

conserved regions were selected. The first is a region that includes the end of the second transmembrane region, a cytoplasmic loop as well as the third transmembrane region. The second pattern corresponds to the core of the fifth transmembrane region.

5

-Consensus pattern: [GA]-[GAS]-[LIVMFYWA SEQ ID NO:41)]-[LIVM SEQ ID NO:4)]-[GAS]-D-x-[LIVMFYWT SEQ ID NO:47)]-[LIVMFYW SEQ ID NO:26)]-G-x(3)-[TAV]-[IV]-x(3)-[GSTAV SEQ ID NO:420)]-x-[LIVMF SEQ ID NO:2)]-x(3)-[GA]

-Consensus pattern: [FYT]-x(2)-[LMFY SEQ ID NO:184)]-[FYV]-[LIVMFYWA SEQ ID NO:41)]-x-[IVG]-N-[LIVMAG SEQ ID NO:286)]-G-[GSA]-[LIMF SEQ ID NO:421)]

10

[1] Paulsen I.T., Skurray R.A. Trends Biochem. Sci. 19:404-404(1994).

[2] Steiner H.-Y., Naider F., Becker J.M. Mol. Microbiol. 16:825-834(1995).

15

427. Pumilio-family RNA binding domains (aka PUM-HD, Pumilio homology domain)

Puf domains are necessary and sufficient for sequence specific

RNA binding in fly Pumilio and worm FBF-1 and FBF-2. Both proteins

20 function as translational repressors in early embryonic development

by binding sequences in the 3' UTR of target mRNAs (e.g. the

nanos response element (NRE) in fly Hunchback mRNA, or the point

mutation element (PME) in worm fem-3 mRNA). Other proteins that contain Puf domains are

also plausible RNA binding proteins. JSN1_YEAST, for instance, appears to also contain a

25 single RRM domain by HMM analysis.

Puf domains usually occur as a tandem repeat of 8 domains.

The Pfam model does not necessarily recognize all 8 domains in

all sequences; some sequences appear to have 5 or 6 domains on

initial analysis, but further analysis suggests the presence

30 of additional divergent domains.

[1] Zhang B, Gallegos M, Puoti A, Durkin E, Fields S, Kimble J,

Wickens MP. Nature 1997;390:477-484. [2] Zamore PD, Williamson JR, Lehmann R.

RNA 1997;3:1421-1433.

428. PWWP domain. The PWWP domain is named after a conserved Pro-Trp-Trp-Pro motif.

5 The function of the domain is currently unknown. Number of members: 19

[1] Medline: 98282232. WHSC1, a 90 kb SET domain-containing gene, expressed in early development and homologous to a Drosophila dysmorphia gene maps in the Wolf-Hirschhorn syndrome critical region and is fused to IgH in t(4;14) multiple myeloma. Stec I, Wright TJ, van Ommen GJB, de Boer PAJ, van Haeringen A, Moorman AFM, Altherr MR, den Dunnen JT; Hum Mol Genet 1998;7:1071-1082.

429. PX domain

15 Eukaryotic domain of unknown function present in phox proteins, PLD isoforms, a PI3K isoform.

Number of members: 71

[1]

Medline: 97084820

20 Novel domains in NADPH oxidase subunits, sorting nexins, and PtdIns 3-kinases: binding partners of SH3 domains?

Ponting CP;

Protein Sci 1996;5:2353-2357.

25

430. ParA family ATPase

[1]

Medline: 91141297

30 A family of ATPases involved in active partitioning of diverse bacterial plasmids.

Motallebi-Veshareh M, Rouch DA, Thomas CM;

Mol Microbiol 1990;4:1455-1463.

Number of members: 122

400

The structure of this repeat has been predicted to be a beta-helix [2].

The repeat can be approximately described as A(D/N)LXX, where X can be any amino acid. Number of members: 75

5 [1]

Medline: 96062225

The hglK gene is required for localization of heterocyst-specific glycolipids in the cyanobacterium *Anabaena* sp. strain PCC 7120.

10 Black K, Buikema WJ, Haselkorn R;
J Bacteriol 1995;177:6440-6448.

[2]Medline: 98318059

Structure and distribution of pentapeptide repeats in bacteria.

15 Bateman A, Murzin A, Teichmann SA;
Protein Sci 1998;7:1477-1480.

[3]Medline: 98316713

Characterisation of an Arabidopsis cDNA encoding a thylakoid lumen protein related to a novel 'pentapeptide repeat' family of proteins.

20 Kieselbach T, Mant A, Robinson C, Schroder WP;
FEBS Lett 1998;428:241-244.

25 434. Polypeptide deformylase

[1]

Medline: 97002011

A new subclass of the zinc metalloproteases superfamily revealed by the solution structure of peptide deformylase.

30 Meinnel T, Blanquet S, Dardel F;
J Mol Biol 1996;262:375-386.

[2]Medline: 98332750

Solution structure of nickel-peptide deformylase.

Dardel F, Ragusa S, Lazennec C, Blanquet S, Meinnel T;

J Mol Biol 1998;280:501-513.

Number of members: 21

5

435. Peptidyl-tRNA hydrolase signatures

Peptidyl-tRNA hydrolase (EC 3.1.1.29) (PTH) is a bacterial enzyme that cleaves peptidyl-tRNA or N-acyl-aminoacyl-tRNA to yield free peptides or N-acyl-amino acids and tRNA. The natural substrate for this enzyme may be peptidyl-tRNA which drop off the ribosome during protein synthesis [1,2]. Bacterial PTH has been found [2,3] to be evolutionary related to yeast hypothetical protein YHR189w.

PTH and YHR189w are proteins of about 200 amino acid residues. As signature patterns, two conserved regions were selected that each contain an histidine.

The first of these regions is located in the N-terminal section, the other in the central part.

-Consensus pattern: [FY]-x(2)-T-R-H-N-x-G-x(2)-[LIVMFA SEQ ID NO:81]](2)-[DE]

-Consensus pattern: [GS]-x(3)-H-N-G-[LIVM SEQ ID NO:4)]-[KR]-[DNS]-[LIVMT SEQ ID NO:1]]

[1] Garcia-Villegas M.R., De La Vega F.M., Galindo J.M., Segura M., Buckingham R.H., Guarneros G. EMBO J. 10:3549-3555(1991).

[2] De La Vega F.M., Galindo J.M., Old I.G., Guarneros G. Gene 169:97-100(1996).

[3] Ouzounis C., Bork P., Casari G., Sander C. Protein Sci. 4:2424-2428(1995).

436. (Peptidase M17) Cytosol aminopeptidase signature

Cytosol aminopeptidase is a eukaryotic cytosolic zinc-dependent exopeptidase that catalyzes the removal of unsubstituted amino-acid residues from the N-terminus of proteins. This enzyme is often known as leucine aminopeptidase (EC 3.4.11.1) (LAP) but has been shown [1] to be identical with prolyl aminopeptidase (EC 3.4.11.5). Cytosol aminopeptidase is a hexamer of identical

chains, each of which binds two zinc ions.

Cytosol aminopeptidase is highly similar to *Escherichia coli* pepA, a manganese dependent aminopeptidase. Residues involved in zinc ion-binding [2] in the mammalian enzyme are absolutely conserved in pepA where they presumably bind manganese.

A cytosol aminopeptidase from *Rickettsia prowazekii* [3] and one from *Arabidopsis thaliana* also belong to this family.

As a signature pattern for these enzymes, a perfectly conserved octapeptide was selected which contains two residues involved in binding metal ions: an aspartate and a glutamate.

-Consensus pattern: N-T-D-A-E-G-R-L [The D and the E are zinc/manganese ligands]

-Note: these proteins belong to family M17 in the classification of peptidases [4,E1].

[1] Matsushima M., Takahashi T., Ichinose M., Miki K., Kurokawa K., Takahashi K. Biochem. Biophys. Res. Commun. 178:1459-1464(1991).

[2] Burley S.K., David P.R., Sweet R.M., Taylor A., Lipscomb W.N. J. Mol. Biol. 224:113-140(1992).

[3] Wood D.O., Solomon M.J., Speed R.R. J. Bacteriol. 175:159-165(1993).

[4] Rawlings N.D., Barrett A.J. Meth. Enzymol. 248:183-228(1995).

437. Assemblin (Peptidase family S21)

[1]

Medline: 96399137

Three-dimensional structure of human cytomegalovirus protease.

Shieh HS, Kurumbail RG, Stevens AM, Stegeman RA, Sturman EJ, Pak JY, Wittwer AJ, Palmier MO, Wiegand RC, Holwerda BC,

Stallings WC;

Nature 1996;383:279-282.

Number of members: 29

438. Pollen proteins Ole e I family signature

The following plant pollen proteins, whose biological function is not yet known, are structurally related [1]:

- 5 - Olive tree pollen major allergen (Ole e I).
- Tomato anther-specific protein LAT52. - Maize pollen-specific protein ZmC13.

These proteins are most probably secreted and consist of about 145 residues.

As shown in the following schematic representation, there are six cysteines which are conserved in the sequence of these proteins. They seem to be

10 involved in disulfide bonds.

xxxxxxCxXX

*****'C': conserved cysteine involved in a disulfide bond.

'*': position of the pattern.

- 15 -Consensus pattern: [EQ]-G-x-V-Y-C-D-T-C-R [The two C's are probably involved in disulfide bonds]

[1] Villalba M., Batanero E., Lopez-Otin C., Sanchez L.M., Monsalve R.I., Gonzalez De La Pena M.A., Lahoz C., Rodriguez R. Eur. J. Biochem. 216:863-869(1993).

20

439. Pollen allergen

This family contains allergens lol PI, PII and PIII from *Lolium perenne*.

Number of members: 49

25 [1]

Medline: 90105394

Complete primary structure of a *Lolium perenne* (perennial rye grass) pollen allergen, Lol p III: comparison with known Lol p I and II sequences.

- 30 Ansari AA, Shenbagamurthi P, Marsh DG;
Biochemistry 1989;28:8665-8670.

440. Porphobilinogen deaminase cofactor-binding site

Porphobilinogen deaminase (EC 4.3.1.8), or hydroxymethylbilane synthase, is an enzyme involved in the biosynthesis of porphyrins and related macrocycles. It catalyzes the assembly of four porphobilinogen (PBG) units in a head to tail fashion to form hydroxymethylbilane.

The enzyme covalently binds a dipyrromethane cofactor to which the PBG subunits are added in a stepwise fashion. In the *Escherichia coli* enzyme (gene hemC), this cofactor has been shown [1] to be bound by the sulfur atom of a cysteine. The region around this cysteine is conserved in porphobilinogen deaminases from various prokaryotic and eukaryotic sources.

-Consensus pattern: E-R-x-[LIVMFA SEQ ID NO:81)]-x(3)-[LIVMF SEQ ID NO:2)]-x-G-[GSA]-C-x-[IVT]-P-[LIVMF SEQ ID NO:2)]-[GSA] [C is the cofactor attachment site]

[1] Miller A.D., Hart G.J., Packman L.C., Battersby A.R. Biochem. J. 254:915-918(1988).

441. Presenilin

Mutations in presenilin-1 are a major cause of early onset Alzheimer's disease [2]. It has been found that presenilin-1 (Swiss:P49768) binds to beta-catenin in vivo [4]. This family also contains SPE proteins from *C.elegans*.

Number of members: 23

[1]

Medline: 98045995

Presenilins and Alzheimer's disease.

Kim TW, Tanzi RE;

Curr Opin Neurobiol 1997;7:683-688.

[2]Medline: 98045995

Presenilins and Alzheimer's disease.

Kim TW, Tanzi RE;

Curr Opin Neurobiol 1997;7:683-688.

[3]Medline: 98099802

Interaction of presenilins with the filamin family of

actin-binding proteins.

Zhang W, Han SW, McKeel DW, Goate A, Wu JY;

J Neurosci 1998;18:914-922.

[4]Medline: 99004850

5 Destabilisation of beta-catenin by mutations in presenilin-1

potentiates neuronal apoptosis.

Zhang Z, Hartmann H, Do VM, Abramowski D, Sturchler-Pierrat

C, Staufenbiel M, Sommer B, van de Wetering M, Clevers H,

Saftig P, De Strooper B, He X, Yankner BA;

10 Nature 1998;395:698-702.

442. (Pribosyltran) Purine/pyrimidine phosphoribosyl transferases signature

Phosphoribosyltransferases (PRT) are enzymes that catalyze the synthesis of

15 beta-n-5'-monophosphates from phosphoribosylpyrophosphate (PRPP) and an enzyme

specific amine. A number of PRT's are involved in the biosynthesis of purine,

pyrimidine, and pyridine nucleotides, or in the salvage of purines and

pyrimidines. These enzymes are:

- Adenine phosphoribosyltransferase (EC 2.4.2.7) (APRT), which is involved in
20 purine salvage.

- Hypoxanthine-guanine or hypoxanthine phosphoribosyltransferase (EC 2.4.2.8)
(HGPRT or HPRT), which are involved in purine salvage.

- Orotate phosphoribosyltransferase (EC 2.4.2.10) (OPRT), which is involved
in pyrimidine biosynthesis.

25 - Amido phosphoribosyltransferase (EC 2.4.2.14), which is involved in purine
biosynthesis.

- Xanthine-guanine phosphoribosyltransferase (EC 2.4.2.22) (XGPRT), which is
involved in purine salvage.

In the sequence of all these enzymes there is a small conserved region which

30 may be involved in the enzymatic activity and/or be part of the PRPP binding
site [1].

-Consensus pattern: [LIVMFYWCTA SEQ ID NO:428)]-[LIVM SEQ ID NO:4)]-[LIVMA SEQ ID NO:30)]-[LIVMFC SEQ ID NO:90)]-[DE]-D-[LIVMS SEQ ID NO:429)]-[LIVM SEQ ID NO:4)]-[STAVD SEQ ID NO:430)]-[STAR SEQ ID NO:136)]-[GAC]-x-[STAR SEQ ID NO:136)]

5 -Note: in position 11 of the pattern most of these enzymes have Gly.

[1] Hershey H.V., Taylor M.W. Gene 43:287-293(1986).

10 443. (Pro CA)

Prokaryotic-type carbonic anhydrases signatures

Carbonic anhydrases (EC 4.2.1.1) (CA) are zinc metalloenzymes which catalyze the reversible hydration of carbon dioxide. In *Escherichia coli*, CA (gene cynT) is involved in recycling carbon dioxide formed in the bicarbonate-dependent decomposition of cyanate by cyanase (gene cynS). By this action, it prevents the depletion of cellular bicarbonate [1]. In photosynthetic bacteria and plant chloroplast, CA is essential to inorganic carbon fixation [2]. Prokaryotic and plant chloroplast CA are structurally and evolutionary related and form a family distinct from the one which groups the many different forms of eukaryotic CA's (see <PDOC00146>). Hypothetical proteins yadF from *Escherichia coli* and HI1301 from *Haemophilus influenzae* also belong to this family. Two signature patterns were developed for this family of enzymes. Both patterns contain conserved residues that could be involved in binding zinc (cysteine and histidine).

25 -Consensus pattern: C-[SA]-D-S-R-[LIVM SEQ ID NO:4)]-x-[AP]

-Consensus pattern: [EQ]-Y-A-[LIVM SEQ ID NO:4)]-x(2)-[LIVM SEQ ID NO:4)]-x(4)-[LIVMF SEQ ID NO:2)](3)-x-G-H-x(2)-C-G

[1] Guilloton M.B., Korte J.J., Lamblin A.F., Fuchs J.A., Anderson P.M. J. Biol. Chem. 267:3731-3734(1992).

[2] Fukuzawa H., Suzuki E., Komukai Y., Miyachi S. Proc. Natl. Acad. Sci. U.S.A. 89:4437-4441(1992).

444. (Prolyl_oligopep)

Prolyl oligopeptidase family serine active site

- 5 The prolyl oligopeptidase family [1,2,3] consist of a number of evolutionary related peptidases whose catalytic activity seems to be provided by a charge relay system similar to that of the trypsin family of serine proteases, but which evolved by independent convergent evolution. The known members of this family are listed below.
- 10 - Prolyl endopeptidase (EC 3.4.21.26) (PE) (also called post-proline cleaving enzyme). PE is an enzyme that cleaves peptide bonds on the C-terminal side of prolyl residues. The sequence of PE has been obtained from a mammalian species (pig) and from bacteria (*Flavobacterium meningosepticum* and *Aeromonas hydrophila*); there is a high degree of sequence conservation between these sequences.
- 15 - *Escherichia coli* protease II (EC 3.4.21.83) (oligopeptidase B) (gene prtB) which cleaves peptide bonds on the C-terminal side of lysyl and arginyl residues.
- Dipeptidyl peptidase IV (EC 3.4.14.5) (DPP IV). DPP IV is an enzyme that removes N-terminal dipeptides sequentially from polypeptides having unsubstituted N-termini provided that the penultimate residue is proline.
- 20 - Yeast vacuolar dipeptidyl aminopeptidase A (DPAP A) (gene: STE13) which is responsible for the proteolytic maturation of the alpha-factor precursor.
- Yeast vacuolar dipeptidyl aminopeptidase B (DPAP B) (gene: DAP2).
- Acylamino-acid-releasing enzyme (EC 3.4.19.1) (acyl-peptide hydrolase).
- This enzyme catalyzes the hydrolysis of the amino-terminal peptide bond of an N-acetylated
- 25 protein to generate a N-acetylated amino acid and a protein with a free amino-terminus.

A conserved serine residue has experimentally been shown (in *E.coli* proteaseII as well as in pig and bacterial PE) to be necessary for the catalytic mechanism. This serine, which is part of the catalytic triad (Ser, His, Asp), is generally located about 150 residues away from the C-

30 terminal extremity of these enzymes (which are all proteins that contains about 700 to 800 amino acids).

Consensus pattern: D-x(3)-A-x(3)-[LIVMFYW SEQ ID NO:26)]-x(14)-G-x-S-x-G-G-[LIVMFYW SEQ ID NO:26)](2) [S is the active site residue] Sequences known to belong to this class detected by the pattern ALL, except for yeast DPAP A.

5 Note: these proteins belong to families S9A/S9B/S9C in the classification of peptidases [4].

[1] Rawlings N.D., Polgar L., Barrett A.J. Biochem. J. 279:907-911(1991).

[2] Barrett A.J., Rawlings N.D.

10

[3] Polgar L., Szabo E.

[4] Rawlings N.D., Barrett A.J. Meth. Enzymol. 244:19-61(1994).

15

445. (Pterin 4a)

Pterin 4 alpha carbinolamine dehydratase

20

Pterin 4 alpha carbinolamine dehydratase is aka DCoH (dimerisation cofactor of hepatocyte nuclear factor 1-alpha).

Number of members: 11

25

[1] Cronk JD, Endrizzi JA, Alber T; Medline: 97052967 "High-resolution structures of the bifunctional enzyme and transcriptional coactivator DCoH and its complex with a product analogue." Protein Sci 1996;5:1963-1972.

446. (Pyridox oxidase)

30

Pyridoxamine 5'-phosphate oxidase signature

Pyridoxamine 5'-phosphate oxidase (EC 1.4.3.5) is a FMN flavoprotein involved in the de novo synthesis of pyridoxine (vitamin B6) and pyridoxal phosphate. It oxidizes

pyridoxamine-5-P (PMP) and pyridoxine-5-P (PNP) to pyridoxal-5-P. The sequences of the enzyme from bacterial (genes *pdxH* or *fprA*) [1] and fungal (gene *PDX3*) [2] sources show that this protein has been highly conserved throughout evolution.

PdxH is evolutionary related [3] to one of the enzymes in the phenazine biosynthesis protein pathway, *phzD* (also known as *phzG*). As a signature pattern, a highly conserved region was selected located in the C-terminal part of these enzymes.

-Consensus pattern: [LIVF SEQ ID NO:127)]-E-F-W-[QHG]-x(4)-R-[LIVM SEQ ID NO:4)]-H-[DNE]-R

[1] Lam H.-M., Winkler M.E. J. Bacteriol. 174:6033-6045(1992).

[2] Loubbardi A., Karst F., Guilloton M., Marcireau C. J. Bacteriol. 177:1817-1823(1995).

[3] Pierson L.S. III, Gaffney T., Lam S., Gong F. FEMS Microbiol. Lett. 134:299-307(1995).

447. (Pyrophosphatase)

Inorganic pyrophosphatase signature

Inorganic pyrophosphatase (EC 3.6.1.1) (PPase) [1,2] is the enzyme responsible for the hydrolysis of pyrophosphate (PPi) which is formed principally as the product of the many biosynthetic reactions that utilize ATP. All known PPases require the presence of divalent metal cations, with magnesium conferring the highest activity. Among other residues, a lysine has been postulated to be part or close to the active site. PPases have been sequenced from bacteria such as *Escherichia coli* (homohexamer), thermophilic bacteria PS-3 and *Thermus thermophilus*, from the archaeobacteria *Thermoplasma acidophilum*, from fungi (homodimer), from a plant, and from bovine retina. In yeast, a mitochondrial isoform of PPase has been characterized which seems to be involved in energy production and whose activity is stimulated by uncouplers of ATP synthesis.

The sequences of PPases share some regions of similarities. As signature patterns a region was selected that contains three conserved aspartates that are involved in the binding of cations.

-Consensus pattern: D-[SGDN SEQ ID NO:431)]-D-[PE]-[LIVMF SEQ ID NO:2)]-D-[LIVMGAC SEQ ID NO:432)]

[The three D's bind divalent metal cations]

5

[1] Lahti R., Kolakowski L.F. Jr., Heinonen J., Vihinen M., Pohjanoksa K., Cooperman B.S. *Biochim. Biophys. Acta* 1038:338-345(1990).

[2] Cooperman B.S., Baykov A.A., Lahti R. *Trends Biochem. Sci.* 17:262-266(1992).

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448. (Peptidase S26)

Signal peptidases I signatures.

15

Signal peptidases (SPases) [1] (aka leader peptidases) remove the signal peptides from secretory proteins. In prokaryotes three types of SPases are known: type I (gene *lepB*) which is responsible for the processing of the majority of exported pre-proteins; type II (gene *lsp*) which only process lipoproteins, and a third type involved in the processing of pili subunits. SPase I (EC 3.4.21.89) is an integral membrane protein that is anchored in the cytoplasmic membrane by one (in *B. subtilis*) or two (in *E. coli*) N-terminal transmembrane domains with the main part of the protein protruding in the periplasmic space. Two residues have been shown [2,3] to be essential for the catalytic activity of SPase I: a serine and an lysine. SPase I is evolutionary related to the yeast mitochondrial inner membrane protease subunit 1 and 2 (genes *IMP1* and *IMP2*) which catalyze the removal of signal peptides required for the targeting of proteins from the mitochondrial matrix, across the inner membrane, into the inter-membrane space [4]. In eukaryotes the removal of signal peptides is effected by an oligomeric enzymatic complex composed of at least five subunits: the signal peptidase complex (SPC). The SPC is located in the endoplasmic reticulum membrane. Two components of mammalian SPC, the 18 Kd (SPC18) and the 21 Kd (SPC21) subunits as well as the yeast SEC11 subunit have been shown [5] to share regions of sequence similarity with prokaryotic SPases I and yeast *IMP1/IMP2*. Three signature patterns have been developed for these proteins. The first signature contains the putative active site serine, the second signature contains the putative active site lysine which is not conserved in the SPC subunits, and the

20

25

30

third signature corresponds to a conserved region of unknown biological significance which is located in the C-terminal section of all these proteins.

Consensus pattern: [GS]-x-S-M-x-[PS]-[AT]-[LF] [S is an active site residue]-

5 Consensus pattern: K-R-[LIVMSTA SEQ ID NO:433]](2)-G-x-[PG]-G-[DE]-x-[LIVM SEQ ID NO:4)]-x-[LIVMFY SEQ ID NO:18)] [K is an active site residue]-

Consensus pattern: [LIVMFYW SEQ ID NO:26]](2)-x(2)-G-D-[NH]-x(3)-[SND]-x(2)-[SG]-

[1] Dalbey R.E., von Heijne G. Trends Biochem. Sci. 17:474-478(1992).[2] Sung M.,
10 Dalbey R.E. J. Biol. Chem. 267:13154-13159(1992).[3] Black M.T. J. Bacteriol. 175:4957-4961(1993).[4] Nunnari J., Fox T.D., Walter P. Science 262:1997-2004(1993).[5] van Dijk J.M., de Jong A., Vehmaanpera J., Venema G., Bron S. EMBO J. 11:2819-2828(1992).[6] Rawlings N.D., Barrett A.J. Meth. Enzymol. 244:19-61(1994).[E1]

15

449. (Peptidase C1) Eukaryotic thiol (cysteine) proteases active sites. Eukaryotic thiol proteases (EC 3.4.22.-) [1] are a family of proteolytic enzymes which contain an active site cysteine. Catalysis proceeds through a thioester intermediate and is facilitated by a nearby histidine side chain; an asparagine completes the essential catalytic triad. The proteases
20 which are currently known to belong to this family are listed below (references are only provided for recently determined sequences). - Vertebrate lysosomal cathepsins B (EC 3.4.22.1), H (EC 3.4.22.16), L (EC 3.4.22.15), and S (EC 3.4.22.27) [2]. - Vertebrate lysosomal dipeptidyl peptidase I (EC 3.4.14.1) (also known as cathepsin C) [2]. - Vertebrate calpains (EC 3.4.22.17). Calpains are intracellular calcium- activated thiol protease that
25 contain both a N-terminal catalytic domain and a C-terminal calcium-binding domain. - Mammalian cathepsin K, which seems involved in osteoclastic bone resorption [3]. - Human cathepsin O [4]. - Bleomycin hydrolase. An enzyme that catalyzes the inactivation of the antitumor drug BLM (a glycopeptide). - Plant enzymes: barley aleurain (EC 3.4.22.16), EP-B1/B4; kidney bean EP-C1, rice bean SH-EP; kiwi fruit actinidin (EC 3.4.22.14); papaya
30 latex papain (EC 3.4.22.2), chymopapain (EC 3.4.22.6), caricain (EC 3.4.22.30), and proteinase IV (EC 3.4.22.25); pea turgor-responsive protein 15A; pineapple stem bromelain (EC 3.4.22.32); rape COT44; rice oryzain alpha, beta, and gamma; tomato low-temperature induced, Arabidopsis thaliana A494, RD19A and RD21A. - House-dust mites allergens

DerP1 and EurM1. - Cathepsin B-like proteinases from the worms *Caenorhabditis elegans* (genes gcp-1, cpr-3, cpr-4, cpr-5 and cpr-6), *Schistosoma mansoni* (antigen SM31) and *Japonica* (antigen SJ31), *Haemonchus contortus* (genes AC-1 and AC-2), and *Ostertagia ostertagi* (CP-1 and CP-3). - Slime mold cysteine proteinases CP1 and CP2. - Cruzipain from
 5 *Trypanosoma cruzi* and *brucei*. - Throphozoite cysteine proteinase (TCP) from various *Plasmodium* species. - Proteases from *Leishmania mexicana*, *Theileria annulata* and *Theileria parva*. - Baculoviruses cathepsin-like enzyme (v-cath). - *Drosophila* small optic lobes protein (gene sol), a neuronal protein that contains a calpain-like domain. - Yeast thiol protease BLH1/YCP1/LAP3. - *Caenorhabditis elegans* hypothetical protein C06G4.2, a calpain-like
 10 protein. Two bacterial peptidases are also part of this family: - Aminopeptidase C from *Lactococcus lactis* (gene pepC) [5]. - Thiol protease tpr from *Porphyromonas gingivalis*. Three other proteins are structurally related to this family, but may have lost their proteolytic activity. - Soybean oil body protein P34. This protein has its active site cysteine replaced by a glycine. - Rat testin, a sertoli cell secretory protein highly similar to cathepsin L but with the
 15 active site cysteine is replaced by a serine. Rat testin should not be confused with mouse testin which is a LIM-domain protein (see <PDOC00382>). - *Plasmodium falciparum* serine-repeat protein (SERA), the major blood stage antigen. This protein of 111 Kd possesses a C-terminal thiol-protease-like domain [6], but the active site cysteine is replaced by a serine. The sequences around the three active site residues are well conserved and can be used as
 20 signature patterns.

Consensus pattern: Q-x(3)-[GE]-x-C-[YW]-x(2)-[STAGC SEQ ID NO:45)]-[STAGCV SEQ ID NO:159)] [C is the active site residue]- Note: the residue in position 4 of the pattern is almost always cysteine; the only exceptions are calpains (Leu), bleomycin hydrolase (Ser)
 25 and yeast YCP1 (Ser). -Note: the residue in position 5 of the pattern is always Gly except in papaya protease IV where it is Glu.

Consensus pattern: [LIVMGSTAN SEQ ID NO:160)]-x-H-[GSACE SEQ ID NO:161)]-[LIVM SEQ ID NO:4)]-x-[LIVMAT SEQ ID NO:162)](2)-G-x-[GSADNH SEQ ID NO:163)] [H is the active site residue]-

30 Consensus pattern: [FYCH SEQ ID NO:164)]-[WI]-[LIVT SEQ ID NO:165)]-x-[KRQAG SEQ ID NO:166)]-N-[ST]-W-x(3)-[FYW]-G-x(2)-G- [LFYW SEQ ID NO:167)]-[LIVMFYG SEQ ID NO:168)]-x-[LIVMF SEQ ID NO:2)] [N is the active site residue] -

Note: these proteins belong to family C1 (papain-type) and C2 (calpains) in the classification of peptidases [7,E1].-

[1] Dufour E. Biochimie 70:1335-1342(1988).[2] Kirschke H., Barrett A.J., Rawlings N.D.
5 Protein Prof. 2:1587-1643(1995).[3] Shi G.-P., Chapman H.A., Bhairi S.M., Deleeuw C.,
Reddy V.Y., Weiss S.J. FEBS Lett. 357:129-134(1995).[4] Velasco G., Ferrando A.A.,
Puente X.S., Sanchez L.M., Lopez-Otin C. J. Biol. Chem. 269:27136-27142(1994).[5]
Chapot-Chartier M.P., Nardi M., Chopin M.C., Chopin A., Gripon J.C. Appl. Environ.
Microbiol. 59:330-333(1993).[6] Higgins D.G., McConnell D.J., Sharp P.M. Nature
10 340:604-604(1989).[7] Rawlings N.D., Barrett A.J. Meth. Enzymol. 244:461-486(1994).

450. (peptidase M24) Aminopeptidase P and proline dipeptidase signature (1).

Aminopeptidase P (EC 3.4.11.9) is the enzyme responsible for the release of any N-terminal
15 amino acid adjacent to a proline residue. Proline dipeptidase(EC 3.4.13.9) (prolidase) splits
dipeptides with a prolyl residue in the carboxyl terminal position. Bacterial aminopeptidase P
II (gene pepP) [1], proline dipeptidase (gene pepQ)[2], and human proline dipeptidase (gene
PEPD) [3] are evolutionary related. These proteins are manganese metalloenzymes. Yeast
hypothetical proteins YER078c and YFR006w and Mycobacterium tuberculosis hypothetical
20 protein MtCY49.29c also belong to this family. As a signature pattern for these enzymes a
conserved region that contains three histidine residues has been developed

Consensus pattern: [HA]-[GSYR SEQ ID NO:434)]-[LIVMT SEQ ID NO:1)]-[SG]-H-x-
[LIV]-G-[LIVM SEQ ID NO:4)]-x-[IV]-H-[DE]-

[1] Yoshimoto T., Tone H., Honda T., Osatomi K., Kobayashi R., Tsuru D. J. Biochem.
105:412-416(1989).[2] Nakahigashi K., Inokuchi H. Nucleic Acids Res. 18:6439-
6439(1990).[3] Endo F., Tanoue A., Nakai H., Hata A., Indo Y., Titani K., Matsuda I. J.
Biol. Chem. 264:4476-4481(1989).[4] Rawlings N.D., Barrett A.J. Meth. Enzymol. 248:183-
30 228(1995).

Methionine aminopeptidase signatures. (2). Methionine aminopeptidase (EC 3.4.11.18)
(MAP) is responsible for the removal of the amino-terminal (initiator) methionine from

nascent eukaryotic cytosolic and cytoplasmic prokaryotic proteins if the penultimate amino acid is small and uncharged. All MAP studied to date are monomeric proteins that require cobalt ions for activity. Two subfamilies of MAP enzymes are known to exist [1,2]. While being evolutionary related, they only share a limited amount of sequence similarity mostly clustered around the residues shown, in the *Escherichia coli* MAP [3], to be involved in cobalt-binding. The first family consists of enzymes from prokaryotes as well as eukaryotic MAP-1, while the second group is made up of archebacterial MAP and eukaryotic MAP-2. The second subfamily also includes proteins which do not seem to be MAP, but that are clearly evolutionary related such as mouse proliferation-associated protein 1 and fission yeast curved DNA-binding protein. For each of these subfamilies, a specific signature pattern that includes residues known to be involved in cobalt-binding has been developed.

Consensus pattern: [MFY]-x-G-H-G-[LIVMC SEQ ID NO:142)]-[GSH]-x(3)-H-x(4)-[LIVM SEQ ID NO:4)]-x-[HN]- [YWV] [H is a cobalt ligand]-

Consensus pattern: [DA]-[LIVMY SEQ ID NO:141)]-x-K-[LIVM SEQ ID NO:4)]-D-x-G-x-[HQ]-[LIVM SEQ ID NO:4)]-[DNS]-G-x(3)- [DN] [The second D and the last D/N are cobalt ligands]

[1] Arfin S.M., Kendall R.L., Hall L., Weaver L.H., Stewart A.E., Matthews B.W., Bradshaw R.A. Proc. Natl. Acad. Sci. U.S.A. 92:7714-7718(1995).[2] Keeling P.J., Doolittle W.F. Trends Biochem. Sci. 21:285-286(1996).[3] Roderick S.L., Mathews B.W. Biochemistry 32:3907-3912(1993).[4] Rawlings N.D., Barrett A.J. Meth. Enzymol. 248:183-228(1995).

451. Cytochrome P450 cysteine heme-iron ligand signature

Cytochrome P450's [1,2,3,E1] are a group of enzymes involved in the oxidative metabolism of a high number of natural compounds (such as steroids, fatty acids, prostaglandins, leukotrienes, etc) as well as drugs, carcinogens and mutagens. Based on sequence similarities, P450's have been classified into about forty different families [4,5]. P450's are proteins of 400 to 530 amino acids; the only exception is *Bacillus BM-3* (CYP102) which is a protein of 1048 residues that contains a N-terminal P450 domain followed by a reductase domain.

P450's are heme proteins. A conserved cysteine residue in the C-terminal part of P450's is involved in binding the heme iron in the fifth coordination site. From a region around this residue, a ten residue signature was developed specific to P450's.

- 5 Consensus pattern: [FW]-[SGNH SEQ ID NO:170)]-x-[GD]-x-[RHPT SEQ ID NO:435)]-x-C-[LIVMFAP SEQ ID NO:347)]-[GAD] [C is the heme iron ligand]-

[1] Nebert D.W., Gonzalez F.J. Annu. Rev. Biochem. 56:945-993(1987).

[2] Coon M.J., Ding X., Pernecky S.J., Vaz A.D.N. FASEB J. 6:669-673(1992).

- 10 [3] Guengerich F.P. J. Biol. Chem. 266:10019-10022(1991).

[4] Nelson D.R., Kamataki T., Waxman D.J., Guengerich F.P., Estrabrook R.W., Feyereisen R., Gonzalez F.J., Coon M.J., Gunsalus I.C., Gotoh O., Okuda K., Nebert D.W. DNA Cell Biol. 12:1-51(1993).

[5] Degtyarenko K.N., Archakov A.I. FEBS Lett. 332:1-8(1993).

15

452. (Pec Lyase) Pectate lyase

This enzyme forms a right handed beta helix structure. Pectate lyase is an enzyme involved in the maceration and soft rotting of plant tissue.

- 20 [1] Yoder MD, Keen NT, Jurnak F, Science 1993;260:1503-1507.

453. (pep M24) Aminopeptidase P and proline dipeptidase signature (pep1)

Aminopeptidase P (EC 3.4.11.9) is the enzyme responsible for the release of any N-terminal amino acid adjacent to a proline residue. Proline dipeptidase(EC 3.4.13.9) (prolidase) splits dipeptides with a prolyl residue in the carboxyl terminal position. Bacterial aminopeptidase P II (gene pepP) [1], proline dipeptidase (gene pepQ)[2], and human proline dipeptidase (gene PEPD) [3] are evolutionary related. These proteins are manganese metalloenzymes. Yeast hypothetical proteins YER078c and YFR006w and Mycobacterium tuberculosis .hypothetical protein MtCY49.29c also belong to this family. As a signature pattern for these enzymes a conserved region was selected that contains three histidine residues.

30

Consensus pattern: [HA]-[GSYR SEQ ID NO:434)]-[LIVMT SEQ ID NO:1)]-[SG]-H-x-
[LIV]-G-[LIVM SEQ ID NO:4)]-x-[IV]-H-[DE]-

[1] Yoshimoto T., Tone H., Honda T., Osatomi K., Kobayashi R., Tsuru D. J. Biochem.
105:412-416(1989).

[2] Nakahigashi K., Inokuchi H. Nucleic Acids Res. 18:6439-6439(1990).

[3] Endo F., Tanoue A., Nakai H., Hata A., Indo Y., Titani K., Matsuda I. J. Biol. Chem.
264:4476-4481(1989).

[4] Rawlings N.D., Barrett A.J. Meth. Enzymol. 248:183-228(1995).

Methionine aminopeptidase signatures (pep2)

Methionine aminopeptidase (EC 3.4.11.18) (MAP) is responsible for the removal of the
amino-terminal (initiator) methionine from nascent eukaryotic cytosolic and cytoplasmic
prokaryotic proteins if the penultimate amino acid is small and uncharged. All MAP studied
to date are monomeric proteins that require cobalt ions for activity. Two subfamilies of MAP
enzymes are known to exist [1,2]. While being evolutionary related, they only share a limited
amount of sequence similarity mostly clustered around the residues shown, in the Escherichia
coli MAP [3], to be involved in cobalt-binding. The first family consists of enzymes from
prokaryotes as well as eukaryotic MAP-1, while the second group is made up of
archeobacterial MAP and eukaryotic MAP-2. The second subfamily also includes proteins
which do not seem to be MAP, but that are clearly evolutionary related such as mouse
proliferation-associated protein 1 and fission yeast curved DNA-binding protein. For each of
these subfamilies, a specific signature pattern was developed that includes residues known to
be involved in cobalt-binding.

Consensus pattern: [MFY]-x-G-H-G-[LIVMC SEQ ID NO:142)]-[GSH]-x(3)-H-x(4)-[LIVM
SEQ ID NO:4)]-x-[HN]- [YWV] [H is a cobalt ligand]-

Consensus pattern: [DA]-[LIVMY SEQ ID NO:141)]-x-K-[LIVM SEQ ID NO:4)]-D-x-G-x-
[HQ]-[LIVM SEQ ID NO:4)]-[DNS]-G-x(3)- [DN] [The second D and the last D/N are
cobalt ligands]

[1] Arfin S.M., Kendall R.L., Hall L., Weaver L.H., Stewart A.E., Matthews B.W.,
Bradshaw R.A. Proc. Natl. Acad. Sci. U.S.A. 92:7714-7718(1995).

[2] Keeling P.J., Doolittle W.F. Trends Biochem. Sci. 21:285-286(1996).

[3] Roderick S.L., Mathews B.W. Biochemistry 32:3907-3912(1993).

[4] Rawlings N.D., Barrett A.J. Meth. Enzymol. 248:183-228(1995).

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454. Peroxidases signatures

Peroxidases (EC 1.11.1.-) [1] are heme-binding enzymes that carry out a variety of biosynthetic and degradative functions using hydrogen peroxide as the electron acceptor. Peroxidases are widely distributed throughout bacteria, fungi, plants, and vertebrates. In peroxidases the heme prosthetic group is protoporphyrin IX and the fifth ligand of the heme iron is a histidine (known as the proximal histidine). Another histidine residue (the distal histidine) serves as an acid-base catalyst in the reaction between hydrogen peroxide and the enzyme. The regions around these two active site residues are more or less conserved in a majority of peroxidases [2,3]. The enzymes in which one or both of these regions can be found are listed below. - Yeast cytochrome c peroxidase (EC 1.11.1.5). - Myeloperoxidase (EC 1.11.1.7) (MPO). MPO is found in granulocytes and monocytes and plays a major role in the oxygen-dependent microbicidal system of neutrophils. - Lactoperoxidase (EC 1.11.1.7) (LPO). LPO is a milk protein which acts as an antimicrobial agent. - Eosinophil peroxidase (EC 1.11.1.7) (EPO). An enzyme found in the cytoplasmic granules of eosinophils. - Thyroid peroxidase (EC 1.11.1.8) (TPO). TPO plays a central role in the biosynthesis of thyroid hormones. It catalyzes the iodination and coupling of the hormonogenic tyrosines in thyroglobulin to yield the thyroid hormones T3 and T4. - Fungal ligninases. Ligninase catalyzes the first step in the degradation of lignin. It depolymerizes lignin by catalyzing the C(alpha)-C(beta) cleavage of the propyl side chains of lignin. - Plant peroxidases (EC 1.11.1.7). Plants express a large number of isozymes of peroxidases. Some of them play a role in cell-suberization by catalyzing the deposition of the aromatic residues of suberin on the cell wall, some are expressed as a defense response toward wounding, others are involved in the metabolism of auxin and the biosynthesis of lignin. - Prokaryotic catalase-peroxidases. Some bacterial species produce enzymes that exhibit both catalase and broad-spectrum peroxidase activities [4]. Examples of such enzymes are: catalase HP I from *Escherichia coli* (gene katG) and perA from *Bacillus stearothermophilus*.

Consensus pattern: [DET]-[LIVMTA SEQ ID NO:311)]-x(2)-[LIVM SEQ ID NO:4)]-[LIVMSTAG SEQ ID NO:44)]-[SAG]-[LIVMSTAG SEQ ID NO:44)]-H- [STA]-[LIVMFY SEQ ID NO:18)] [H is the proximal heme-binding ligand] -

Consensus pattern: [SGATV SEQ ID NO:436)]-x(3)-[LIVMA SEQ ID NO:30)]-R-[LIVMA SEQ ID NO:30)]-x-[FW]-H-x-[SAC] [H is an active site residue]-

[1] Dawson J.H. Science 240:433-439(1988).

[2] Kimura S., Ikeda-Saito M. Proteins 3:113-120(1988).

[3] Henrissat B., Saloheimo M., Lavaitte S., Knowles J.K.C. Proteins 8:251-257(1990).

[4] Welinder K.G. Biochim. Biophys. Acta 1080:215-220(1991).

455. pfkB family of carbohydrate kinases signatures

It has been shown [1,2,3] that the following carbohydrate and purine kinases are evolutionary related and can be grouped into a single family, which is known [1] as the 'pfkB family': - Fructokinase (EC 2.7.1.4) (gene scrK). - 6-phosphofructokinase isozyme 2 (EC 2.7.1.11) (phosphofructokinase-2) (gene pfkB). pfkB is a minor phosphofructokinase isozyme in Escherichia coli and is not evolutionary related to the major isozyme (gene pfkA). Plants 6-phosphofructokinase also belong to this family. - Ribokinase (EC 2.7.1.15) (gene rbsK). - Adenosine kinase (EC 2.7.1.20) (gene ADK). - 2-dehydro-3-deoxygluconokinase (EC 2.7.1.45) (gene: kdgK). - 1-phosphofructokinase (EC 2.7.1.56) (fructose 1-phosphate kinase) (gene fruK). - Inosine-guanosine kinase (EC 2.7.1.73) (gene gsk). - Tagatose-6-phosphate kinase (EC 2.7.1.144) (phosphotagatokinase) (gene lacC). - Escherichia coli hypothetical protein yeiC. - Escherichia coli hypothetical protein yeiL. - Escherichia coli hypothetical protein yhfQ. - Escherichia coli hypothetical protein yihV. - Bacillus subtilis hypothetical protein yxdC. - Yeast hypothetical protein YJR105w. All the above kinases are proteins of from 280 to 430 amino acid residues that share a few region of sequence similarity. Two of these regions were selected as signature patterns. The first pattern is based on a region rich in glycine which is located in the N-terminal section of these enzymes; while the second pattern is based on a conserved region in the C-terminal section.

Consensus pattern: [AG]-G-x(0,1)-[GAP]-x-N-x-[STA]-x(6)-[GS]-x(9)-G-

Consensus pattern: [DNSK SEQ ID NO:437)]-[PSTV SEQ ID NO:438)]-x-[SAG](2)-[GD]-D-x(3)-[SAGV SEQ ID NO:25)]-[AG]- [LIVMFYA SEQ ID NO:98)]-[LIVMSTAP SEQ ID NO:439)]

- 5 [1] Wu L.-F., Reizer A., Reizer J., Cai B., Tomich J.M., Saier M.H. Jr. J. Bacteriol. 173:3117-3127(1991).
 [2] Orchard L.M.D., Kornberg H.L. Proc. R. Soc. Lond., B, Biol. Sci. 242:87-90(1990).
 [3] Blatch G.L., Scholle R.R., Woods D.R. Gene 95:17-23(1990).

10

456. Phospholipase A2 active sites signatures

Phospholipase A2 (EC 3.1.1.4) (PA2) [1,2] is an enzyme which releases fatty acids from the second carbon group of glycerol. PA2's are small and rigid proteins of 120 amino-acid residues that have four to seven disulfide bonds. PA2 binds a calcium ion which is required for activity. The side chains of two conserved residues, a histidine and an aspartic acid, participate in a 'catalytic network'. Many PA2's have been sequenced from snakes, lizards, bees and mammals. In the latter, there are at least four forms: pancreatic, membrane-associated as well as two less characterized forms. The venom of most snakes contains multiple forms of PA2. Some of them are presynaptic neurotoxins which inhibit neuromuscular transmission by blocking acetylcholine release from the nerve termini. Two different signature patterns were derived for PA2's. The first is centered on the active site histidine and contains three cysteines involved in disulfide bonds. The second is centered on the active site aspartic acid and also contains three cysteines involved in disulfide bonds.

- 25 Consensus pattern: C-C-x(2)-H-x(2)-C [H is the active site residue] This pattern will not detect some snake toxins homologous with PA2 but which have lost their catalytic activity as well as otoconin-22, a Xenopus protein from the aragonitic otoconia which is also unlikely to be enzymatically active.

Consensus pattern: [LIVMA SEQ ID NO:30)]-C-{LIVMFYWPCST SEQ ID NO:440)}-C-D-x(5)-C [D is the active site residue] The majority of functional and non-functional PA2's. Undetected sequences are bee PA2, gila monster PA2's, PA2 PL-X from habu and PA2 PA-5 from mulga.

30

[1] Davidson F.F., Dennis E.A. J. Mol. Evol. 31:228-238(1990).

[2] Gomez F., Vandermeers A., Vandermeers-Piret M.-C., Herzog R., Rathe J., Stievenart M., Winand J., Christophe J. Eur. J. Biochem. 186:23-33(1989).

5

457. Phosphorylase pyridoxal-phosphate attachment site. Phosphorylases (EC 2.4.1.1) [1] are important allosteric enzymes in carbohydrate metabolism. They catalyze the formation of glucose 1-phosphate from polyglucose such as glycogen, starch or maltodextrin. Enzymes from different sources differ in their regulatory mechanisms and their natural substrates.

10

However, all known phosphorylases share catalytic and structural properties. They are pyridoxal-phosphate dependent enzymes; the pyridoxal-P group is attached to a lysine residue around which the sequence is highly conserved and can be used as a signature pattern to detect this class of enzymes.

15

Consensus pattern: E-A-[SC]-G-x-[GS]-x-M-K-x(2)-[LM]-N [K is the pyridoxal-P attachment site]-

[1] Fukui T., Shimomura S., Nakano K. Mol. Cell. Biochem. 42:129-144(1982).

20

458. Protein kinases signatures and profile

Eukaryotic protein kinases [1 to 5] are enzymes that belong to a very extensive family of proteins which share a conserved catalytic core common to both serine/threonine and tyrosine protein kinases. There are a number of conserved regions in the catalytic domain of protein kinases. Two of these regions were selected to build signature patterns. The first region, which is located in the N-terminal extremity of the catalytic domain, is a glycine-rich stretch of residues in the vicinity of a lysine residue, which has been shown to be involved in ATP binding. The second region, which is located in the central part of the catalytic domain, contains a conserved aspartic acid residue which is important for the catalytic activity of the enzyme [6]; Two signature patterns were derived for that region: one specific for serine/threonine kinases and the other for tyrosine kinases. A profile was also developed which is based on the alignment in [1] and covers the entire catalytic domain.

30

Consensus pattern: [LIV]-G-{P}-G-{P}-[FYWMGSTNH SEQ ID NO:441)]-[SGA]-{PW}-
 [LIVCAT SEQ ID NO:442)]-{PD}-x- [GSTACLIVMFY SEQ ID NO:443)]-x(5,18)-
 [LIVMFYWCSTAR SEQ ID NO:444)]-[AIVP SEQ ID NO:445)]-[LIVMFAGCKR SEQ ID
 NO:446)]-K [K binds ATP]. The majority of known protein kinases belong to the class
 5 detected by this pattern, but it fails to find a number of them, especially viral kinases which
 are quite divergent in this region and are completely missed by this pattern.

Consensus pattern: [LIVMFYC SEQ ID NO:6)]-x-[HY]-x-D-[LIVMFY SEQ ID NO:18)]-K-
 x(2)-N-[LIVMFYCT SEQ ID NO:447)](3) [D is an active site residue]. Most serine/
 threonine specific protein kinases belong to this class detected by the pattern with 10
 10 exceptions (half of them viral kinases) and also Epstein-Barr virus BGLF4 and Drosophila
 ninaC which have respectively Ser and Arg instead of the conserved Lys and which are
 therefore detected by the tyrosine kinase specific pattern described below.

Consensus pattern: [LIVMFYC SEQ ID NO:6)]-x-[HY]-x-D-[LIVMFY SEQ ID NO:18)]-
 [RSTAC SEQ ID NO:448)]-x(2)-N-[LIVMFYC SEQ ID NO:6)](3) [D is an active site
 15 residue] ALL tyrosine specific protein kinases with the exception of human ERBB3 and
 mouse blk belong to this class detected by the pattern. This pattern will also detect most
 bacterial aminoglycoside phosphotransferases [8,9] and herpesviruses gangciclovir kinases
 [10]; which are proteins structurally and evolutionary related to protein kinases. This profile
 also detects receptor guanylate cyclases and 2-5A-dependent ribonucleases. Sequence
 20 similarities between these two families and the eukaryotic protein kinase family have been
 noticed before. It also detects Arabidopsis thaliana kinase- like protein TMKL1 which seems
 to have lost its catalytic activity. If a protein analyzed includes the two protein kinase
 signatures, the probability of it being a protein kinase is close to 100%. Eukaryotic-type
 protein kinases have also been found in prokaryotes such as Myxococcus xanthus [11] and
 25 Yersinia pseudotuberculosis.

[1] Hanks S.K., Hunter T. FASEB J. 9:576-596(1995).

[2] Hunter T. Meth. Enzymol. 200:3-37(1991).

[3] Hanks S.K., Quinn A.M. Meth. Enzymol. 200:38-62(1991).

30 [4] Hanks S.K. Curr. Opin. Struct. Biol. 1:369-383(1991).

[5] Hanks S.K., Quinn A.M., Hunter T. Science 241:42-52(1988).

[6] Knighton D.R., Zheng J., Ten Eyck L.F., Ashford V.A., Xuong N.-H., Taylor S.S.,
 Sowadski J.M. Science 253:407-414(1991).

[7] Bairoch A., Claverie J.-M. Nature 331:22(1988).

[8] Benner S. Nature 329:21-21(1987).

[9] Kirby R. J. Mol. Evol. 30:489-492(1992).

[10] Littler E., Stuart A.D., Chee M.S. Nature 358:160-162(1992).

5 [11] Munoz-Dorado J., Inouye S., Inouye M. Cell 67:995-1006(1991).

Receptor tyrosine kinase class II signature

A number of growth factors stimulate mitogenesis by interacting with a family of cell surface receptors which possess an intrinsic, ligand-sensitive, protein tyrosine kinase activity [1].

10 These receptor tyrosine kinases (RTK) all share the same topology: an extracellular ligand-binding domain, a single transmembrane region and a cytoplasmic kinase domain. However they can be classified into at least five groups. The prototype for class II RTK's is the insulin receptor, a heterotetramer of two alpha and two beta chains linked by disulfide bonds. The alpha and beta chains are cleavage products of a precursor molecule. The alpha chain
15 contains the ligand binding site, the beta chain transverses the membrane and contains the tyrosine protein kinase domain. The receptors currently known to belong to class II are: - Insulin receptor from vertebrates. - Insulin growth factor I receptor from mammals. - Insulin receptor-related receptor (IRR), which is most probably a receptor for a peptide belonging to the insulin family. - Insects insulin-like receptors. - Molluscan insulin-related peptide(s)
20 receptor (MIP-R). - Insulin-like peptide receptor from Branchiostoma lanceolatum. - The Drosophila developmental protein sevenless, a putative receptor for positional information required for the formation of the R7 photoreceptor cells. - The trk family of receptors (NTRK1, NTRK2 and NTRK3), which are high affinity receptors for nerve growth factor and related neurotrophic factors (BDNF and NT-3). And the following uncharacterized receptors:
25 - ROS. - LTK (TYK1). - EDDR1 (cak, TRKE, RTK6). - NTRK3 (Tyro10, TKT). - A sponge putative receptor tyrosine kinase. While only the insulin and the insulin growth factor I receptors are known to exist in the tetrameric conformation specific to class II RTK's, all the above proteins share extensive homologies in their kinase domain, especially around the putative site of autophosphorylation. Hence, a signature pattern was developed for this class
30 of RTK's, which includes the tyrosine residue, itself probably autophosphorylated.

Consensus pattern: [DN]-[LIV]-Y-x(3)-Y-Y-R [The second Y is the autophosphorylation site]

[1] Yarden Y., Ullrich A. Annu. Rev. Biochem. 57:443-478(1988).

Receptor tyrosine kinase class III signature

5 A number of growth factors stimulate mitogenesis by interacting with a family of cell surface receptors which possess an intrinsic, ligand-sensitive, protein tyrosine kinase activity [1]. These receptor tyrosine kinases (RTK) all share the same topology: an extracellular ligand-binding domain, a single transmembrane region and a cytoplasmic kinase domain. However they can be classified into at least five groups. The class III RTK's are characterized by the
10 presence of five to seven immunoglobulin-like domains [2] in their extracellular section. Their kinase domain differs from that of other RTK's by the insertion of a stretch of 70 to 100 hydrophilic residues in the middle of this domain. The receptors currently known to belong to class III are: - Platelet-derived growth factor receptor (PDGF-R). PDGF-R exists as a homo- or heterodimer of two related chains: alpha and beta [3]. - Macrophage colony stimulating
15 factor receptor (CSF-1-R) (also known as the *fms* oncogene). - Stem cell factor (mast cell growth factor) receptor (also known as the *kit* oncogene). - Vascular endothelial growth factor (VEGF) receptors Flt-1 and Flk-1/KDR [4]. - Fl cytokine receptor Flk-2/Flt-3 [5]. - The putative receptor Flt-4 [7]. a signature pattern Was developed for this class of RTK's which is based on a conserved region in the kinase domain.

20

Consensus pattern: G-x-H-x-N-[LIVM SEQ ID NO:4]-V-N-L-L-G-A-C-T-

[1] Yarden Y., Ullrich A. Annu. Rev. Biochem. 57:443-478(1988).

[2] Hunkapiller T., Hood L. Adv. Immunol. 44:1-63(1989).

25 [3] Lee K.-H., Bowen-Pope D.F., Reed R.R. Mol. Cell. Biol. 10:2237-2246(1990).

[4] Terman B.I., Dougher-Vermazen M., Carrion M.E., Dimitrov D., Armellino D.C., Gospodarowicz D., Boehlen P. Biochem. Biophys. Res. Commun. 187:1579-1586(1992).

[5] Lyman S.D., James L., Vanden Bos T., de Vries P., Brasel K., Gliniak B., Hollingsworth L.T., Picha K.S., McKenna H.J., Splett R.R. Cell 75:1157-1167(1993).

30 [6] Galland F., Karamysheva A., Pebusque M.J., Borg J.P., Rottapel R., Dubreuil P., Rosnet O., Birnbaum D. Oncogene 8:1233-1240(1993).

Receptor tyrosine kinase class V signatures

A number of growth factors stimulate mitogenesis by interacting with a family of cell surface receptors which possess an intrinsic, ligand-sensitive, protein tyrosine kinase activity [1].

These receptor tyrosine kinases (RTK) all share the same topology: an extracellular ligand-binding domain, a single transmembrane region and a cytoplasmic kinase domain. However

they can be classified into at least five groups on the basis of sequence similarities. The extracellular domain of class V RTK's consist of a region of about 300 amino acids, amongst which 16 conserved cysteines probably involved in disulfide bonds; this region is followed

by two copies of a fibronectin type III domain. The ligands for these receptors are proteins of about 200 to 300 residues collectively known as Ephrins. The receptors currently known to

belong to class V are [2,3,E1]: - EPHA1 (Eph-1; Esk). - EPHA2 (Eck; Mpk-5; Sek-2). -

EPHA3 (Etk-1; Hek; Mek4; Tyro4; Rek4; Cek4). - EPHA4 (Sek; Hek8; Mpk-3; Cek8). -

EPHA5 (Ehk-1; Hek7; Bsk; Cek7). - EPHA6 (Ehk-2). - EPHA7 (Ehk-3; Hek11; Mdk-1;

Ebk). - EPHA8 (Eek). - EPHB1 (Eph-2; Elk; Net). - EPHB2 (Eph-3; Hek5; Drt; Erk; Nuk;

Sek-3; Cek5; Qek5). - EPHB3 (Hek-2; Mdk-5). - EPHB4 (Htk; Mdk-2; Myk-1). - EPHB5

(Cek9). The EPHA subtype receptors bind to GPI-anchored ephrins while the EPHB subtype

receptors bind to type-I membrane ephrins. Two signature patterns were developed for this

class of RTK's, which each include some of the conserved cysteine residues.

Consensus pattern: F-x-[DN]-x-[GAW]-[GA]-C-[LIVM SEQ ID NO:4)]-[SA]-[LIVM SEQ

ID NO:4)](2)-[SA]-[LV]-[KRHQ SEQ ID NO:449)]-[LIVA SEQ ID NO:219)]-x(3)-[KR]-

C-[PSAW SEQ ID NO:450)] [The two C's are probably involved in disulfide bonds]

Consensus pattern: C-x(2)-[DE]-G-[DEQ]-W-x(2,3)-[PAQ]-[LIVMT SEQ ID NO:1)]-[GT]-

x-C-x-C-x(2)-G-[HFY]-[EQ] [The three C's are probably involved in disulfide bonds]

[1] Yarden Y., Ullrich A. Annu. Rev. Biochem. 57:443-478(1988).

[2] Sajjadi F.G., Pasquale E.B., Subramani S. New Biol. 3:769-778(1991).

[3] Wicks I.P., Wilkinson D., Salvaris E., Boyd A.W. Proc. Natl. Acad. Sci. U.S.A. 89:1611-1615(1992).

459. Protein kinase C terminal domain

460. Plant thionins signature

Thionins are small, basic, plant proteins generally toxic to animal cells [1]. They seem to exert their toxic effect at the level of the cell membrane but their exact function is not known. They consist of a polypeptide chain of forty five to fifty amino acids with three to four internal

disulfide bonds. They are found in seeds but also in the cell wall of leaves [2]. Thionins are processed from larger precursor proteins [3]. Crambin [4], a hydrophobic plant seed protein, also belongs to this family. The pattern to detect this family of proteins includes three of the six cysteine residues involved in disulfide bonds. +-----+ | +-----

-----+ | || | xxCCxxxxxxxxxxxxCxxxxxxxxCxxxCxxCxxxxxCxxxxxxxx
***** || | +-----+'C': conserved cysteine involved in a disulfide bond.'*':

position of the pattern.

Consensus pattern: C-C-x(5)-R-x(2)-[FY]-x(2)-C [The three C's are involved in disulfide bonds] The proteins from the gamma-thionin family are not related to the above proteins and are described in a separate section.

[1] Vernon L.P., Evett G.E., Zeikus R.D., Gray W.R. Arch. Biochem. Biophys. 238:18-29(1985).

[2] Bohlmann H., Clausen S., Behnke S., Giese H., Hiller C., Reimann-Phillip U., Schrader G., Barkholt V., Apel K. EMBO J. 7:1559-1565(1988).

[3] Bohlmann H., Apel K. Mol. Gen. Genet. 207:446-454(1987).

[4] Teeter M.M., Mazer J.A., L'Italien J.J. Biochemistry 20:5437-5443(1981).

461. Polyprenyl synthetases signatures

A variety of isoprenoid compounds are synthesized by various organisms. For example in eukaryotes the isoprenoid biosynthetic pathway is responsible for the synthesis of a variety of end products including cholesterol, dolichol, ubiquinone or coenzyme Q. In bacteria this pathway leads to the synthesis of isopentenyl tRNA, isoprenoid quinones, and sugar carrier lipids. Among the enzymes that participate in that pathway, are a number of polyprenyl synthetase enzymes which catalyze a 1'4-condensation between 5 carbon isoprene units.

Currently the sequence of some of these enzymes is known: - Eukaryotic farnesyl pyrophosphate synthetase (FPP synthetase) (EC 2.5.1.1 / EC 2.5.1.10) which catalyzes the

sequential condensation of isopentenyl pyrophosphate (IPP) with dimethylallyl pyrophosphate (DMAPP), and then with the resultant geranyl pyrophosphate to form farnesyl pyrophosphate. FPP synthetase is a cytoplasmic dimeric enzyme. - Prokaryotic farnesyl pyrophosphate synthetase (gene *ispA*). - Prokaryotic octaprenyl diphosphate synthase (gene *ispB*). - Prokaryotic heptaprenyl diphosphate synthase (EC 2.5.1.30). - Eukaryotic geranylgeranyl pyrophosphate synthetase (GGPP synthetase) (EC 2.5.1.1 / EC 2.5.1.10 / EC 2.5.1.29) which catalyzes the sequential addition of the three molecules of IPP onto DMAPP to form geranylgeranyl pyrophosphate. In plants GGPP synthase is a chloroplast enzyme involved in the biosynthesis of terpenoids; in fungi, such as *Neurospora crassa* (gene *al-3*), this enzyme is involved in the biosynthesis of carotenoids. - Prokaryotic GGPP synthetase, which are involved in the biosynthesis of carotenoids (gene *crtE*). Such an enzyme is also encoded in the cyanelle genome of *Cyanophora paradoxa*. - Eukaryotic hexaprenyl pyrophosphate synthetase, which is involved in the biosynthesis of coenzyme Q and which catalyzes the formation of all trans- polyprenyl pyrophosphates generally ranging in length of between 6 and 10 isoprene units depending on the species. HP synthetase is a mitochondrial membrane-associated enzyme. It has been shown [1 to 5] that all the above enzymes share some regions of sequence similarity. Two of these regions are rich in aspartic-acid residues and could be involved in the catalytic mechanism and/or the binding of the substrates. signature patterns were developed for both regions. Possible additional members of this family of proteins are: - *Bacillus subtilis* spore germination protein C3 (gene *gerC3*). Both proteins are most probably also enzymes involved in isoprenoid metabolism [6].

Consensus pattern: [LIVM SEQ ID NO:4]](2)-x-D-D-x(2,4)-D-x(4)-R-R-[GH]-

Consensus pattern: [LIVMFY SEQ ID NO:18)]-G-x(2)-[FYL]-Q-[LIVM SEQ ID NO:4)]-x-D-D-[LIVMFY SEQ ID NO:18)]-x-[DNG]

[1] Ashby M.N., Edwards P.A. J. Biol. Chem. 265:13157-13164(1990).

[2] Fujisaki S., Hara H., Nishimura Y., Horiuchi K., Nishino T. J. Biochem. 108:995-1000(1990).

[3] Carattoli A., Romano N., Ballario P., Morelli G., Macino G. J. Biol. Chem. 266:5854-5859(1991).

[4] Kuntz M., Roemer S., Suire C., Hugueney P., Weil J.H., Schantz R., Camara B. Plant J. 2:25-34(1992).

- [5] Math S.K., Hearst J.E., Poulter C.D. Proc. Natl. Acad. Sci. U.S.A. 89:6761-6764(1992).
[6] Bairoch A. Unpublished observations (1993).

5 462. Potato inhibitor I family signature

The potato inhibitor I family is one of the numerous families of serine proteinase inhibitors. Members of this protein family are found in plants; in the seeds of barley or beans [1,2,3], and in potato or tomato leaves where they accumulate in response to mechanical damage [4,5]. An inhibitor belonging to this family is also found in leech [6]. It is interesting to note
10 that, currently, this is the only proteinase inhibitor family to be found both in plant and animal kingdoms. Structurally these inhibitors are small (60 to 90 residues) and in contrast with other families of protease inhibitors, they lack disulfide bonds. They have a single inhibitory site. The consensus pattern includes three out of the four residues conserved in all members of this family and is located in the N-terminal half.

15 Consensus pattern: [FYW]-P-[EQH]-[LIV](2)-G-x(2)-[STAGV SEQ ID NO:451)]-x(2)-A-
Barley subtilisin-chymotrypsin inhibitor-2b has Glu instead of Gly. There is a trypsin inhibitor from the cucurbitaceae *Momordica charantia* [7], which is said to belong to the potato inhibitor I family but which shows only a very weak similarity with the other members
20 of this family.

- [1] Svendsen I., Hejgaard J., Chavan J.K. Carlsberg Res. Commun. 49:493-502(1984).
[2] Svendsen I., Boisen S., Hejgaard J. Carlsberg Res. Commun. 47:45-53(1982).
[3] Nozawa H., Yamagata H., Aizono Y., Yoshikawa M., Iwasaki T. J. Biochem. 106:1003-
25 1008(1989).
[4] Cleveland T.E., Thornburg R.W., Ryan C.A. Plant Mol. Biol. 8:199-207(1987).
[5] Lee J.S., Brown W.E., Graham J.S., Pearce G., Fox E.A., Dreher T.W., Ahern K.G., Pearson G.D., Ryan C.A. Proc. Natl. Acad. Sci. U.S.A. 83:7277-7281(1986).
[6] Seemuller U., Eulitz M., Fritz H., Strobl A. Hoppe-Seyler's Z. Physiol. Chem. 361:1841-
30 1846(1980).
[7] Zeng F.-Y., Qian R.-Q., Wang Y. FEBS Lett. 234:35-38(1988).

463. (pp binding) Phosphopantetheine attachment site

Phosphopantetheine (or pantetheine 4' phosphate) is the prosthetic group of acyl carrier proteins (ACP) in some multienzyme complexes where it serves as a 'swinging arm' for the attachment of activated fatty acid and amino-acid groups [1]. Phosphopantetheine is attached to a serine residue in these proteins [2]. ACP proteins or domains have been found in various enzyme systems which are listed below (references are only provided for recently determined sequences). - Fatty acid synthetase (FAS), which catalyzes the formation of long-chain fatty acids from acetyl-CoA, malonyl-CoA and NADPH. Bacterial and plant chloroplast FAS are composed of eight separate subunits which correspond to the different enzymatic activities; ACP is one of these polypeptides. Fungal FAS consists of two multifunctional proteins, FAS1 and FAS2; the ACP domain is located in the N-terminal section of FAS2. Vertebrate FAS consists of a single multifunctional enzyme; the ACP domain is located between the beta-ketoacyl reductase domain and the C-terminal thioesterase domain [3]. - Polyketide antibiotics synthase enzyme systems. Polyketides are secondary metabolites produced from simple fatty acids, by microorganisms and plants. ACP is one of the polypeptidic components involved in the biosynthesis of *Streptomyces* polyketide antibiotics actinorhodin, curamycin, granatacin, monensin, oxytetracycline and tetracenomycin C. - *Bacillus subtilis* putative polyketide synthases pksK, pksL and pksM which respectively contain three, five and one ACP domains. - The multifunctional 6-methylsalicylic acid synthase (MSAS) from *Penicillium patulum*. This is a multifunctional enzyme involved in the biosynthesis of a polyketide antibiotic and which contains an ACP domain in the C-terminal extremity. - Multifunctional mycocerosic acid synthase (gene mas) from *Mycobacterium bovis*. - Gramicidin S synthetase I (gene grsA) from *Bacillus brevis*. This enzyme catalyzes the first step in the biosynthesis of the cyclic antibiotic gramicidin S. - Tyrocidine synthetase I (gene tycA) from *Bacillus brevis*. The reaction carried out by tycA is identical to that catalyzed by grsA - Gramicidin S synthetase II (gene grsB) from *Bacillus brevis*. This enzyme is a multifunctional protein that activates and polymerizes proline, valine, ornithine and leucine. GrsB contains four ACP domains. - Erythronolide synthase proteins 1, 2 and 3 from *Saccharopolyspora erythraea* which is involved in the biosynthesis of the polyketide antibiotic erythromycin. Each of these proteins contain two ACP domains. - Conidial green pigment synthase from *Aspergillus nidulans*. - ACV synthetase from various fungi. This enzyme catalyzes the first step in the biosynthesis of penicillin and cephalosporin. It contains three ACP domains. - Enterobactin synthetase component F (gene entF) from *Escherichia*

coli. This enzyme is involved in the ATP-dependent activation of serine during enterobactin (enterochelin) biosynthesis. - Cyclic peptide antibiotic surfactin synthase subunits 1, 2 and 3 from *Bacillus subtilis*. Subunits 1 and 2 contains three related domains while subunit 3 only contains a single domain. - HC-toxin synthetase (gene HTS1) from *Cochliobolus carbonum*.

5 This enzyme synthesizes HC-toxin, a cyclic tetrapeptide. HTS1 contains four ACP domains. - Fungal mitochondrial ACP [9], which is part of the respiratory chain NADH dehydrogenase (complex I). - Rhizobium nodulation protein nodF, which probably acts as an ACP in the synthesis of the nodulation Nod factor fatty acyl chain. The sequence around the phosphopantetheine attachment site is conserved in all these proteins and can be used as a
10 signature pattern. A profile was also developed that spans the complete ACP-like domain.

Consensus pattern: [DEQGSTALMKRH SEQ ID NO:452)]-[LIVMFYSTAC SEQ ID NO:453)]-[GNQ]-[LIVMFYAG SEQ ID NO:351)]-[DNEKHS SEQ ID NO:454)]-S-[LIVMST SEQ ID NO:48)]-{PCFY SEQ ID NO:455)}-[STAGCPQLIVMF SEQ ID
15 NO:456)]-[LIVMATN SEQ ID NO:457)]-[DENQGTAKRHLM SEQ ID NO:458)]-[LIVMWSTA SEQ ID NO:459)]-[LIVGSTACR SEQ ID NO:460)]-x(2)-[LIVMFSA SEQ ID NO:81)] [S is the pantetheine attachment site]

[1] Concise Encyclopedia Biochemistry, Second Edition, Walter de Gruyter, Berlin New-
20 York (1988).

[2] Pugh E.L., Wakil S.J. J. Biol. Chem. 240:4727-4733(1965).

[3] Witkowski A., Rangan V.S., Randhawa Z.I., Amy C.M., Smith S. Eur. J. Biochem. 198:571-579(1991).

[6] Scotti C., Piatti M., Cuzzoni A., Perani P., Tognoni A., Grandi G., Galizzi A., Albertini
25 A.M. Gene 130:65-71(1993).

[9] Sackmann U., Zensen R., Rohlen D., Jahnke U., Weiss H. Eur. J. Biochem. 200:463-469(1991).

30 464. (Prenyltrans) Terpene synthases signature

The following enzymes catalyze mechanistically related reactions which involve the highly complex cyclic rearrangement of squalene or its 2,3 oxide: - Lanosterol synthase (EC 5.4.99.7) (oxidosqualene--lanosterol cyclase), which catalyzes the cyclization of (S)-2,3-

epoxysqualene to lanosterol, the initial precursor of cholesterol, steroid hormones and vitamin D in vertebrates and of ergosterol in fungi (gene ERG7). - Cycloartenol synthase (EC 5.4.99.8) (2,3-epoxysqualene--cycloartenol cyclase), a plant enzyme that catalyzes the cyclization of (S)-2,3- epoxysqualene to cycloartenol. - Hopene synthase (EC 5.4.99.-) (squalene--hopene cyclase), a bacterial enzyme that catalyzes the cyclization of squalene into hopene, a key step in hopanoid (triterpenoid) metabolism. These enzymes are evolutionary related [1] proteins of about 70 to 85 Kd. As a signature pattern, a highly conserved region was selected which is rich in aromatic residues and which is located in the C-terminal section.

10 Consensus pattern: [DE]-G-S-W-x-G-x-W-[GA]-[LIVM SEQ ID NO:4])-x-[FY]-x-Y-[GA]

[1] Corey E.J., Matsuda S.P.T., Bartel B. Proc. Natl. Acad. Sci. U.S.A. 90:11628-11632(1993).

15

465. Prion protein signatures

Prion protein (PrP) [1,2,3] is a small glycoprotein found in high quantity in the brains of humans or animals infected with a number of degenerative neurological diseases such as Kuru, Creutzfeldt-Jacob disease (CJD), scrapie or bovine spongiform encephalopathy (BSE).

PrP is encoded in the host genome and expressed both in normal and infected cells. It has a tendency to aggregate yielding polymers called rods. Structurally, PrP is a protein consisting of a signal peptide, followed by an N-terminal domain that contains tandem repeats of a short motif (PHGGGWGQ in mammals, PHNPGY in chicken), itself followed by a highly conserved domain. It then comes a C-terminal hydrophobic domain post-translationally removed when PrP is attached to the extracellular side of the cell membrane by a GPI-anchor. The structure of PrP is shown in the following schematic representation: +---+-----+---

*****_-----****_----+-----+ |Sig| Tandem repeats | C C S | | +---+-----+---

-----|-----|---|+----+ +-----+ | GPI'C': conserved cysteine involved in a disulfide bond.'*': position of the patterns. As signature pattern for PrP, a perfectly conserved alanine- and glycine-rich region of 16 residues was selected as well as a region centered on the second cysteine involved in the disulfide bond.

Consensus pattern: A-G-A-A-A-A-G-A-V-V-G-G-L-G-G-Y-

Consensus pattern: E-x-[ED]-x-K-[LIVM SEQ ID NO:4)](2)-x-[KR]-[LIVM SEQ ID NO:4)](2)-x-[QE]-M-C-x(2)- Q-Y [C is involved in a disulfide bond]

[1] Stahl N., Prusiner S.B. FASEB J. 5:2799-2807(1991).

5 [2] Brunori M., Chiara Silvestrini M., Pocchiari M. Trends Biochem. Sci. 13:309-313(1988).

[3] Prusiner S.B. Annu. Rev. Microbiol. 43:345-374(1989).

466. Cyclophilin-type peptidyl-prolyl cis-trans isomerase signature and profile (pro
10 isomerase)

Cyclophilin [1] is the major high-affinity binding protein in vertebrates for the immunosuppressive drug cyclosporin A (CSA). It exhibits a peptidyl- prolyl cis-trans isomerase activity (EC 5.2.1.8) (PPIase or rotamase). PPIase is an enzyme that accelerates protein folding by catalyzing the cis-transisomerization of proline imidic peptide bonds in
15 oligopeptides [2]. It is probable that CSA mediates some of its effects via an inhibitory action on PPIase. Cyclophilin is a cytosolic protein which belongs to a family [3,4,5]that also includes the following isozymes: - Cyclophilin B (or S-cyclophilin), a PPIase which is retained in an endoplasmic reticulum compartment. - Cyclophilin C, a cytoplasmic PPIase. - Mitochondrial matrix cyclophilin (cyp3). - A PPIase which seems specific for the folding of
20 rhodopsin and is an integral membrane protein anchored by a C-terminal transmembrane region. This protein was first characterized in Drosophila (gene ninaA). - Bacterial periplasmic PPIase (gene ppiA). - Bacterial cytosolic PPIase (gene ppiB). - Natural-killer cell cyclophilin-related protein. This large protein (about 160 Kd) is a component of a putative tumor-recognition complex involved in the function of NK cells. It contains a cyclophilin-type PPIase domain. - Mammalian nucleoporin Nup358 [6], a nuclear pore complex protein of 358 Kd that contains a C-terminal cyclophilin-type PPIase domain. - Yeast hypothetical protein YJR032w. - Fission yeast hypothetical protein SpAC21E11.05c. - Caenorhabditis elegans hypothetical protein T27D1.1. The sequences of the different forms of cyclophilin-type PPIases are well conserved. As a signature pattern, a conserved region was selected in
25 the central part of these enzymes.
30

Consensus pattern: [FY]-x(2)-[STCNLV SEQ ID NO:461)]-x-F-H-[RH]-[LIVMN SEQ ID NO:382)]-[LIVM SEQ ID NO:4)]-x(2)-F- [LIVM SEQ ID NO:4)]-x-Q-[AG]-G- FKBP's, a

family of proteins that bind the immunosuppressive drug FK506, are also PPIases, but their sequence is not at all related to that of cyclophilin.

[1] Stamnes M.A., Rutherford S.L., Zuker C.S. Trends Cell Biol. 2:272-276(1992).

5 [2] Fischer G., Schmid F.X. Biochemistry 29:2205-2212(1990).

[3] Trandinh C.C., Pao G.M., Saier M.H. Jr. FASEB J. 6:3410-3420(1992).

[4] Galat A. Eur. J. Biochem. 216:689-707(1993).

[5] Hacker J., Fischer G. Mol. Microbiol. 10:445-456(1993).

10 [6] Wu J., Matunis M.J., Kraemer D., Blobel G., Coutavas E. J. Biol. Chem. 270:14209-14213(1995).

467. Profilin signature

Profilin [1,2] is a small eukaryotic protein that binds to monomeric actin(G-actin) in a 1:1 ratio thus preventing the polymerization of actin into filaments (F-actin). It can also, in certain circumstance promotes actin polymerization. Profilin also binds to polyphosphoinositides such as PIP2. Overall sequence similarity among profilin from organisms which belong to different phyla (ranging from fungi to mammals) is low, but the N-terminal region is relatively well conserved. That region is thought to be involved in the binding to actin. The signature pattern for profilin is based on conserved residues at the N-terminal extremity. A protein structurally similar to profilin is present in the genome of variola and vaccinia viruses (gene A42R).

Consensus pattern: <x(0,1)-[STA]-x(0,1)-W-[DENQH SEQ ID NO:462)]-x-[YI]-x-[DEQ]

25 [1] Haarer B.K., Brown S.S. Cell Motil. Cytoskeleton 17:71-74(1990).

[2] Sohn R.H., Goldschmidt-Clermont P. BioEssays 16:465-472(1994).

30 468. Protamine P1 signature

Protamines are small, highly basic proteins, that substitute for histones in sperm chromatin during the haploid phase of spermatogenesis. They pack sperm DNA into a highly condensed, stable and inactive complex. There are two different types of mammalian

protamine, called P1 and P2. P1 has been found in all species studied, while P2 is sometimes absent. There seems to be a single type of avian protamine whose sequence is closely related to that of mammalian P1 [1]. As a signature for this family of proteins, a conserved region was selected at the N-terminal extremity of the sequence.

5

Consensus pattern: [AV]-R-[NFY]-R-x(2,3)-[ST]-x-S-x-S-

[1] Oliva R., Goren R., Dixon G.H. J. Biol. Chem. 264:17627-17630(1989).

10

469. Sperm histone P2 (protamine P2)

This protein also known as protamine P2 can substitute for histones in the chromatin of sperm. The alignment contains both the sequence of the mature P2 protein and its propeptide.

15

470. Proteasome A-type subunits signature

The proteasome (or macropain) (EC 3.4.99.46) [1 to 5,E1] is an eukaryotic and archaeobacterial multicatalytic proteinase complex that seems to be involved in an ATP/ubiquitin-dependent nonlysosomal proteolytic pathway. In eukaryotes the proteasome is composed of about 28 distinct subunits which form a highly ordered ring-shaped structure (20S ring) of about 700 Kd. Most proteasome subunits can be classified, on the basis on sequence similarities into two groups, A and B. Subunits that belong to the A-type group are proteins of from 210 to 290 amino acids that share a number of conserved sequence regions. Subunits that are known to belong to this family are listed below. - Vertebrate subunits C2 (nu), C3, C8, C9, iota and zeta. - Drosophila PROS-25, PROS-28.1, PROS-29 and PROS-35. - Yeast C1 (PRS1), C5 (PRS3), C7-alpha (Y8) (PRS2), Y7, Y13, PRE5, PRE6 and PUP2. - Arabidopsis thaliana subunits alpha and PSM30. - Thermoplasma acidophilum alpha-subunit. In this archaeobacteria the proteasome is composed of only two different subunits. As a signature pattern for proteasome A-type subunits the best conserved region was selected, which is located in the N-terminal part of these proteins.

30

Consensus pattern: [FY]-x(4)-[STNV SEQ ID NO:463)]-x-[FYW]-S-P-x-G-[RKH]-x(2)-Q-[LIVM SEQ ID NO:4)]-[DE]-Y-[SAD]-x(2)-[SAG]-. These proteins belong to family T1 in the classification of peptidases [6,E2].

- 5 [1] Rivett A.J. Biochem. J. 291:1-10(1993).
- [2] Rivett A.J. Arch. Biochem. Biophys. 268:1-8(1989).
- [3] Goldberg A.L., Rock K.L Nature 357:375-379(1992).
- [4] Wilk S. Enzyme Protein 47:187-188(1993).
- [5] Hilt W., Wolf D.H. Trends Biochem. Sci. 21:96-102(1996).
- 10 [6] Rawlings N.D., Barrett A.J. Meth. Enzymol. 244:19-61(1994).

Proteasome B-type subunits signature

- The proteasome (or macropain) (EC 3.4.99.46) [1 to 5,E1] is an eukaryotic and archaeobacterial multicatalytic proteinase complex that seems to be involved in an
- 15 ATP/ubiquitin-dependent nonlysosomal proteolytic pathway. In eukaryotes the proteasome is composed of about 28 distinct subunits which form a highly ordered ring-shaped structure (20S ring) of about 700 Kd. Most proteasome subunits can be classified, on the basis on sequence similarities into two groups, A and B. Subunits that belong to the B-type group are proteins of from 190 to 290 amino acids that share a number of conserved sequence regions.
- 20 Subunits that are known to belong to this family are listed below. - Vertebrate subunits C5, beta, delta, epsilon, theta (C10-II), LMP2/RING12, C13 (LMP7/RING10), C7-I and MECL-1. - Yeast PRE1, PRE2 (PRG1), PRE3, PRE4, PRS3, PUP1 and PUP3. - Drosophila L(3)73AI. - Fission yeast pts1. - Thermoplasma acidophilum beta-subunit. In this
- 25 archaeobacteria the proteasome is composed of only two different subunits. As a signature pattern for proteasome B-type subunits the best conserved region was selected, which is located in the N-terminal part of these proteins.

- Consensus pattern: [LIVMA SEQ ID NO:30)]-[GSA]-[LIVMF SEQ ID NO:2)]-x-[FYLVGAC SEQ ID NO:464)]-x(2)-[GSACFY SEQ ID NO:465)]-[LIVMSTAC SEQ ID
- 30 NO:151)](3)-[GAC]-[GSTACV SEQ ID NO:466)]-[DES]-x(15)-[RK]-x(12,13)-G-x(2)-[GSTA SEQ ID NO:19)]-D-. These proteins belong to family T1 in the classification of peptidases [6,E2].

- [1] Rivett A.J. Biochem. J. 291:1-10(1993).
- [2] Rivett A.J. Arch. Biochem. Biophys. 268:1-8(1989).
- [3] Goldberg A.L., Rock K.L Nature 357:375-379(1992).
- [4] Wilk S. Enzyme Protein 47:187-188(1993).
- 5 [5] Hilt W., Wolf D.H. Trends Biochem. Sci. 21:96-102(1996).
- [6] Rawlings N.D., Barrett A.J. Meth. Enzymol. 244:19-61(1994).

471. (pyr redox) Pyridine nucleotide-disulphide oxidoreductases class-I active site

- 10 The pyridine nucleotide-disulphide oxidoreductases are FAD flavoproteins which contains a pair of redox-active cysteines involved in the transfer of reducing equivalents from the FAD cofactor to the substrate. On the basis of sequence and structural similarities [1] these enzymes can be classified into two categories. The first category groups together the following enzymes [2 to 6]: - Glutathione reductase (EC 1.6.4.2) (GR). - Higher eukaryotes
- 15 thioredoxin reductase (EC 1.6.4.5). - Trypanothione reductase (EC 1.6.4.8). - Lipoamide dehydrogenase (EC 1.8.1.4), the E3 component of alpha-ketoacid dehydrogenase complexes. - Mercuric reductase (EC 1.16.1.1). The sequence around the two cysteines involved in the redox-active disulfide bond is conserved and can be used as a signature pattern.
- 20 Consensus pattern: G-G-x-C-[LIVA SEQ ID NO:219)]-x(2)-G-C-[LIVM SEQ ID NO:4)]-P [The two C's form the active site disulfide bond]. In positions 6 and 7 of the pattern all known sequences have Asn-(Val/ Ile) with the exception of GR from plant chloroplasts and from cyanobacteria which have Ile-Arg [7].
- 25 [1] Kurlyan J., Krishna T.S.R., Wong L., Guenther B., Pahler A., Williams C.H. Jr., Model P. Nature 352:172-174(1991).
- [2] Rice D.W., Schulz G.E., Guest J.R. J. Mol. Biol. 174:483-496(1984).
- [3] Brown N.L. Trends Biochem. Sci. 10:400-402(1985).
- [4] Carothers D.J., Pons G., Patel M.S. Arch. Biochem. Biophys. 268:409-425(1989).
- 30 [5] Walsh C.T., Bradley M., Nadeau K. Trends Biochem. Sci. 16:305-309(1991).
- [6] Gasdaska P.Y., Gasdaska J.R., Cochran S., Powis G. FEBS Lett. 373:5-9(1995).
- [7] Creissen G., Edwards E.A., Enard C., Wellburn A., Mullineaux P. Plant J. 2:129-131(1991).

472. (pyridoxal deC) DDC / GAD / HDC / TyrDC pyridoxal-phosphate attachment site (pyridoxal deC)

- 5 Three different enzymes - all pyridoxal-dependent decarboxylases - seem to share regions of sequence similarity [1,2,3,4], especially in the vicinity of the lysine residue which serves as the attachment site for the pyridoxal-phosphate (PLP) group. These enzymes are: - Glutamate decarboxylase (EC 4.1.1.15) (GAD). Catalyzes the decarboxylation of glutamate into the neurotransmitter GABA (4-aminobutanoate). - Histidine decarboxylase (EC 4.1.1.22) (HDC).
10 Catalyzes the decarboxylation of histidine to histamine. There are two completely unrelated types of HDC: those that use PLP as a cofactor (found in Gram-negative bacteria and mammals), and those that contain a covalently bound pyruvoyl residue (found in Gram-positive bacteria). - Aromatic-L-amino-acid decarboxylase (EC 4.1.1.28) (DDC), also known as L-dopa decarboxylase or tryptophan decarboxylase. DDC catalyzes the decarboxylation of
15 tryptophan to tryptamine. It also acts on 5-hydroxy- tryptophan and dihydroxyphenylalanine (L-dopa). - Tyrosine decarboxylase (EC 4.1.1.25) (TyrDC) which converts tyrosine into tyramine, a precursor of isoquinoline alkaloids and various amides. These enzymes are collectively known as group II decarboxylases [3,4].

- 20 Consensus pattern: S-[LIVMFYW SEQ ID NO:26)]-x(5)-K-[LIVMFYWG SEQ ID NO:467)](2)-x(3)-[LIVMFYW SEQ ID NO:26)]-x-[CA]- x(2)-[LIVMFYWQ SEQ ID NO:468)]-x(2)-[RK] [K is the pyridoxal-P attachment site]

[1] Jackson F.R. J. Mol. Evol. 31:325-329(1990).

- 25 [2] Joseph D.R., Sullivan P., Wang Y.-M., Kozak C., Fenstermacher D.A., Behrendsen M.E., Zahnow C.A. Proc. Natl. Acad. Sci. U.S.A. 87:733-737(1990).

[3] Sandmeier E., Hale T.I., Christen P. Eur. J. Biochem. 221:997-1002(1994).

[4] Ishii S., Mizuguchi H., Nishino J., Hayashi H., Kagamiyama H. J. Biochem. 120:369-376(1996).

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473. Regulator of chromosome condensation (RCC1) signatures (RCC1)

The regulator of chromosome condensation (RCC1) [1] is a eukaryotic protein which binds to chromatin and interacts with ran, a nuclear GTP-binding protein, to promote the loss of bound GDP and the uptake of fresh GTP, thus acting as a guanine-nucleotide dissociation stimulator (GDS)[2]. The interaction of RCC1 with ran probably plays an important role in the regulation of gene expression. RCC1, known as PRP20 or SRM1 in yeast, pim1 in fission yeast and BJI in Drosophila, is a protein that contains seven tandem repeats of a domain of about 50 to 60 amino acids. As shown in the following schematic representation, the repeats make up the major part of the length of the protein. Outside the repeat region, there is just a small N-terminal domain of about 40 to 50 residues and, in the Drosophila protein only, a C-terminal domain of about 130 residues.

+---+-----+-----+-----+-----+-----+-----+-----+-----+
 --+-----+ |N-t.|Rpt. 1 |Rpt. 2 |Rpt. 3 |Rpt. 4 |Rpt. 5 |Rpt. 6 |Rpt. 7 | C-terminal | +---+---
 ---+-----+-----+-----+-----+-----+-----+-----+-----+ In Drosophila two signature patterns for RCC1 were developed. The first is found in the N-terminal part of the second repeat; this is the most conserved part of RCC1. The second is derived from conserved positions in the C-terminal part of each repeat and detects up to five copies of the repeated domain. The RCC1-type of repeat is also found in the X-linked retinitis pigmentosa GTPase regulator [3].

Consensus pattern: G-x-N-D-x(2)-[AV]-L-G-R-x-T-

Consensus pattern: [LIVMFA SEQ ID NO:81]-[STAGC SEQ ID NO:45]](2)-G-x(2)-H-[STAGLI SEQ ID NO:469)]-[LIVMFA SEQ ID NO:81)]-x-[LIVM SEQ ID NO:4)]-

[1] Dasso M. Trends Biochem. Sci. 18:96-101(1993).

[2] Boguski M.S., McCormick F. Nature 366:643-654(1993).

[3] Roepman R., Van Duijnhoven G., Rosenberg T., Pinckers A.J.L.G., Bleeker-Wagemakers L.M., Bergen A.A.B., Post J., Beck A., Reinhardt R., Ropers H.-H., Cremers F., Berger W. Hum. Mol. Genet. 5:1035-1041(1996).

474. RNA 3'-terminal phosphate cyclase signature (RCT)

RNA 3'-terminal phosphate cyclase (EC 6.5.1.4) [1,2] catalyzes the conversion of 3'-phosphate to a 2',3'-cyclic phosphodiester at the end of RNA. The biological role of this enzyme is unknown but it is likely to function in some aspects of cellular RNA processing.

The reaction catalyzed by the enzyme occurs in three steps: 1) adenylation of the enzyme by ATP; 2) the enzyme acts on RNA-3'terminal phosphate to produce RNA-3'terminal diphosphate adenylate; 3) Release of AMP and cyclisation by a non catalytic nucleophilic attack by the adjacent 2'hydroxyl on the phosphorus in the diester linkage. This enzyme, which has been characterized in human (where there seems to be at least three isozymes) and *Escherichia coli* (gene *rtCA*), seems to be taxonomically widespread. It is found in insects, plants, fungi (gene *RTC1* in yeast) and in archaeobacteria. RNA cyclase is a protein of from 36 to 42 Kd. The best conserved region, which is used as a signature pattern, is a glycine-rich stretch of residues located in the central part of the sequence and which is reminiscent of various ATP, GTP or AMP glycine-rich loops. In this context, the conserved Arg (His in the *E. coli* enzyme) could be the AMP-binding residue.

Consensus pattern: [RH]-G-x(2)-P-x-G(3)-x-[LIV]-

- [1] Genschik P., Billy E., Swianiewicz M., Filipowicz W. *EMBO J.* 16:2955-2967(1997).
[2] Filipowicz W., Vincente O. *Meth. Enzymol.* 181:499-510(1990).

475. REV protein (anti-repression trans-activator protein)

476. Prokaryotic-type class I peptide chain release factors signature (RF-1)

Peptide chain release factors (RFs) are required for the termination of protein biosynthesis [1]. At present two classes of RFs can be distinguished. Class I RFs bind to ribosomes that have encountered a stop codon at their decoding site and induce release of the nascent polypeptide. Class II RFs are GTP-binding proteins that interact with class I RFs and enhance class I RF activity. In prokaryotes there are two class I RFs that act in a codon specific manner[2]: RF-1 (gene *prfA*) mediates UAA and UAG-dependent termination while RF-2 (gene *prfB*) mediates UAA and UGA-dependent termination. RF-1 and RF-2 are structurally and evolutionary related proteins which have been shown [3] to make up a family that also contains the following proteins: - Fungal MRF1, a mitochondrial RF (m-RF) which recognizes the UAA and UAG codons. - *Escherichia coli* RF-H, a protein of unknown function. - *Escherichia coli* hypothetical protein *yaeJ* and a close *Pseudomonas putida*

homolog. A highly conserved region located in the central part of the 40 to 45 Kd RF-1/2 and m-RF and in the N-terminal of the 15 to 16Kd RF-H and yaeJ is used as a signature pattern.

Consensus pattern: [AR]-[STA]-x-G-x-G-G-Q-[HNGCS SEQ ID NO:470)]-V-N-x(3)-[ST]-A-[IV]

Note that prokaryotic-type class I RFs display no significant sequence similarity to prokaryotic-type class II which belong to the family of GTP-binding elongation factors nor to eukaryotic class I or class II RFs.

[1] Tate W.P. , Poole E.S., Mannering S.M. Prog. Nucleic Acids. Res. Mol. Biol. 52:293-335(1996).

[2] Craigen W.J., Lee C.C., Caskey C.T. Mol. Microbiol. 4:861-865(1990).

[3] Pel H.J., Rep M., Grivell L.A. Nucleic Acids Res. 20:4423-4428(1992).

477. RIO1/ZK632.3/MJ0444 family signature

The following uncharacterized proteins are evolutionary related [1]: - Yeast protein RIO1. - *Caenorhabditis elegans* hypothetical protein ZK632.3. - *Methanococcus jannaschii* hypothetical protein MJ0444. - *Thermoplasma acidophilum* hypothetical protein if rpoA2 3'region. The eukaryotic members of this family are proteins of about 55 to 60 Kd, while the archbacterial ones are half that size. The central part of these proteins is highly conserved. The best conserved region is used as a signature pattern.

Consensus pattern: [LIVM SEQ ID NO:4)]-V-H-[GA]-D-L-S-E-[FY]-N-x-[LIVM SEQ ID NO:4)]

[1] Bairoch A. Unpublished observations (1997).

478. (RIP) Shiga/ricin ribosomal inactivating toxins active site signature. A number of bacterial and plant toxins act by inhibiting protein synthesis in eukaryotic cells. The toxins of the Shiga and ricin family inactivate 60S ribosomal subunits by an N-glycosidic cleavage which releases a specific adenine base from the sugar-phosphate backbone of 28S rRNA

[1,2,3]. The toxins which are known to function in this manner are: - Shiga toxin from *Shigella dysenteriae* [4]. This toxin is composed of one copy of an enzymatically active A subunit and five copies of a B subunit responsible for binding the toxin complex to specific receptors on the target cell surface. - Shiga-like toxins (SLT) are a group of *Escherichia coli* toxins very similar in their structure and properties to Shiga toxin. The sequence of two types of these toxins, SLT-1 [5] and SLT-2 [6], is known. - Ricin, a potent toxin from castor bean seeds. Ricin consists of two glycosylated chains linked by a disulfide bond. The A chain is enzymatically active. The B chain is a lectin with a binding preference for galactosides. Both chains are encoded by a single polypeptidic precursor. Ricin is classified as a type-II ribosome-inactivating protein (RIP); other members of this family are agglutinin, also from castor bean, and abrin from the seeds of the bean *Abrus precatorius* [7]. - Single chain ribosome-inactivating proteins (type-I RIP) from plants. Examples of such proteins are: barley protein synthesis inhibitors I and II, mongolian snake-gourd trichosanthin, sponge gourd luffin-A and -B, garden four-o'clock MAP, common pokeberry PAP-S and soapwort saporin-6 [7]. All these toxins are structurally related. A conserved glutamic residue has been implicated [8] in the catalytic mechanism; it is located near a conserved arginine which also plays a role in catalysis [9]. The signature that has been developed for these proteins includes these catalytic residues.

Consensus pattern: [LIVMA SEQ ID NO:30)]-x-[LIVMSTA SEQ ID NO:433)](2)-x-E-[SAGV SEQ ID NO:25)]-[STAL SEQ ID NO:471)]-R-[FY]-[RKNQS SEQ ID NO:472)]-x-[LIVM SEQ ID NO:4)]-[EQS]-x(2)-[LIVMF SEQ ID NO:2)] [E and R are active site residues]-

[1] Endo Y., Tsurugi K., Takeda Y., Ogasawara T., Igarashi K. Eur. J. Biochem. 171:45-50(1988).[2] May M.J., Hartley M.R., Roberts L.M., Krieg P.A., Osborn R.W., Lord J.M. EMBO J. 8:301-308(1989).[3] Funatsu G., Islam M.R., Minami Y., Sung-Sil K., Kimura M. Biochimie 73:1157-1161(1991).[4] Strockbine N.A., Jackson M.P., Sung L.M., Holmes R.K., O'Brien A.D. J. Bacteriol. 170:1116-1122(1988).[5] Calderwood S.B., Auclair F., Donohue-Rolfe A., Keusch G.T., Mekalanos J.J. Proc. Natl. Acad. Sci. U.S.A. 84:4364-4368(1987).[6] Jackson M.P., Neill R.J., O'Brien A.D., Holmes R.K., Newland J.W. FEMS Microbiol. Lett. 44:109-114(1987).[7] Barbieri L., Battelli M.G., Stirpe F. Biochim. Biophys. Acta 1154:237-282(1993).[8] Hovde C.J., Calderwood S.B., Mekalanos J.J.,

Collier R.J. Proc. Natl. Acad. Sci. U.S.A. 85:2568-2572(1988).[9] Monzingo A.F., Collins E.J., Ernst S.R., Irvin J.D., Robertus J.D. J. Mol. Biol. 233:705-715(1993).

5 479. Bacterial RNA polymerase, alpha chain (RNA pol A bac)

Members of this family include alpha subunit from eubacteria and alpha subunits from chloroplasts. The alpha subunit of RNA polymerase consists of two independently folded domains, referred to as amino-terminal and carboxyl terminal domains. The amino terminal domain is involved in the interaction with the other subunits of the RNA polymerase. The
10 carboxyl-terminal domain interacts with the DNA and activators. The amino acid sequence of the alpha subunit is conserved in prokaryotic and chloroplast RNA polymerases. There are three regions of particularly strong conservation, two in the amino-terminal and one in the carboxyl-Comment: terminal [3].

[1] Zhang G, Darst SA; Science 1998;281:262-266. [2] Jeon YH, Negishi T, Shirakawa M,
15 Yamazaki T, Fujita N, Ishihama A, Kyogoku Y; Science 1995;270:1495-1497. [3] Ebright RH, Busby S; Curr Opin Genet Dev 1995;5:197-203. [4] Murakami K, Kimura M, Owens JT, Meares CF, Ishihama A; Proc Natl Acad Sci USA 1997;94:1709-1714.

20 480. RNA polymerase beta subunit (RNA pol B)

RNA polymerases catalyse the DNA dependent polymerisation of RNA. Prokaryotes contain a single RNA polymerase compared to three in eukaryotes (not including mitochondrial and chloroplast polymerases). Each RNA polymerase complex contains two related members of this family, in each case they are the two largest subunits.

25 [1] Falkenburg D, Dworniczak B, Faust DM, Bautz EK; J Mol Biol 1987;195:929-937.

481. RNA polymerases H / 23 Kd subunits signature

In eukaryotes, there are three different forms of DNA-dependent RNA polymerases (EC
30 2.7.7.6) transcribing different sets of genes. Each class of RNA polymerase is an assemblage of ten to twelve different polypeptides. In archaeobacteria, there is generally a single form of RNA polymerase which also consist of an oligomeric assemblage of 10 to 13 polypeptides. Archaeobacterial subunit H (gene rpoH) [1,2] is a small protein of about 8.5 to 10 Kd, it is

442

evolutionary related to the C-terminal part of a 23 Kd component shared by all three forms of eukaryotic RNA polymerases (gene RPB5 in yeast and POLR2E in mammals). As a signature pattern a conserved region was selected which is located at the N-terminal extremity of subunit H; this region contains two histidines that could play a role in the binding of a metal ion.

Consensus pattern: H-[NEI]-[LIVM SEQ ID NO:4]-V-P-x-H-x(2)-[LIVM SEQ ID NO:4]-x(2)-[DE]

[1] Klenk H.-P., Palm P., Lottspeich F., Zillig W. Proc. Natl. Acad. Sci. U.S.A. 89:407-410(1992).

[2] Thiru A., Hodach M., Eloranta J.J., Kostourou V., Weinzierl R.O., Matthews S.; J. Mol. Biol. 287:753-760(1999).

482. RNA polymerases K / 14 to 18 Kd subunits signature

In eukaryotes, there are three different forms of DNA-dependent RNA polymerases (EC 2.7.7.6) transcribing different sets of genes. Each class of RNA polymerase is an assemblage of ten to twelve different polypeptides. In archaeobacteria, there is generally a single form of RNA polymerase which also consist of an oligomeric assemblage of 10 to 13 polypeptides. A component of 14 to 18 Kd shared by all three forms of eukaryotic RNA polymerases and which has been sequenced in budding yeast (gene RPB6 or RPO26), in fission yeast (gene rpb6 or rpo15), in human and in African swine fever virus [1] is evolutionary related [2] to archaeobacterial subunit K (gene rpoK). The archaeobacterial protein is colinear with the C-terminal part of the eukaryotic subunit.

Consensus pattern: [ST]-x-[FY]-E-x-[AT]-R-x-[LIVM SEQ ID NO:4]-[GSA]-x-R-[SA]-x-Q

[1] Lu Z., Kutish G.F., Sussman M.D., Rock D.L. Nucleic Acids Res. 21:2940-2940(1993).

[2] McKune K., Woychik N.A. J. Bacteriol. 176:4754-4756(1994).

483. RNA polymerases L / 13 to 16 Kd subunits signature

In eukaryotes, there are three different forms of DNA-dependent RNA polymerases (EC 2.7.7.6) transcribing different sets of genes. Each class of RNA polymerase is an assemblage of ten to twelve different polypeptides. In archaeobacteria, there is generally a single form of RNA polymerase which also consist of an oligomeric assemblage of 10 to 13 polypeptides. It has been shown that small subunits of about 13 to 16 Kd found in all three types of eukaryotic polymerases are highly conserved. Subunits known to belong to this family are: - Budding yeast RPC19 subunit from RNA polymerases I and III [1]. - Budding yeast RPB11 subunit from RNA polymerase II [2]. - Mammalian RPB11 (gene POLR2K) from RNA polymerase II. - *Caenorhabditis elegans* hypothetical protein F58A4.9. - *Methanococcus jannaschii* RNA polymerase subunit L (gene rpoL). - *Sulfolobus acidocaldarius* RNA polymerase subunit L (gene rpoL) [3]. As a signature pattern a conserved region was selected which is located at the N-terminal extremity of these polymerase subunits; this region contains two cysteines that could play a role in the binding of a metal ion.

Consensus pattern: [DE](2)-H-[ST]-[LIVM SEQ ID NO:4)]-[GAP]-N-x(11)-V-x-[FM]-x(2)-Y-x(3)- H-P

[1] Dequard-Chablat M., Riva M., Carles C., Sentenac A. J. Biol. Chem. 266:15300-15307(1991).

[2] Woychik N.A., McKune K., Lane W.S., Young R.A. Gene Expr. 3:77-82(1993).

[3] Langer D. EMBL/GenBank: X70805.

484. RNA polymerases N / 8 Kd subunits signature

In eukaryotes, there are three different forms of DNA-dependent RNA polymerases (EC 2.7.7.6) transcribing different sets of genes. Each class of RNA polymerase is an assemblage of ten to twelve different polypeptides. In archaeobacteria, there is generally a single form of RNA polymerase which also consist of an oligomeric assemblage of 10 to 13 polypeptides. Archaeobacterial subunit N (gene rpoN) [1] is a small protein of about 8 Kd, it is evolutionary related [2] to a 8.3 Kd component shared by all three forms of eukaryotic RNA polymerases (gene RPB10 in yeast and POLR2J in mammals) as well as to African swine fever virus protein CP80R [3]. As a signature pattern a conserved region was selected which is located at

the N-terminal extremity of these polymerase subunits; this region contains two cysteines that could play a role in the binding of a metal ion.

Consensus pattern: [LIVMF SEQ ID NO:2)](2)-P-[LIVM SEQ ID NO:4)]-x-C-F-[ST]-C-G-

[1] Langer D., Hain J., Thuriaux P., Zillig W. Proc. Natl. Acad. Sci. U.S.A. 92:5768-5772(1995).

[2] McKune K., Woychik N.A. J. Bacteriol. 176:4754-4756(1994).

[3] Yanez R.J., Rodriguez J.M., Nogal M.L., Yuste L., Enriquez C., Rodriguez J.F., Vinuela E. Virology 208:249-278(1995).

485. Ribonuclease HII

[1] Mian IS; Nucleic Acids Res 1997;25:3187-3189.

486. Ribonuclease PH signature

Prokaryotic ribonuclease PH (EC 2.7.7.56) (RNase PH) [1] is a phosphorolytic exoribonuclease that removes nucleotide residues following the -CCA terminus of tRNA and adds nucleotides to the ends of RNA molecules by using nucleoside diphosphates as substrates. RNase PH is a conserved protein of about 240 amino-acid residues. It is evolutionary related to *Caenorhabditis elegans* hypothetical protein B0564.1. As a signature pattern, the most highly conserved region was selected which is located in the central part of these proteins.

Consensus sequence: C-[DE]-[LIVM SEQ ID NO:4)](2)-Q-[GTA]-D-G-[SG]-x(2)-[TA]-A

[1] Kelly K.O., Deutscher M.P. J. Biol. Chem. 267:17153-17158(1992).

487. RanBP1 domain

[1] Di Matteo G, Fuschi P, Zerfass K, Moretti S, Ricordy R, Cenciarelli C, Tripodi M, Jansen-Durr P, Lavia P; Cell Growth Differ 1995;6:1213-1224.

488. Rhodanese signatures

Rhodanese (thiosulfate sulfurtransferase) (EC 2.8.1.1) [1,2] is an enzyme which catalyzes the transfer of the sulfane atom of thiosulfate to cyanide, to form sulfite and thiocyanate. In vertebrates, rhodanese is a mitochondrial enzyme of about 300 amino-acid residues involved in forming iron-sulfur complexes and cyanide detoxification. A cysteine residue takes part in the catalytic mechanism. Some bacterial proteins closely related to rhodanese are also thought to express a sulfotransferase activity. These are: - *Azotobacter vinelandii* rhdA. - *Escherichia coli* sseA [3]. - *Saccharopolyspora erythraea* cysA [4]. - *Synechococcus* strain PCC 7942 rhdA [5]. RhdA is a periplasmic protein probably involved in the transport of sulfur compounds. Two patterns for the rhodanese family were developed. They are based on highly conserved regions, one which is located in the N-terminal region, the other at the C-terminal extremity of the enzyme.

Consensus pattern: [FY]-x(3)-H-[LIV]-P-G-A-x(2)-[LIVF SEQ ID NO:127])

Consensus pattern: [FY]-[DEAP SEQ ID NO:473)]-G-[SA]-W-x-E-[FYW]

[1] Westley J. Meth. Enzymol. 77:285-291(1981).

[2] Weiland K.L., Dooley T.P. Biochem. J. 275:227-231(1991).

[3] Rudd K.E. Unpublished observations (1993).

[4] Donadio S., Shafiee A., Hutchinson C.R. J. Bacteriol. 172:350-360(1990).

[5] Laudenbach D.E., Ehrhardt D., Green L., Grossman A.R. J. Bacteriol. 173:2751-2760(1991).

489. Ribonuclease III family signature

Prokaryotic ribonuclease III (EC 3.1.26.3) (gene *rnc*) [1] is an enzyme that digests double-stranded RNA. It is involved in the processing of ribosomal RNA precursors and of some mRNAs. RNase III is evolutionary related [2] to the following proteins: - Fission yeast *pac1*, a ribonuclease that probably inhibits mating and meiosis by degrading a specific mRNA required for sexual development. - Yeast ribonuclease III (gene *RNT1*), a dsRNA-specific nuclease that cleaves eukaryotic preribosomal RNA at various sites. - *Caenorhabditis elegans* hypothetical protein F26E4.13. - *Paramecium bursaria* chloroella virus 1 protein A464R. - *Synechocystis* strain PCC 6803 hypothetical protein slr0346. - Fission yeast hypothetical

protein SpAC8A4.08c, a protein with a N-terminal helicase domain and a C-terminal RNase III domain. - *Caenorhabditis elegans* hypothetical protein K12H4.8, a protein with the same structure as SpAC8A4.08c. These proteins share regions of sequence similarity; one of which is a highly conserved stretch of 9 residues which has been developed as a signature pattern.

5

Consensus pattern: [DEQ]-[RQ]-[LM]-E-[FYW]-[LV]-G-D-[SAR]-

[1] Nashimoto H., Uchida H. Mol. Gen. Genet. 201:25-29(1985).

[2] Mian I.S. Nucleic Acids Res. 25:3187-3195(1997).

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490. Rieske iron-sulfur protein signatures

Ubiquinol-cytochrome c reductase (EC 1.10.2.2) (also known as the bc1 complex or complex III) is one of the electron transport chains of mitochondria and of some aerobic prokaryotes;

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it catalyzes the oxidoreduction of ubiquinol and cytochrome c. In the chloroplast of plants and in cyanobacteria plastoquinone-plastocyanin reductase (EC 1.10.99.1) (also known as the b6f complex) is functionally similar and catalyzes the oxidoreduction of plastoquinol and cytochrome f. One of the components of these electron transfer systems is an iron-sulfur protein with a 2Fe-2S cluster, which is called the Rieske protein [1,2]. The Rieske protein

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contains approximately 190 amino acid residues. The iron-sulfur cluster is complexed to the protein through cysteine and histidine residues. Two perfectly conserved regions in Rieske proteins contain all the residues that bind the iron-sulfur cluster. Both regions contain two cysteines and a histidine. The first cysteine and the histidine are 2Fe-2S ligands while the remaining cysteines form a disulfide bond [3]. Two conserved regions were selected as

25

signature patterns.

Consensus pattern: C-[TK]-H-L-G-C-[LIVST SEQ ID NO:474)] [The first C and the H are 2Fe-2S ligands] [The second C is involved in a disulfide bond]

Consensus pattern: C-P-C-H-x-[GSA] [The first C and the H are 2Fe-2S ligands] [The second C is involved in a disulfide bond]

30

[1] Gatti F.L., Meinhardt S.W., Ohnishi T., Tzagoloff A. J. Mol. Biol. 205:421-435(1989).

[2] Kallas T., Spiller S., Malkin R. Proc. Natl. Acad. Sci. U.S.A. 85:5794-5798(1988).

[3] Iwata S., Saynovits M., Link T.A., Michel H. Structure 4:567-579(1996).

491. Ribosomal protein L1 signature

5 Ribosomal protein L1 is the largest protein from the large ribosomal subunit. In *Escherichia coli*, L1 is known to bind to the 23S rRNA. It belongs to a family of ribosomal proteins which, on the basis of sequence similarities [1, 2], groups: - Eubacterial L1. - Algal and plant chloroplast L1. - Cyanelle L1. - Archaeobacterial L1. - Vertebrate L10A. - Yeast SSM1. As a signature pattern, the best conserved region was selected located in the central section of
10 these proteins. It is located at the end of an alpha helix thought to be involved in RNA-binding.

Consensus pattern: [IM]-x(2)-[LIVA SEQ ID NO:219)]-x(2,3)-[LIVM SEQ ID NO:4)]-G-x(2)-[LMS]-[GSNH SEQ ID NO:475)]-[PTKR SEQ ID NO:476)]-[KRAV SEQ ID
15 NO:477)]-G-x-[LIMF SEQ ID NO:421)]-P-[DENSTKQ SEQ ID NO:478)]

[1] Nikonov S.V., Nevskaya N., Eliseikina I.A., Fomenkova N.P., Nikulin A., Ossina N., Garber M., Jonsson B.-H., Briand C., Al-Karadaghi S., Svensson L.A., Aevvarsson A., Liljas A. EMBO J. 15:1350-1359(1996).
20 [2] Olvera J., Wool I.G. 2.3.CO;2-"Biochem. Biophys. Res. Commun. 220:954-957(1996).

492. Ribosomal protein L10 signature

25 Ribosomal protein L10 is one of the proteins from the large ribosomal subunit. L10 is a protein of 162 to 185 amino-acid residues which has only been found so far in eubacteria. A conserved region located in the N-terminal section of these proteins was used as a signature pattern.

Consensus pattern: [DEH]-x(2)-[GS]-[LIVMF SEQ ID NO:2)]-[STN]-[VA]-x-[DEQK SEQ
30 ID NO:479)]-[LIVMA SEQ ID NO:30)]-x(2)- [LIM]-R

493. Ribosomal protein L10e signature

A number of eukaryotic and archaeobacterial ribosomal proteins can be grouped on the basis of sequence similarities. One of these families consists of: - Vertebrate L10 (QM) [1]. - Plant L10. - *Caenorhabditis elegans* L10 (F10B5.1). - Yeast L10 (QSR1). - *Methanococcus jannaschii* MJ0543. These proteins have 174 to 232 amino-acid residues. A conserved region located in the central section was selected as a signature pattern.

Consensus pattern: R-x-A-[FYW]-G-K-[PA]-x-G-x(2)-A-R-V

[1] Chan Y.-L., Diaz J.-J., Denoroy L., Madjar J.-J., Wool I.G. 2.3.CO;2-"Biochem. Biophys. Res. Commun. 255:952-956(1996).

494. Ribosomal protein L11 signature

Ribosomal protein L11 is one of the proteins from the large ribosomal subunit. In *Escherichia coli*, L11 is known to bind directly to the 23S rRNA. It belongs to a family of ribosomal proteins which, on the basis of sequence similarities [1,2], groups:

- Eubacterial L11.
- Plant chloroplast L11 (nuclear-encoded).
- Read algal chloroplast L11.
- Cyanelle L11.
- Archaeobacterial L11.
- Mammalian L12.
- Plants L12.
- Yeast L12 (YL15).

L11 is a protein of 140 to 165 amino-acid residues. A conserved region located in the C-terminal section of these proteins was selected as a signature pattern. In *Escherichia coli*, the C-terminal half of L11 has been shown [3] to be in an extended and loosely folded conformation and is likely to be buried within the ribosomal structure.

Consensus pattern: [RKN]-x-[LIVM SEQ ID NO:4)]-x-G-[ST]-x(2)-[SNQ]-[LIVM SEQ ID NO:4)]-G-x(2)-[LIVM SEQ ID NO:4)]-x(0,1)-[DENG SEQ ID NO:360)]

[1] Pucciarelli G., Remacha M., Ballesta J.P.G.; Nucleic Acids Res. 18:4409-4416(1990).

[2] Otaka E., Hashimoto T., Mizuta K., Suzuki K.; Protein Seq. Data Anal. 5:301-313(1993).

5 [3] Choli T. Biochem. Int. 19:1323-1338(1989).

495. Ribosomal protein L7/L12 C-terminal domain

[1] Leijonmarck M, Liljas A; J Mol Biol 1987;195:555-579.

10

496. Ribosomal protein L13 signature

Ribosomal protein L13 is one of the proteins from the large ribosomal subunit.

In Escherichia coli, L13 is known to be one of the early assembly proteins of

15 the 50S ribosomal subunit. It belongs to a family of ribosomal proteins which, on the basis of sequence similarities [1], groups: - Eubacterial L13.

- Plant chloroplast L13 (nuclear-encoded). - Red algal chloroplast L13.

- Archaeobacterial L13. - Mammalian L13a (Tum P198). - Yeast Rp22 and Rp23.

L11 is a protein of 140 to 250 amino-acid residues. As a signature pattern, a

20 conserved region was selected located in the C-terminal section of these proteins.

Consensus pattern: [LIVM SEQ ID NO:4)]-[KRV]-[GK]-M-[LIV]-[PS]-x(4,5)-[GS]-
[NQEKRA SEQ ID NO:480)]-x(5)-[LIVM SEQ ID NO:4)]-x-[AIV]-[LFY]-x-[GDN]

25

[1] Chan Y.-L., Olvera J., Glueck A., Wool I.G. J. Biol. Chem. 269:5589-5594(1994).

497. Ribosomal protein L13e signature

30 A number of eukaryotic ribosomal proteins can be grouped on the basis of sequence similarities [1]. One of these families consists of:

- Vertebrate L13 (was previously known as Breast Basic Conserved protein 1

(BBC1)). - Drosophila L13. - Plant L13. - Yeast probable L13 (YM9375.11c).

These proteins have 199 to 218 amino-acid residues. As a signature pattern, a stretch of about 16 residues in the first third of these proteins selected.

-Consensus pattern: [KR]-Y-x(2)-K-[LIVM SEQ ID NO:4]-R-[STA]-G-[KR]-G-F-[ST]-L-x-E

[1] Olvera J., Wool I.G. Biochem. Biophys. Res. Commun. 201:102-107(1994).

498. Ribosomal protein L14 signature

Ribosomal protein L14 is one of the proteins from the large ribosomal subunit.

In eubacteria, L14 is known to bind directly to the 23S rRNA. It belongs to a family of ribosomal proteins which, on the basis of sequence similarities [1], groups: - Eubacterial L14. - Algal and plant chloroplast L14. - Cyanelle L14.

- Archaeobacterial L14. - Yeast L17A. - Mammalian L23.
- Caenorhabditis elegans L23 (B0336.10). - Higher eukaryotes mitochondrial L14.
- Yeast mitochondrial Yml38 (gene MRPL38).

L14 is a protein of 119 to 137 amino-acid residues. As a signature pattern, a conserved region located in the C-terminal half of these proteins was selected.

-Consensus pattern: [GA]-[LIV](3)-x(9,10)-[DNS]-G-x(4)-[FY]-x(2)-[NT]-x(2)-V-[LIV]

[1] Otake E., Hashimoto T., Mizuta K., Suzuki K. Protein Seq. Data Anal. 5:301-313(1993).

499. Ribosomal protein L15 signature

Ribosomal protein L15 is one of the proteins from the large ribosomal subunit.

In Escherichia coli, L15 is known to bind the 23S rRNA. It belongs to a family of ribosomal proteins which, on the basis of sequence similarities [1], groups: - Eubacterial L15. - Plant chloroplast L15 (nuclear-encoded).

- Archaeobacterial L15. - Vertebrate L27a. - Tetrahymena thermophila L29.
- Fungi L27a (L29, CRP-1, CYH2).

L15 is a protein of 144 to 154 amino-acid residues. As a signature pattern, a conserved region was selected in the C-terminal section of these proteins.

-Consensus pattern: K-[LIVM SEQ ID NO:4])(2)-[GASL SEQ ID NO:349)]-x-[GT]-x-
5 [LIVMA SEQ ID NO:30)]-x(2,5)-[LIVM SEQ ID NO:4)]-x-[LIVMF SEQ ID NO:2)]-x(3,4)-
[LIVMFCA SEQ ID NO:350)]-[ST]-x(2)-A-x(3)-[LIVM SEQ ID NO:4)]-x(3)-G

[1] Otake E., Hashimoto T., Mizuta K., Suzuki K. Protein Seq. Data Anal. 5:301-
313(1993).

500. Ribosomal protein L15e signature

A number of eukaryotic and archaeobacterial ribosomal proteins can be grouped on the basis of sequence similarities [1]. One of these families consists of:

- 15 - Mammalian L15. - Insect L15. - Plant L15. - Yeast YL10 (L13) (Rp15r).
- Thermoplasma acidophilum L15.

These proteins have about 200 amino acid residues. As a signature pattern, a conserved region was selected located in the central section.

-Consensus pattern: [DE]-[KR]-A-R-x-L-G-[FY]-x-[SAP]-x(2)-G-[LIVMFY SEQ ID
20 NO:18)](4)-R-x-R-
[IV]-x-R-G

[1] Zwickl P., Lupas A., Baumeister W.

Biochem. Biophys. Res. Commun. 209:684-688(1995).

25 501. Ribosomal protein L17 signature

Ribosomal protein L17 is one of the proteins from the large ribosomal subunit. L17 belongs to a family of ribosomal proteins which, on the basis of sequence similarities, groups: - Eubacterial L17.

- 30 - Yeast mitochondrial YmL8 (gene MRPL8).

Eubacterial L17 is a protein of 120 to 130 amino-acid residues. Yeast YmL8 is twice larger (238 residues), the sequence of its N-terminal half is colinear with that of eubacterial L17. As a signature pattern, a conserved region in

the N-terminal section was selected.

-Consensus pattern: I-x-[ST]-[GT]-x(2)-[KR]-x-K-x(6)-[DE]-x-[LIMV SEQ ID NO:34)]-[LIVMT SEQ ID NO:1)]-T-x-[STAG SEQ ID NO:20)]-[KR]

5

502. Ribosomal protein L18e signature

A number of eukaryotic and archaeobacterial ribosomal proteins can be grouped on the basis of sequence similarities. One of these families consists of:

- 10 - Vertebrate L18 (known as L14 in *Xenopus*) [1]. - Plant L18.
- Yeast L18 (Rp28). - *Halobacterium marismortui* H129.
- *Sulfolobus acidocaldarius* H129e.

These proteins have 115 to 187 amino-acid residues., A stretch of about 13 residues in the first third of these proteins has been selected as a signature pattern.

- 15 -Consensus pattern: [KRE]-x-L-x(2)-[PS]-[KR]-x(2)-[RH]-[PSA]-x-[LIVM SEQ ID NO:4)]-[NS]-
[LIVM SEQ ID NO:4)]-x-[RK]-[LIVM SEQ ID NO:4)]
[1] Puder M., Barnard G.F., Staniunas R.J., Steele G.D. Jr., Chen L.B.
Biochim. Biophys. Acta 1216:134-136(1993).

20

503. Ribosomal L18p family

It has been shown that the amino terminal 93 amino acids of Swiss:P09895 are necessary and sufficient to bind 5S rRNA in vitro. The carboxyl-terminal half of the protein, comprising amino acids 151-296, serves to localize the protein to the nucleolus [1].

Number of members: 26

[1]

30 Medline: 96212235

Distinct domains in ribosomal protein L5 mediate 5 S rRNA binding and nucleolar localization.

Michael WM, Dreyfuss G;

J Biol Chem 1996;271:11571-11574.

504. Ribosomal protein L19 signature

5 Ribosomal protein L19 is one of the proteins from the large ribosomal subunit.

In *Escherichia coli*, L19 is known to be located at the 30S-50S ribosomal subunit interface and may play a role in the structure and function of the aminoacyl-tRNA binding site. It belongs to a family of ribosomal proteins which, on the basis of sequence similarities, groups: - Eubacterial L19.

10 - Red algal chloroplast L19. - Cyanelle L19.

L19 is a protein of 120 to 130 amino-acid residues.,

A conserved region in the C-terminal section has been selected as a signature pattern.

-Consensus pattern: [LIVM SEQ ID NO:4)]-x-[KRGTI SEQ ID NO:481)]-x-[GSAI SEQ ID NO:482)]-[KRQDA SEQ ID NO:483)]-[VG]-[RSN]-X(0,1)-[KR]-

15 [SA]-[KY]-[KLI]-[LYS]-Y-[LIM]-R

505. Ribosomal protein L19e signature

A number of eukaryotic and archaeobacterial ribosomal proteins can be grouped

20 on the basis of sequence similarities. One of these families consists of:

- Mammalian ribosomal protein L19 [1]. - *Drosophila* ribosomal protein L19 [2].

- Slime mold (*D. discoideum*) vegetative specific protein V14 [3].

- Yeast ribosomal protein L19 (YL14). - Archeobacterial ribosomal protein L19E.

These proteins have 148 to 203 amino-acid residues.

25 A stretch of about 20 residues in the N-terminal part of these

proteins has been selected as a signature pattern.

-Consensus pattern: Q-[KR]-R-[LIVM SEQ ID NO:4)]-x-[SA]-x(4)-[CV]-G-x(3)-[IV]-[WK]-[LIVF SEQ ID NO:127)]-

[DN]-P

30 [1] Chan Y.-L., Lin A., McNally J., Peleg D., Meyuhas O., Wool I.G.

J. Biol. Chem. 262:1111-1115(1987).[2] Hart K., Klein T., Wilcox M.

Mech. Dev. 43:101-110(1993).[3] Singleton C.K., Manning S.S., Ken R.

Nucleic Acids Res. 17:9679-9692(1989).

506. Ribosomal protein L1e signature (Ribosomal_L4)

A number of eukaryotic and archaeobacterial ribosomal proteins can be grouped on the basis of sequence similarities. One of these families consists [1,2,3, 4] of: - Vertebrate L1 (L4). - Drosophila L1. - Plant L1. - Yeast L2 (Rp2). - Fission yeast L2. - Halobacterium marismortui HmaL4 (HL6). - Methanococcus jannaschii MJ0177.

These proteins have 246 (archaeobacteria) to 427 (human) amino acids. A conserved region in the N-terminal part of these proteins has been selected as a signature pattern.

-Consensus pattern: N-x(3)-[KRM]-x(2)-A-[LIVT SEQ ID NO:165)]-x-S-A-[LIV]-x-A-[ST]-[SGA]-x(7)-[RK]-[GS]-H

[1] Rafti F., Gargiulo G., Manzi A., Malva C., Graziani F.

Nucleic Acids Res. 17:456-456(1989).[2] Presutti C., Villa T., Bozzoni I.

Nucleic Acids Res. 21:3900-3900(1993).

[3] Bagni C., Mariottini P., Annesi F., Amaldi F.

Biochim. Biophys. Acta 1216:475-478(1993).

[3] Arndt E., Kroemer W., Hatakeyama T. J. Biol. Chem. 265:3034-3039(1990).

507. Ribosomal protein L2 signature

Ribosomal protein L2 is one of the proteins from the large ribosomal subunit.

In Escherichia coli, L2 is known to bind to the 23S rRNA and to have peptidyltransferase activity. It belongs to a family of ribosomal proteins which, on the basis of sequence similarities [1,2], groups: - Eubacterial L2.

- Algal and plant chloroplast L2. - Cyanelle L2. - Archaeobacterial L2.

- Plant L2. - Slime mold L2. - Marchantia polymorpha mitochondrial L2.

- Paramecium tetraurelia mitochondrial L2. - Fission yeast K5, K37 and KD4.

- Yeast YL6. - Vertebrate L8.

The best conserved region located in the C-terminal section of these proteins has been selected as a signature pattern.

-Consensus pattern: P-x(2)-R-G-[STAIV SEQ ID NO:130)](2)-x-N-[APK]-x-[DE]

[1] Marty I., Meyer Y.

Nucleic Acids Res. 20:1517-1522(1992).

[2] Otaka E., Hashimoto T., Mizuta K., Suzuki K.

5 Protein Seq. Data Anal. 5:301-313(1993).

508. Ribosomal protein L20 signature

Ribosomal protein L20 is one of the proteins from the large ribosomal subunit.

10 In Escherichia coli, L20 is known to bind directly to the 23S rRNA. It belongs to a family of ribosomal proteins which, on the basis of sequence similarities [1], groups: - Eubacterial L20. - Algal and plant chloroplast L20.

- Cyanelle L20.

15 L20 is a protein of about 120 amino-acid residues. A conserved region located in the central section of these proteins has been selected as a signature pattern.

-Consensus pattern: K-x(3)-[KRC]-x-[LIVM SEQ ID NO:4)]-W-[IV]-[STNALV SEQ ID NO:484)]-R-[LIVM SEQ ID NO:4)]-[NS]-x(3)-[RKHS SEQ ID NO:485)]

[1] Otaka E., Hashimoto T., Mizuta K., Suzuki K.

20 Protein Seq. Data Anal. 5:301-313(1993).

509. Ribosomal protein L21e signature

A number of eukaryotic and archaebacterial ribosomal proteins can be grouped

25 on the basis of sequence similarities. One of these families consists of:

- Mammalian L21 [1]. - Entamoeba histolytica L21 [2].

- Caenorhabditis elegans L21 (C14B9.7). - Yeast L21E (URP1) [3].

- Halobacterium marismortui HL31 [4].

30 These proteins have 160 (eukaryotes) or 95 (archaeobacteria) amino-acid residues. A conserved region in the central part of these proteins has been selected as a signature pattern.

-Consensus pattern: G-[DE]-x-V-x(10)-[GV]-x(2)-[FYH]-x(2)-[FY]-x-G-x-T-G

[1] Devi K.R.G., Chan Y.-L., Wool I.G.

Biochem. Biophys. Res. Commun. 162:364-370(1989).

[2] Petter R., Rozenblatt S., Nuchamowitz Y., Mirelman D.

Mol. Biochem. Parasitol. 56:329-333(1992).

[3] Jank B., Waldherr M., Schweyen R.J. Curr. Genet. 23:15-18(1993).

5 [4] Hatakeyama T., Kimura M. Eur. J. Biochem. 172:703-711(1988).

510. Ribosomal protein L21 signature

Ribosomal protein L21 is one of the proteins from the large ribosomal subunit.

10 In *Escherichia coli*, L21 is known to bind to the 23S rRNA in the presence of L20. It belongs to a family of ribosomal proteins which, on the basis of sequence similarities, groups: - Eubacterial L21.

- *Marchantia polymorpha* chloroplast L21. - *Cyanelle* L21.

- Spinach chloroplast L21 (nuclear-encoded).

15 Eubacterial L21 is a protein of about 100 amino-acid residues, the mature form of the spinach chloroplast L21 has 200 residues. A conserved region located in the C-terminal section of these proteins has been selected as a signature pattern.

-Consensus pattern: [IVT]-x(3)-[KR]-x(3)-[KRQ]-K-x(6)-G-[HF]-R-[RQ]-x(2)-[ST]

20

511. Ribosomal protein L22 signature

Ribosomal protein L22 is one of the proteins from the large ribosomal subunit.

In *Escherichia coli*, L22 is known to bind 23S rRNA. It belongs to a family of ribosomal proteins which, on the basis of sequence similarities [1,2,3],

25 groups: - Eubacterial L22.

- Algal and plant chloroplast L22 (in legumes L22 is encoded in the nucleus instead of the chloroplast). - *Cyanelle* L22. - Archaeobacterial L22.

- Mammalian L17. - Plant L17. - Yeast YL17.

30 A conserved region located in the C- terminal section of these proteins has been selected as a signature pattern.

-Consensus pattern: [RKQN SEQ ID NO:486]-x(4)-[RH]-[GAS]-x-G-[KRQS SEQ ID NO:487])-x(9)-[HDN]-[LIVM SEQ ID NO:4])-x-

[LIVMS SEQ ID NO:429])-x-[LIVM SEQ ID NO:4)]

- [1] Gantt J.S., Baldauf S.L., Calie P.J., Weeden N.F., Palmer J.D.
EMBO J. 10:3073-3078(1991).[2] Madsen L.H., Kreiberg J.D., Gausing K.
Curr. Genet. 19:417-422(1991).
[3] Otake E., Hashimoto T., Mizuta K., Suzuki K.
5 Protein Seq. Data Anal. 5:301-313(1993).

512. Ribosomal protein L23 signature

Ribosomal protein L23 is one of the proteins from the large ribosomal subunit.

- 10 In *Escherichia coli*, L23 is known to bind a specific region on the 23S rRNA;
in yeast, the corresponding protein binds to a homologous site on the 26S rRNA
[1]. It belongs to a family of ribosomal proteins which, on the basis of
sequence similarities [2,3,4], groups: - Eubacterial L23.
- Algal and plant chloroplast L23. - Archaeobacterial L23. - Mammalian L23A.
15 - *Caenorhabditis elegans* L23A (F55D10.2). - Fungi L25.
- Yeast mitochondrial YmL41 (gene MRPL41 or MRP20).

A small conserved region in the C-terminal section of these proteins, which is
probably involved in rRNA-binding has been selected as a signature pattern [2].

- 20 -Consensus pattern: [RK](2)-[AM]-[IVFYT SEQ ID NO:488)]-[IV]-[RKT]-L-[STANEQK
SEQ ID NO:489)]-x(7)-[LIVMFT SEQ ID NO:282)]
[1] El Baradi T.T.A.L., Raue H.A., van de Regt C.H.F., Verbree E.C.,
Planta R.J. EMBO J. 4:210-2107(1985).
[2] Raue H.A., Otake E., Suzuki K. J. Mol. Evol. 28:418-426(1989).
25 [3] Fearon K., Mason T.L. J. Biol. Chem. 267:5162-5170(1992).
[4] Otake E., Hashimoto T., Mizuta K.
Protein Seq. Data Anal. 5:285-300(1993).

30 513. Ribosomal protein L24 signature

Ribosomal protein L24 is one of the proteins from the large ribosomal subunit.

L24 belongs to a family of ribosomal proteins which, on the basis of sequence
similarities, groups: - Eubacterial L24.

458

- Plant chloroplast L24 (nuclear-encoded). - Red algal L24. - Vertebrate L26.
- Yeast L26 (YL33). - Archaeobacterial HmaL24 (HL15).
- A probable ribosomal protein from *Sulfolobus acidocaldarius* [1].

In their mature form, these proteins have 103 to 150 amino-acid residues.

- 5 A conserved stretch of 20 residues in their N-terminal section has been selected as a signature pattern.

-Consensus pattern: [GDEN SEQ ID NO:490)]-D-x-V-x-[IV]-[LIVMA SEQ ID NO:30)]-x-G-x(2)-[KRA]-[GNQ]-x(2,3)-[GA]-x-[IV]

- 10 [1] Ouzounis C., Kyripides N., Sander C.
Nucleic Acids Res. 23:565-570(1995).

514. Ribosomal protein L24e signature

- 15 A number of eukaryotic and archaeobacterial ribosomal proteins can be grouped on the basis of sequence similarities. One of these families consists [1] of:

- Mammalian ribosomal protein L24.
- Yeast ribosomal protein L30A/B (Rp29) (YL21).
- *Kluyveromyces lactis* ribosomal protein L30.
- 20 - *Arabidopsis thaliana* ribosomal protein L24 homolog.
- *Haloarcula marismortui* ribosomal protein HL21/HL22.
- *Methanococcus jannaschii* MJ1201.

These proteins have 60 to 160 amino-acid residues. The most conserved region, which is located in the N-terminal region of these proteins has been selected as a signature pattern.

- 25 -Consensus pattern: [FY]-x-[GSH]-x(2)-[IV]-x-P-G-x-G-x(2)-[FYV]-x-[KRHE SEQ ID NO:491)]-x-D

[1] Chan Y.-L., Olvera J., Wool I.G.

Biochem. Biophys. Res. Commun. 202:1176-1180(1994).

30

515. Ribosomal protein L27 signature

Ribosomal protein L27 is one of the proteins from the large ribosomal subunit.

L27 belongs to a family of ribosomal proteins which, on the basis of sequence

similarities [1,2], groups: - Eubacterial L27.

- Plant chloroplast L27 (nuclear-encoded). - Algal chloroplast L27.

- Yeast mitochondrial YmL2 (gene MRPL2 or MRP7).

The schematic relationship between these groups of proteins is shown below.

5 Eub. L27 NxxxxxxxxAlgal L27 Nxxxxxxxx

Plant L27 ttttNxxxxxxxxxxxxxx

Yeast MRP7 tttNxx

***'t': transit peptide.

'N': N-terminal of mature protein. '*': position of the pattern.

10 -Consensus pattern: G-x-[LIVM SEQ ID NO:4](2)-x-R-Q-R-G-x(5)-G

[1] Elhag G.A., Bourque D.P. Biochemistry 31:6856-6864(1992).

[2] Otake E., Hashimoto T., Mizuta K.

Protein Seq. Data Anal. 5:285-300(1993).

15

516. Ribosomal L28 family

The ribosomal 28 family includes L28 proteins from bacteria

and chloroplasts. The L24 protein from yeast Swiss:P36525

also contains a region of similarity to prokaryotic L28

20 proteins. L24 from yeast is also found in the large

ribosomal subunit

Number of members: 24

25 517. Ribosomal protein L29 signature

Ribosomal protein L29 is one of the proteins from the large ribosomal subunit.

L29 belongs to a family of ribosomal proteins which, on the basis of sequence

similarities [1], groups: - Eubacterial L29. - Red algal L29.

- Archaeobacterial L29. - Mammalian L35 - Caenorhabditis elegans L35 (ZK652.4).

30 - Yeast L35.

L29 is a protein of 63 to 138 amino-acid residues.

A conserved region located in the central section of L29 has been selected as a signature pattern.

-Consensus pattern: [KNQS SEQ ID NO:492)]-[PSTL SEQ ID NO:493)]-x(2)-[LIMFA SEQ ID NO:494)]-[KRGSAN SEQ ID NO:495)]-x-[LIVYSTA SEQ ID NO:496)]-[KR]-[KRHQS SEQ ID NO:497)]-[DESTANRL SEQ ID NO:498)]-[LIV]-A-[KRCQVT SEQ ID NO:499)]-[LIVMA SEQ ID NO:30)]

- 5 [1] Otake E., Hashimoto T., Mizuta K.
Protein Seq. Data Anal. 5:285-300(1993).

518. Ribosomal protein L3 signature

- 10 Ribosomal protein L3 is one of the proteins from the large ribosomal subunit.
In *Escherichia coli*, L3 is known to bind to the 23S rRNA and may participate
in the formation of the peptidyltransferase center of the ribosome. It belongs
to a family of ribosomal proteins which, on the basis of sequence
similarities [1,2,3,4], groups: - Eubacterial L3. - Red algal L3. - Cyanelle L3.
15 - Archaeobacterial *Halobacterium marismortui* HmaL3 (HL1).
- Yeast L3 (also known as trichodermin resistance protein) (gene TCM1).
- *Arabidopsis thaliana* L3 (genes ARP1 and ARP2). - Mammalian L3 (L4).
- Mammalian mitochondrial L3. - Yeast mitochondrial YmL9 (gene MRPL9).
A conserved region located in the central section of these proteins has been selected
20 as a signature pattern.

-Consensus pattern: [FL]-x(6)-[DN]-x(2)-[AGS]-x-[ST]-x-G-[KRH]-G-x(2)-G-x(3)-R

- [1] Arndt E., Kroemer W., Hatakeyama T. J. Biol. Chem. 265:3034-3039(1990).
[2] Graack H.-R., Grohmann L., Kitakawa M., Schaefer K.L., Kruft V.
Eur. J. Biochem. 206:373-380(1992).
25 [3] Herwig S., Kruft V., Wittmann-Liebold B.
Eur. J. Biochem. 207:877-885(1992).
[4] Otake E., Hashimoto T., Mizuta K., Suzuki K.
Protein Seq. Data Anal. 5:301-313(1993).

30

519. Ribosomal protein L30 signature

Ribosomal protein L30 is one of the proteins from the large ribosomal subunit.
L30 belongs to a family of ribosomal proteins which, on the basis of sequence

similarities [1], groups: - Eubacterial L30. - Archaeobacterial L30.

- Drosophila L7. - Slime mold L7. - Mammalian L7. - Fungi L7 (YL8).

- Yeast mitochondrial L33.

L30 from eubacteria are small proteins of about 60 residues, those from
5 archaeobacteria are proteins of about 150 residues. Eukaryotic L7 are proteins
of about 250 to 270 residues. The schematic relationship between the three
groups of proteins is shown below. Eub. L30 NxxxxxxxxxxC

Arc. L30 NxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxC

Euk. L7 NxxC

10 *****': position of the pattern.

The signature pattern for this family of ribosomal proteins spans the
N-terminal half of the region common to all these proteins.

-Consensus pattern: [IVT]-[LIVM SEQ ID NO:4)]-x(2)-[LF]-x-[LI]-x-[KRHQEG SEQ ID
NO:500)]-x(2)-[STNQH SEQ ID NO:501)]-x-

15 [IVT]-x(10)-[LMS]-[LIV]-x(2)-[LIVA SEQ ID NO:219)]-x(2)-[LMFY SEQ ID NO:184)]-
[IVT]

[1] Mizuta K., Hashimoto T., Otake E.

Nucleic Acids Res. 20:1011-1016(1992).

20

520. Ribosomal protein L31 signature

Ribosomal protein L31 is one of the proteins from the large ribosomal subunit.

L31 is a protein of 66 to 97 amino-acid residues which has only been found so
far in eubacteria and in some algal chloroplasts.

25 A conserved region located in the central section of these proteins has been selected as
a signature pattern.

-Consensus pattern: H-P-F-[FY]-[TI]-x(9)-G-R-[AIV]-x-[KRQ]

30 521. Ribosomal protein L31e signature

A number of eukaryotic and archaeobacterial ribosomal proteins can be grouped
on the basis of sequence similarities. One of these families consists of:

- Mammalian L31 [1]. - Chlamydomonas reinhardtii L31. - Yeast L34.

- *Halobacterium marismortui* HL30 [2].

These proteins have 87 to 128 amino-acid residues.

A conserved region, located in the central section has been selected as a signature pattern.

-Consensus pattern: V-[KR]-[LIVM SEQ ID NO:4)]-x(3)-[LIVM SEQ ID NO:4)]-N-x-

[AKH]-x-W-x-[KR]-G

[1] Tanaka T., Kuwano Y., Kuzumaki T., Ishikawa K., Ogata K.

Eur. J. Biochem. 162:45-48(1987).[2] Bergmann U., Arndt E.

Biochim. Biophys. Acta 1050:56-60(1990).

522. Ribosomal protein L33 signature

Ribosomal protein L33 is one of the proteins from the large ribosomal subunit.

In *Escherichia coli*, L33 has been shown to be on the surface of 50S subunit.

L33 belongs to a family of ribosomal proteins which, on the basis of sequence

similarities [1,2,3], groups: - Eubacterial L33.

- Algal and plant chloroplast L33. - Cyanelle L33.

L33 is a small protein of 49 to 66 amino-acid residues. A conserved region located in the central section of L33 has been selected as a signature pattern.

-Consensus pattern: Y-x-[ST]-x-[KR]-[NS]-x(4)-[PATQ SEQ ID NO:502)]-x(1,2)-[LIVM SEQ ID NO:4)]-[EA]-x(2)-

K-[FY]-[CSD]

[1] Kruft V., Kapp U., Wittmann-Liebold B. Biochimie 73:855-860(1991).

[2] Sharp P.M. Gene 139:129-130(1994).

[3] Otake E., Hashimoto T., Mizuta K.

Protein Seq. Data Anal. 5:285-300(1993).

523. Ribosomal protein L34 signature

Ribosomal protein L34 is one of the proteins from the large subunit of the prokaryotic ribosome. It is a small basic protein of 44 to 51 amino-acid residues [1]. L34 belongs to a

family of ribosomal proteins which, on the basis of sequence similarities, groups: -

Eubacterial L34.

- Red algal chloroplast L34. - Cyanelle L34.

A conserved region that corresponds to the N-terminal half of L34 has been selected as a signature pattern.

-Consensus pattern: K-[RG]-T-[FYWL SEQ ID NO:293)]-[EQS]-x(5)-[KRHS SEQ ID NO:503)]-x(4,5)-G-F-x(2)-R

- 5 [1] Old I.G., Margarita D., Saint Girons I.
Nucleic Acids Res. 20:6097-6097(1992).

524. Ribosomal protein L34e signature

10 A number of eukaryotic and archaeobacterial ribosomal proteins can be grouped on the basis of sequence similarities. One of these families consists of:

- Mammalian L34. - Mosquito L31 [1]. - Plant L34 [2].
- Yeast putative ribosomal protein YIL052c. - Methanococcus jannaschii MJ0655.

These proteins have 89 to 129 amino-acid residues.

15 A conserved region located in the N-terminal section of these proteins has been selected as a signature pattern.

-Consensus pattern: Y-x-[ST]-x-S-[NY]-x(5)-[KR]-T-P-G

[1] Lan Q., Niu L.L., Fallon A.M.

Biochim. Biophys. Acta 1218:460-462(1994).

[2] Gao J., Kim S.R., Chung Y.Y., Lee J.M., An G.

20 Plant Mol. Biol. 25:761-770(1994).

525. Ribosomal protein L35Ae signature

25 A number of eukaryotic and archaeobacterial ribosomal proteins can be grouped on the basis of sequence similarities. One of these families consists of:

- Vertebrate L35A. - Caenorhabditis elegans L35A (F10E7.7).
- Yeast L37A/L37B (Rp47). - Pyrococcus woesei L35A homolog [1].

These proteins have 87 to 110 amino-acid residues.

30 A highly conserved stretch of 22 residues in the C-terminal part of these proteins has been selected as a signature pattern.

-Consensus pattern: G-K-[LIVM SEQ ID NO:4)]-x-R-x-H-G-x(2)-G-x-V-x-A-x-F-x(3)-[LI]-P

[1] Ouzounis C., Kyripides N., Sander C.

Nucleic Acids Res. 23:565-570(1995).

526. Ribosomal protein L36 signature

5 Ribosomal protein L36 is the smallest protein from the large subunit of the prokaryotic ribosome. It belongs to a family of ribosomal proteins which, on the basis of sequence similarities [1], groups: - Eubacterial L36. - Algal and plant chloroplast L36. - Cyanelle L36. L36 is a small basic and cysteine-rich protein of 37 amino-acid residues. As a signature pattern, a conserved region that corresponds to positions 11 to 36 in L36 and includes three
10 conserved cysteine residues has been developed.

Consensus pattern: C-x(2)-C-x(2)-[LIVM SEQ ID NO:4)]-x-R-x(3)-[LIVMN SEQ ID NO:382)]-x-[LIVM SEQ ID NO:4)]-x-C-x(3,4)- [KR]-H-x-Q-x-Q-

[1] Otake E., Hashimoto T., Mizuta K. Protein Seq. Data Anal. 5:285-300(1993).

15

527. Ribosomal protein L36e signature

A number of eukaryotic ribosomal proteins can be grouped on the basis of sequence similarities. One of these families consists of: - Mammalian L36 [1].

- Drosophila L36 (M(1)1B). - Caenorhabditis elegans L36 (F37C12.4).

20 - Candida albicans L39. - Yeast YL39.

These proteins have 99 to 104 amino acids.

A conserved region in the central part of these proteins has been selected as a signature pattern.

-Consensus pattern: P-Y-E-[KR]-R-x-[LIVM SEQ ID NO:4)]-[DE]-[LIVM SEQ ID NO:4)](2)-[KR]

25

[1] Chan Y.-L., Paz V., Olvera J., Wool I.G.

Biochem. Biophys. Res. Commun. 192:849-853(1993).

30 528. Ribosomal protein L39e signature

A number of eukaryotic and archaeobacterial ribosomal proteins can be grouped on the basis of sequence similarities. One of these families consists of:

- Mammalian L39 [1]. - Plants L39. - Yeast L46 [2]. - Archeobacterial L39e [3].

465

These proteins are very basic. About 50 residues long, they are the smallest proteins of eukaryotic-type ribosomes. A conserved region in the C-terminal section of these proteins has been selected as a signature pattern.

-Consensus pattern: [KRA]-T-x(3)-[LIVM SEQ ID NO:4)]-[KRQF SEQ ID NO:504)]-x-

5 [NHS]-x(3)-R-[NHY]-W-R-R

[1] Lin A., McNally J., Wool I.G. J. Biol. Chem. 259:487-490(1984).

[2] Leer R.J., van Raamsdonk-Duin M.M.C., Kraakman P., Mager W.H.,
Planta R.J. Nucleic Acids Res. 13:701-709(1985).

[3] Ramirez C., Louie K.A., Matheson A.T. FEBS Lett. 250:416-418(1989).

10

529. Ribosomal L40e family

Bovine L40 has been identified as a secondary RNA binding protein [1]. L40 is fused to a ubiquitin protein [2].

15 Number of members: 27

[1]

Medline: 88203200

RNA binding proteins of the large subunit of bovine
mitochondrial ribosomes.

20 Piatyszek MA, Denslow ND, O'Brien TW;

Nucleic Acids Res 1988;16:2565-2583.

[2]Medline: 96011832

The carboxyl extensions of two rat ubiquitin fusion proteins
are ribosomal proteins S27a and L40.

25 Chan YL, Suzuki K, Wool IG;

Biochem Biophys Res Commun 1995;215:682-690.

530. (Ribosomal L44) Ribosomal protein L44e signature

30 A number of eukaryotic and archaebacterial ribosomal proteins can be grouped
on the basis of sequence similarities. One of these families consists of:

- Mammalian L44 [1]. - Trypanosoma brucei L44.

- Caenorhabditis elegans L44 (C09H10.2). - Fungal L44 (L41).

- *Halobacterium marismortui* LA [2].

These proteins have 92 to 105 amino-acid residues.

A conserved region located in the C-terminal part of these proteins has been selected as a signature pattern.

5 -Consensus pattern: K-x-[TV]-K-K-x(2)-L-[KR]-x(2)-C

[1] Gallagher M.J., Chan Y.-L., Lin A., Wool I.G. DNA 7:269-273(1988).

[2] Bergmann U., Wittmann-Liebold B.

Biochim. Biophys. Acta 1173:195-200(1993)

10

531. Ribosomal protein L5 signature

Ribosomal protein L5 is one of the proteins from the large ribosomal subunit.

In *Escherichia coli*, L5 is known to be involved in binding 5S RNA to the large ribosomal subunit. It belongs to a family of ribosomal proteins which, on the

15 basis of sequence similarities [1,2,3,4], groups: - Eubacterial L5.

- Algal chloroplast L5. - Cyanelle L5. - Archaeobacterial L5. - Mammalian L11.

- *Tetrahymena thermophila* L21. - Slime mold L5 (V18). - Yeast L16 (39A).

- Plants mitochondrial L5.

L5 is a protein of about 180 amino-acid residues.

20 A conserved region, located in the first third of these proteins has been selected as a signature pattern.

-Consensus pattern: [LIVM SEQ ID NO:4)]-x(2)-[LIVM SEQ ID NO:4)]-[STAVC SEQ ID NO:505)]-[GE]-[QV]-x(2)-[LIVMA SEQ ID NO:30)]-x-[STC]-

x-[STAG SEQ ID NO:20)]-[KRH]-x-[STA]

25 [1] Hatakeyama T., Hatakeyama T. Biochim. Biophys. Acta 1039:343-347(1990).

[2] Rosendahl G., Andreassen P.H., Kristiansen K. Gene 98:161-167(1991).

[3] Yang D., Gunther I., Matheson A.T., Auer J., Spicker G., Boeck A.

Biochimie 73:679-682(1991).

[4] Otake E., Hashimoto T., Mizuta K., Suzuki K.

30 Protein Seq. Data Anal. 5:301-313(1993).

532. ribosomal L5P family C-terminus

This region is found associated with Ribosomal_L5.

Number of members: 60

5 533. Ribosomal protein L6 signatures

Ribosomal protein L6 is one of the proteins from the large ribosomal subunit. In *Escherichia coli*, L6 is known to bind directly to the 23S rRNA and is located at the aminoacyl-tRNA binding site of the peptidyltransferase center. It belongs to a family of ribosomal proteins which, on the basis of sequence similarities [1,2,3,4], groups: -

10 Eubacterial L6.

- Algal chloroplast L6.
- Cyanelle L6.
- Archaeobacterial L6.
- *Marchantia polymorpha* mitochondrial L6.
- 15 - Yeast mitochondrial YmL6 (gene MRPL6).
- Mammalian L9.
- *Drosophila* L9.
- Plants L9.
- Yeast L9 (YL11).

20 While all the above proteins are evolutionary related it is very difficult to derive a pattern that will find them all. Two patterns were therefore created, the first to detect eubacterial, cyanelle and mitochondrial L6, the second to detect archaeobacterial L6 as well as eukaryotic L9.

-Consensus pattern: [PS]-[DENS SEQ ID NO:405)]-x-Y-K-[GA]-K-G-[LIVM SEQ ID
25 NO:4)]

-Consensus pattern: Q-x(3)-[LIVM SEQ ID NO:4)]-x(2)-[KR]-x(2)-R-x-F-x-D-G-[LIVM
SEQ ID NO:4)]-Y-[LIVM SEQ ID NO:4)]-x(2)-[KR]

[1] Suzuki K., Olvera J., Wool I.G. *Gene* 93:297-300(1990).

30 [2] Schwank S., Harrer R., Schueller H.-J., Schweizer E. *Curr. Genet.* 24:136-140(1993).

[3] Golden B.L., Ramakrishnan V., White S.W. *EMBO J.* 12:4901-4908(1993).

[4] Otaka E., Hashimoto T., Mizuta K., Suzuki K. *Protein Seq. Data Anal.* 5:301-313(1993).

534. Ribosomal protein L6e signature

A number of eukaryotic and archaeobacterial ribosomal proteins can be grouped on the basis of sequence similarities. One of these families consists of:

- 5 - Mammalian ribosomal protein L6 (L6 was previously known as TAX-responsive enhancer element binding protein 107).
- *Caenorhabditis elegans* ribosomal protein L6 (R151.3).
- Yeast ribosomal protein YL16A/YL16B.
- *Mesembryanthemum crystallinum* ribosomal protein YL16-like.

10 These proteins have 175 (yeast) to 287 (mammalian) amino acids. A highly conserved region in the central part of these proteins has been selected as a signature pattern.

-Consensus pattern: N-x(2)-P-L-R-R-x(4)-[FY]-V-I-A-T-S-x-K

15

535. Ribosomal protein L7Ae signature

A number of eukaryotic and archaeobacterial ribosomal proteins can be grouped on the basis of sequence similarities. One of these families consists of:

- 20 - Vertebrate L7A (SURF3) [1]. - Plant L7A. - Yeast L7A (YL5) (Rp6).
- Yeast protein NHP2 [2]. - Yeast hypothetical protein YEL026w.
- *Bacillus subtilis* hypothetical protein ylxQ. - *Halobacterium marismortui* Hs6.
- *Methanococcus jannaschii* MJ1203.

These proteins have 100 to 265 amino-acid residues.

A conserved region located in the central section has been selected as a signature pattern.

25 -Consensus pattern: [CA]-x(4)-[IV]-P-[FY]-x(2)-[LIVM SEQ ID NO:4]-x-[GSQ]-[KRQ]-x(2)-L-G

[1] Colombo P., Yon J., Garson K., Fried M.

Proc. Natl. Acad. Sci. U.S.A. 89:6358-6362(1992).

[2] Kolodrubetz D., Burgum A. Yeast 7:79-90(1991).

30

536. Ribosomal protein L9 signature

Ribosomal protein L9 is one of the proteins from the large ribosomal subunit.

In *Escherichia coli*, L9 is known to bind directly to the 23S rRNA. It belongs to a family of ribosomal proteins which, on the basis of sequence similarities [1,2], groups: - Eubacterial L9. - Cyanobacterial L9.

- Plant chloroplast L9 (nuclear-encoded). - Red algal chloroplast L9.

- 5 A conserved region, located in the N-terminal section of these proteins has been selected as a signature pattern.

-Consensus pattern: G-x(2)-[GN]-x(4)-V-x(2)-G-[FY]-x(2)-N-[FY]-L-x(5)-[GA]-x(3)-[STN]

[1] Hoffman D.W., Davies C., Gerchman S.E., Kycia J.H., Porter S.J.,

- 10 White S.W., Ramakrishnan V. EMBO J. 13:205-212(1994).

[2] Otaka E., Hashimoto T., Mizuta K., Suzuki K.

Protein Seq. Data Anal. 5:301-313(1993).

15 537. Ribosomal protein S10 signature

Ribosomal protein S10 is one of the proteins from the small ribosomal subunit.

In *Escherichia coli*, S10 is known to be involved in binding tRNA to the ribosomes. It belongs to a family of ribosomal proteins which, on the basis of sequence similarities [1], groups: - Eubacterial S10.

- 20 - Algal chloroplast S10. - Cyanelle S10. - Archaeobacterial S10.
- *Marchantia polymorpha* and *Prototheca wickerhamii* mitochondrial S10.
- *Arabidopsis thaliana* mitochondrial S10 (nuclear encoded). - Vertebrate S20.
- Plant S20. - Yeast URP2.

S10 is a protein of about 100 amino-acid residues.

- 25 A conserved region located in the center of these proteins has been selected as a signature pattern.

-Consensus pattern: [AV]-x(3)-[GDNSR SEQ ID NO:506]-[LIVMSTA SEQ ID NO:433]-x(3)-G-P-[LIVM SEQ ID NO:4]-x-[LIVM SEQ ID NO:4]-P-T

[1] Otaka E., Hashimoto T., Mizuta K.

- 30 Protein Seq. Data Anal. 5:285-300(1993).

538. Ribosomal protein S11 signature

Ribosomal protein S11 [1] plays an essential role in selecting the correct tRNA in protein biosynthesis. It is located on the large lobe of the small ribosomal subunit. S11 belongs to a family of ribosomal proteins which, on the basis of sequence similarities, groups [2]: - Eubacterial S11.

- 5 - Algal and plant chloroplast S11. - Cyanelle S11. - Archaeobacterial S11.
- Marchantia polymorpha and Prototheca wickerhamii mitochondrial S11.
- Acanthamoeba castellanii mitochondrial S11. - Neurospora crassa S14 (crp-2).
- Yeast S14 (RP59 or CRY1).
- Mammalian, Drosophila, Trypanosoma, and plant S14.
- 10 - Caenorhabditis elegans S14 (F37C12.9).

One of the best conserved regions in these proteins was selected as a signature pattern.

-Consensus pattern: [LIVMF SEQ ID NO:2)]-x-[GSTAC SEQ ID NO:99)]-[LIVMF SEQ ID NO:2)]-x(2)-[GSTAL SEQ ID NO:507)]-x(0,1)-[GSN]-

- 15 [LIVMF SEQ ID NO:2)]-x-[LIVM SEQ ID NO:4)]-x(4)-[DEN]-x-T-P-x-[PA]-[STCH SEQ ID NO:508)]-[DN]

[1] Kimura M., Kimura J., Hatakeyama T. FEBS Lett. 240:15-20(1988).

[2] Otake E., Hashimoto T., Mizuta K.

Protein Seq. Data Anal. 5:285-300(1993).

20

539. Ribosomal protein S12 signature

Ribosomal protein S12 is one of the proteins from the small ribosomal subunit.

In Escherichia coli, S12 is known to be involved in the translation initiation

- 25 step. It is a very basic protein of 120 to 150 amino-acid residues. S12 belongs to a family of ribosomal proteins which, on the basis of sequence similarities [1], groups: - Eubacterial S12. - Archaeobacterial S12.

- Algal and plant chloroplast S12. - Cyanelle S12.

- Protozoa and plant mitochondrial S12. - Yeast S28.

- 30 - Drosophila mitochondrial protein tko (Technical KnockOut). - Mammalian S23.

The best conserved regions in these proteins, located in the center of each sequence have been selected as a signature pattern.

-Consensus pattern: [RK]-x-P-N-S-[AR]-x-R

[1] Otaka E., Hashimoto T., Mizuta K.
Protein Seq. Data Anal. 5:285-300(1993).

5 540. Ribosomal protein S12e signature

A number of eukaryotic ribosomal proteins can be grouped on the basis of sequence similarities. One of these families consists of: - Vertebrate S12 [1].

- Trypanosoma brucei S12 [2]. - Caenorhabditis elegans S12 (F54E7.2).

- Drosophila S12. - Yeast S12.

10 These proteins have 130 to 150 amino acids.

A conserved region in the N-terminal part of these proteins has been selected as a signature pattern.

-Consensus pattern: A-L-[KRQP SEQ ID NO:509)]-x-V-L-x(2)-[SA]-x(3)-[DN]-G-L

[1] Lin A., Chan Y.-L., Jones R., Wool I.G.

15 J. Biol. Chem. 262:14343-14351(1987).[2] Marchal C., Ismaili N., Pays E.

Mol. Biochem. Parasitol. 57:331-334(1993).

541. Ribosomal protein S13 signature

20 Ribosomal protein S13 is one of the proteins from the small ribosomal subunit.

In Escherichia coli, S13 is known to be involved in binding fMet-tRNA and, hence, in the initiation of translation. It is a basic protein of 115 to 177

amino-acid residues and belongs to a family of ribosomal proteins which, on the basis of sequence similarities [1,2], groups: - Eubacterial S13.

25 - Plant chloroplast S13 (nuclear encoded). - Red algal chloroplast S13.

- Cyanelle S13. - Archaeobacterial S13. - Plant mitochondrial S13.

- Mammalian and plant S18.

The best conserved regions in these proteins, located in their C-terminal part have been selected as a signature pattern.

30 -Consensus pattern: [KRQS SEQ ID NO:487)]-G-x-R-H-x(2)-[GSNH SEQ ID NO:475)]-x(2)-[LIVMC SEQ ID NO:142)]-R-G-Q

[1] Chan Y.-L., Paz V., Wool I.G.

Biochem. Biophys. Res. Commun. 178:1212-1218(1991).

[2] Otake E., Hashimoto T., Mizuta K.
Protein Seq. Data Anal. 5:285-300(1993).

5 542. Ribosomal protein S14p/S29e (Ribosomal protein S14 signature)

Ribosomal protein S14 is one of the proteins from the small ribosomal subunit. In *Escherichia coli*, S14 is known to be required for the assembly of 30S particles and may also be responsible for determining the conformation of 16S rRNA at the A site. It belongs to a family of ribosomal proteins which, on the basis of sequence similarities [1,2], groups:

- 10 - Eubacterial S14.
- Algal and plant chloroplast S14.
- Cyanelle S14.
- Archaeobacterial *Methanococcus vannielii* S14.
- Plant mitochondrial S14.
- 15 - Yeast mitochondrial MRP2.
- Mammalian S29.
- Yeast YS29A/B.

S14 is a protein of 53 to 115 amino-acid residues. Our signature pattern is based on the few conserved positions located in the center of these proteins.

20 Consensus pattern: [RP]-x(0,1)-C-x(11,12)-[LIVMF SEQ ID NO:2])-x-[LIVMF SEQ ID NO:2)]-[SC]-[RG]-x(3)-[RN]

[1] Chan Y.-L., Suzuki K., Olvera J., Wool I.G. *Nucleic Acids Res.* 21:649-655(1993).

25 [2] Otake E., Hashimoto T., Mizuta K. *Protein Seq. Data Anal.* 5:285-300(1993).

543. Ribosomal protein S15 signature

Ribosomal protein S15 is one of the proteins from the small ribosomal subunit.

- 30 In *Escherichia coli*, this protein binds to 16S ribosomal RNA and functions at early steps in ribosome assembly. It belongs to a family of ribosomal proteins which, on the basis of sequence similarities [1,2], groups:
- Eubacterial S15.
 - Archaeobacterial *Halobacterium marismortui* HmaS15 (HS11).

- Plant chloroplast S15. - Yeast mitochondrial S28. - Mammalian S13.

- *Brugia pahangi* and *Wuchereria bancrofti* S13 (S15). - Yeast S13 (YS15).

S15 is a protein of 80 to 250 amino-acid residues.

A conserved region located in the C-terminal part of these proteins has been

5 selected as a signature pattern.

-Consensus pattern: [LIVM SEQ ID NO:4)]-x(2)-H-[LIVMFY SEQ ID NO:18)]-x(5)-D-
x(2)-[SAGN SEQ ID NO:510)]-x(3)-[LF]-x(9)-

[LIVM SEQ ID NO:4)]-x(2)-[FY]

[1] Dang H., Ellis S.R.

10 Nucleic Acids Res. 18:6895-6901(1990).

[2] Otaka E., Hashimoto T., Mizuta K.

Protein Seq. Data Anal. 5:285-300(1993).

15 544. Ribosomal protein S16 signature

Ribosomal protein S16 is one of the proteins from the small ribosomal subunit. It belongs to a family of ribosomal proteins which, on the basis of sequence similarities [1], groups:

- Eubacterial S16.

20 - Algal and plant chloroplast S16.

- Cyanelle S16.

- *Neurospora crassa* mitochondrial S24 (cyt-21).

S16 is a protein of about 100 amino-acid residues. A conserved region located in the N-terminal extremity of these proteins has been selected as a signature pattern.

25 Consensus pattern: [LIVMT SEQ ID NO:1)]-x-[LIVM SEQ ID NO:4)]-[KR]-L-[STAK SEQ ID NO:331)]-R-x-G-[AKR]

[1] Otaka E., Hashimoto T., Mizuta K. Protein Seq. Data Anal. 5:285-300(1993).

30

545. Ribosomal protein S17 signature

Ribosomal protein S17 is one of the proteins from the small ribosomal subunit.

In *Escherichia coli*, S17 is known to bind specifically to the 5' end of 16S ribosomal RNA and is thought to be involved in the recognition of termination codons. It belongs to a family of ribosomal proteins which, on the basis of sequence similarities [1,2,3], groups: - Eubacterial S17.

- 5 - Plant chloroplast S17 (nuclear encoded). - Red algal chloroplast S17.
- Cyanelle S17. - Archaeobacterial S17. - Mammalian and plant cytoplasmic S11.
- Yeast S18a and S18b (RP41; YS12).

The best conserved regions located in the C-terminal sections of these proteins have been selected as a signature pattern.

- 10 -Consensus pattern: G-D-x-[LIV]-x-[LIVA SEQ ID NO:219)]-x-[QEK]-x-[RK]-P-[LIV]-S
- [1] Gantt J.S., Thompson M.D. J. Biol. Chem. 265:2763-2767(1990).
- [2] Herfurth E., Hirano H., Wittmann-Liebold B.
- Biol. Chem. Hoppe-Seyler 372:955-961(1991).
- [3] Otake E., Hashimoto T., Mizuta K.
- 15 Protein Seq. Data Anal. 5:285-300(1993).

546. Ribosomal protein S17e signature

A number of eukaryotic and archaeobacterial ribosomal proteins can be grouped

- 20 on the basis of sequence similarities. One of these families consists of:

- Vertebrates S17 [1]. - *Drosophila* S17 [2]. - *Neurospora crassa* S17 (crp-3).
- Yeast S17a (RP51A) and S17b (RP51B) [3]. - *Methanococcus jannaschii* MJ0245.

These proteins have from 63 (in archaeobacteria) to 130 to 146 amino acids and are highly conserved. A region in the central part of these proteins has been selected

- 25 as a signature.

-Consensus pattern: A-x-I-x-[ST]-K-x-L-R-N-[KR]-I-A-G-[FY]-x-T-H

- [1] Chen I.-T., Roufa D.J. Gene 70:107-116(1988).
- [2] Maki C., Rhoads D.D., Stewart M.J., van Slyke B., Denell R.E.,
- Roufa D.J. Gene 79:289-298(1989).[3] Abovich N., Rosbash M.
- 30 Mol. Cell. Biol. 4:1871-1879(1984).

547. Ribosomal protein S18 signature

Ribosomal protein S18 is one of the proteins from the small ribosomal subunit. In *Escherichia coli*, S18 has been involved in aminoacyl-tRNA binding[1]. It appears to be situated at the tRNA A-site of the ribosome. It belongs to a family of ribosomal proteins which, on the basis of sequence similarities[2], groups: - Eubacterial S18. - Algal and plant chloroplast S18. - Cyanelle S18. As a signature pattern, a conserved region in the central section of the protein has been selected. This region contains two basic residues which may be involved in RNA-binding.-

Consensus pattern: [IV]-[DY]-Y-x(2)-[LIVMT SEQ ID NO:1)]-x(2)-[LIVM SEQ ID NO:4)]-x(2)-[FYT]-[LIVM SEQ ID NO:4)]- [ST]-[DERP SEQ ID NO:511)]-x-[GY]-K-[LIVM SEQ ID NO:4)]-x(3)-R-[LIVMAS SEQ ID NO:512)]-

[1] McDougall J., Choli T., Kruft V., Kapp U., Wittmann-Liebold B. FEBS Lett. 245:253-260(1989).[2] Otake E., Hashimoto T., Mizuta K. Protein Seq. Data Anal. 5:285-300(1993).

548. Ribosomal protein S19 signature

Ribosomal protein S19 is one of the proteins from the small ribosomal subunit. In *Escherichia coli*, S19 is known to form a complex with S13 that binds strongly to 16S ribosomal RNA. S19 belongs to a family of ribosomal proteins which, on the basis of sequence similarities [1,2], groups: - Eubacterial S19. - Algal and plant chloroplast S19. - Cyanelle S19. - Archaeobacterial S19. - Plant mitochondrial S19. - Eukaryotic S15 ('rig' protein). S19 is a protein of 88 to 144 amino-acid residues. Our signature pattern is based on the few conserved positions located in the C-terminal section of these proteins.

-Consensus pattern: [STDNQ SEQ ID NO:513)]-G-[KRQM SEQ ID NO:514)]-x(6)-[LIVM SEQ ID NO:4)]-x(4)-[LIVM SEQ ID NO:4)]-[GSD]-x(2)-[LF]-[GAS]-[DE]-F-x(2)-[ST]

[1] Kitagawa M., Takasawa S., Kikuchi N., Itoh T., Teraoka H., Yamamoto H., Okamoto H. FEBS Lett. 283:210-214(1991).

[2] Otake E., Hashimoto T., Mizuta K. Protein Seq. Data Anal. 5:285-300(1993).

549. Ribosomal protein S19e signature

A number of eukaryotic and archaeobacterial ribosomal proteins can be grouped on the basis of sequence similarities [1,2]. One of these families consists of: - Mammalian S19. - Drosophila S19.

- 5 - Ascaris lumbricoides S19g (ALEP-1) and S19s. - Yeast YS16 (RP55A and RP55B).
- Aspergillus S16. - Halobacterium marismortui HS12.

These proteins have 143 to 155 amino acids.

A well conserved stretch of 20 residues in the C-terminal part of these proteins has been selected as a signature pattern.

- 10 -Consensus pattern: P-x(6)-[SAN]-x(2)-[LIVMA SEQ ID NO:30)]-x-R-x-[ALIV SEQ ID NO:199)]-[LV]-Q-x-L-[EQ]

[1] Etter A., Aboutanos M., Tobler H., Mueller F.

Proc. Natl. Acad. Sci. U.S.A. 88:1593-1596(1991).

[2] Suzuki K., Olvera J., Wool I.G. Biochimie 72:299-302(1990).

15

550. Ribosomal protein S2 signatures

Ribosomal protein S2 is one of the proteins from the small ribosomal subunit.

- 20 S2 belongs to a family of ribosomal proteins which, on the basis of sequence similarities [1,2], groups: - Eubacterial S2. - Algal and plant chloroplast S2.

- Cyanelle S2. - Archaeobacterial S2.

- Higher eukaryotes P40 (previously thought to be a laminin receptor).

- Yeast NAB1. - Plant mitochondrial S2. - Yeast mitochondrial MRP4.

S2 is a protein of 235 to 394 amino-acid residues.

- 25 Two conserved regions have been selected as signature patterns. One is located in the N-terminal section and the other in the central section.

-Consensus pattern: [LIVMFA SEQ ID NO:81)]-x(2)-[LIVMFYC SEQ ID NO:6)](2)-x-[STAC SEQ ID NO:204)]-[GSTANQEKR SEQ ID NO:515)]-[STALV SEQ ID NO:516)]-[HY]-[LIVMF SEQ ID NO:2)]-G

- 30 -Consensus pattern: P-x(2)-[LIVMF SEQ ID NO:2)](2)-[LIVMS SEQ ID NO:429)]-x-[GDN]-x(3)-[DENL SEQ ID NO:517)]-x(3)-[LIVM SEQ ID NO:4)]-x-E-x(4)-[GNQKRH SEQ ID NO:518)]-[LIVM SEQ ID NO:4)]-[AP]

[1] Davis S.C., Tzagoloff A., Ellis S.R.

J. Biol. Chem. 267:5508-5514(1992).

[2] Tohgo A., Takasawa S., Munakata H., Yonekura H., Hayashi N., Okamoto H.
FEBS Lett. 340:133-138(1994).

5

551. Ribosomal protein S21 signature

Ribosomal protein S21 is one of the proteins from the small ribosomal subunit. So far S21 has only been found in eubacteria. It is a protein of 55 to 70 amino-acid residues. A conserved region in the N-terminal section of the protein has been selected as a signature pattern.

10

Consensus pattern: [DE]-x-A-[LIY]-[KR]-R-F-K-[KR]-x(3)-[KR]

552. Ribosomal protein S21e signature

15 A number of eukaryotic ribosomal proteins can be grouped on the basis of sequence similarities. One of these families consists of: - Mammalian S21 [1].
- Caenorhabditis elegans S21 (F37C12.11). - Rice S21 [2].
- Yeast S21 (Ys25) [3]. - Fission yeast S28 [4].

These proteins have 82 to 87 amino acids.

20 A perfectly conserved nonapeptide in the N-terminal part of these proteins has been selected as a signature pattern.

-Consensus pattern: L-Y-V-P-R-K-C-S-[SA]

[1] Bhat K.S., Morrison S.G. Nucleic Acids Res. 21:2939-2939(1993).

[2] Nishi R., Hashimoto H., Uchimiya H., Kato A.

25 Biochim. Biophys. Acta 1216:113-114(1993).[3] Suzuki K., Otaka E.
Nucleic Acids Res. 16:6223-6223(1988).[4] Itoh T., Okata E., Matsui K.A.
Biochemistry 24:7418-7423(1985).

30 553. Ribosomal protein S24e signature

A number of eukaryotic and archaeobacterial ribosomal proteins can be grouped on the basis of sequence similarities. One of these families consists of:

- Vertebrate S24 [1]. - Yeast Rp50. - Mucor racemosus S24 [2].

- *Halobacterium marismortui* HS15 [3]. - *Methanococcus jannaschii* MJ0394.

These proteins have 101 to 148 amino acids.

A well conserved stretch in the central part of these proteins has been selected as a signature pattern.

5 -Consensus pattern: [FYA]-G-x(2)-[KR]-[STA]-x-G-[FY]-[GA]-x-[LIVM SEQ ID NO:4)]-Y-[DN]-[SDN]

[1] Brown S.J., Jewell A., Maki C.G., Roufa D.J. Gene 91:293-296(1990).

[2] Sosa L., Fonzi W.A., Sypherd P.S.

10 Nucleic Acids Res. 17:9319-9331(1989).[3] Kimura J., Arndt E., Kimura M. FEBS Lett. 224:65-70(1987).

554. Ribosomal protein S26e signature

15 A number of eukaryotic ribosomal proteins can be grouped on the basis of sequence similarities. One of these families consists of: - Mammalian S26 [1]. - Octopus S26 [2]. - *Drosophila* S26 (DS31) [3]. - Plant cytoplasmic S26. - Fungi S26 [4].

These proteins have 114 to 127 amino acids.

20 A conserved octapeptide in the central part of these proteins has been selected as a signature pattern.

-Consensus pattern: [YH]-C-V-S-C-A-I-H

[1] Kuwano Y., Nakanishi O., Nabeshima Y., Tanaka T., Ogata K.

J. Biochem. 97:983-992(1985).[2] Zinov'eva R.D., Tomarev S.I.

25 Dokl. Akad. Nauk SSSR 304:464-469(1989).

[3] Itoh N., Ohta K., Ohta M., Kawasaki T., Yamashina I.

Nucleic Acids Res. 17:2121-2121(1989).[4] Wu M., Tan H.

Gene 150:401-402(1994).

30

555. Ribosomal protein S28e signature

A number of eukaryotic and archaeobacterial ribosomal proteins can be grouped on the basis of sequence similarities. One of these families consists of:

- Mammalian S28 [1]. - Plant S28 [2]. - Fungi S33 [3].
- *Methanococcus jannaschii* MJ1202.

These proteins have from 64 to 78 amino acids.

A highly conserved nonapeptide from the C-terminal extremity of these proteins has been selected as a signature pattern.

-Consensus pattern: E-[ST]-E-R-E-A-R-x-L

[1] Chan Y.-L., Olvera J., Wool I.G.

Biochem. Biophys. Res. Commun. 179:314-318(1991).

[2] Hwang I., Goodman H.M. Plant Physiol. 102:1357-1358(1993).

[3] Hoekstra R., Ferreira P.M., Bootsman T.C., Mager W.H., Planta R.J.
Yeast 8:949-959(1992).

556. Ribosomal protein S3Ae signature

A number of eukaryotic and archaebacterial ribosomal proteins can be grouped on the basis of sequence similarities. One of these families consists of:

- Mammalian S3A (was originally known as v-fos transformation effector protein). - *Caenorhabditis elegans* S3A (F56F3.5).
- Plant cytoplasmic S3A (CYC07) [1]. - Yeast Rp10 (PLC1 and PLC2).
- Fission yeast Rp10 (SpAC13G6.02c). - *Methanococcus jannaschii* MJ0980.

These proteins have from 220 to 250 amino acids.

A conserved stretch in their N-terminal section was selected as a signature pattern.

-Consensus pattern: [LIV]-x-[GH]-R-[IV]-x-E-x-[SC]-L-x-D-L

[1] Liu J.H., Reid D.M.

Plant Physiol. 109:338-338(1995).

557. Ribosomal protein S3 signature

Ribosomal protein S3 is one of the proteins from the small ribosomal subunit.

In *Escherichia coli*, S3 is known to be involved in the binding of initiator Met-tRNA. It belongs to a family of ribosomal proteins which, on the basis of sequence similarities [1], groups: - Eubacterial S3.

- Algal and plant chloroplast S3. - Cyanelle S3. - Archaebacterial S3.

- Plant mitochondrial S3. - Vertebrate S3. - Insect S3.
- *Caenorhabditis elegans* S3 (C23G10.3). - Yeast S3 (Rp13).

S3 is a protein of 209 to 559 amino-acid residues.

A conserved region located in the C-terminal section has been selected as a signature pattern.

- 5 -Consensus pattern: [GSTA SEQ ID NO:19)]-[KR]-x(6)-G-x-[LIVMT SEQ ID NO:1)]-x(2)-[NQSCH SEQ ID NO:519)]-x(1,3)-[LIVFCA SEQ ID NO:520)]-x(3)-[LIV]-[DENQ SEQ ID NO:371)]-x(7)-[LMT]-x(2)-G-x(2)-G

[1] Otake E., Hashimoto T., Mizuta K.

Protein Seq. Data Anal. 5:285-300(1993).

10

558. Ribosomal protein S4 signature

Ribosomal protein S4 is one of the proteins from the small ribosomal subunit.

In *Escherichia coli*, S4 is known to bind directly to 16S ribosomal RNA.

- 15 Mutations in S4 have been shown to increase translational error frequencies.

It belongs to a family of ribosomal proteins which, on the basis of sequence similarities [1,2], groups:

- Eubacterial S4. - Algal and plant chloroplast S4.
- Cyanelle S4. - Archaeobacterial S4. - Mammalian S9. - Yeast YS11 (SUP45).
- *Marchantia polymorpha* mitochondrial S4. - *Dictyostelium discoideum* rp1024.

- 20 - Yeast protein NAM9 [3]. NAM9 has been characterized as a suppressor for ochre mutations in mitochondrial DNA. It could be a ribosomal protein that acts as a suppressor by decreasing translation accuracy.

S4 is a protein of 171 to 205 amino-acid residues (except for NAM9 which is much larger). The signature pattern for this protein is based on a conserved

- 25 region located in the central section of these proteins.

-Consensus pattern: [LIVM SEQ ID NO:4)]-[DE]-x-R-[LI]-x(3)-[LIVMC SEQ ID NO:142)]-[VMFYHQ SEQ ID NO:521)]-[KRT]-x(3)-

[STAGCVF SEQ ID NO:522)]-x-[ST]-x(3)-[SAI]-[KR]-x-[LIVMF SEQ ID NO:2)](2)

[1] Mizuta K., Hashimoto T., Suzuki K.I., Otake E.

- 30 Nucleic Acids Res. 19:2603-2608(1991).

[2] Otake E., Hashimoto T., Mizuta K.

Protein Seq. Data Anal. 5:285-300(1993).

[3] Boguta M., Dmochowska A., Borsuk P., Wrobel K., Gargouri A., Lazowska J.,

Slonimski P., Szczesniak B., Kruszewska A.

Mol. Cell. Biol. 12:402-412(1992).

5 559. Ribosomal protein S4e signature

A number of eukaryotic and archaeobacterial ribosomal proteins can be grouped on the basis of sequence similarities. One of these families consists of:

- Mammalian S4 [1]. Two highly similar isoforms of this protein exist : one coded by a gene on chromosome Y, and the other on chromosome X.

10 - Plant cytoplasmic S4 [2] - Yeast S7 (YS6). - Archeobacterial S4e.

These proteins have 233 to 264 amino acids.

A highly conserved stretch of 15 residues in their N-terminal section has been selected as a signature pattern. Four positions in this region are positively charged residues.

15 -Consensus pattern: H-x-K-R-[LIVMF SEQ ID NO:2)]-[SANK SEQ ID NO:523)]-x-P-x(2)-[WY]-x-[LIVM SEQ ID NO:4)]-x-[KRP]

[1] Fisher E.M., Beer-Romero P., Brown L.G., Ridley A., McNeil J.A., Lawrence J.B., Willard H.F., Bieber F.R., Page D.C.
Cell 63:1205-1218(1990).

20 [2] Braun H.P., Emmermann M., Mentzel H., Schmitz U.K.
Biochim. Biophys. Acta 1218:435-438(1994).

560. Ribosomal protein S5 signature

25 Ribosomal protein S5 is one of the proteins from the small ribosomal subunit. In Escherichia coli, S5 is known to be important in the assembly and function of the 30S ribosomal subunit. Mutations in S5 have been shown to increase translational error frequencies. It belongs to a family of ribosomal proteins which, on the basis of sequence similarities [1,2], groups: - Eubacterial S5.

30 - Cyanelle S5. - Red algal chloroplast S5. - Archaeobacterial S5.

- Mammalian S2 (LLrep3). - Caenorhabditis elegans S2 (C49H3.11).

- Drosophila S2. - Plant S2. - Yeast S4 (SUP44). - Fungi mitochondrial S5.

S5 is a protein of 166 to 254 amino-acid residues. The signature pattern for

this protein is based on a conserved region, rich in glycine residues, and located in the N-terminal section of these proteins.

-Consensus pattern: G-[KRQ]-x(3)-[FY]-x-[ACV]-x(2)-[LIVMA SEQ ID NO:30)]-[LIVM SEQ ID NO:4)]-[AG]-[DN]-

5 x(2)-G-x-[LIVM SEQ ID NO:4)]-G-x-[SAG]-x(5,6)-[DEQ]-[LIVMA SEQ ID NO:30)]-x(2)-A-[LIVMF SEQ ID NO:2)]

[1] All-Robyn J.A., Brown N., Otaka E., Liebman S.W.

Mol. Cell. Biol. 10:6544-6553(1990).[2] Otaka E., Hashimoto T., Mizuta K.

10 Protein Seq. Data Anal. 5:285-300(1993).

561. Ribosomal protein S6 signature

Ribosomal protein S6 is one of the proteins from the small ribosomal subunit.

15 In *Escherichia coli*, S6 is known to bind together with S18 to 16S ribosomal RNA. It belongs to a family of ribosomal proteins which, on the basis of sequence similarities, groups: - Eubacterial S6. - Red algal chloroplast S6. - Cyanelle S6.

S6 is a protein of 95 to 208 amino-acid residues. The signature pattern for
20 this protein is based on a conserved region located in the N-terminal section of these proteins.

-Consensus pattern: G-x-[KRC]-[DENQRH SEQ ID NO:524)]-L-[SA]-Y-x-I-[KRNSA SEQ ID NO:525)]

25

562. Ribosomal protein S6e signature

A number of eukaryotic and archaeobacterial ribosomal proteins can be grouped on the basis of sequence similarities. One of these families consists of:

- Mammalian S6 [1]. - *Drosophila* S6 [2]. - Plant S6 [3]. - Yeast S10 (YS4).
30 - *Halobacterium marismortui* HS13 [4]. - *Methanococcus jannaschii* MJ1260.

S6 is the major substrate of protein kinases in eukaryotic ribosomes [5]; it may have an important role in controlling cell growth and proliferation through the selective translation of particular classes of mRNA.

These proteins have 135 to 249 amino acids.

A conserved stretch of 12 residues in the N-terminal part of these proteins has been selected as a signature pattern.

-Consensus pattern: [LIVM SEQ ID NO:4)]-[STAMR SEQ ID NO:526)]-G-G-x-D-x(2)-G-x-

5 -P-M

[1] Franco R., Rosenfeld M.G. J. Biol. Chem. 265:4321-4325(1990).

[2] Watson K.L., Konrad K.D., Woods D.F., Bryant P.J.

Proc. Natl. Acad. Sci. U.S.A. 89:11302-11306(1992).

[3] Hansen G., Estruch J.J., Spena A.

10 Nucleic Acids Res. 20:5230-5230(1992).

[4] Kimura M., Arndt E., Hatakeyama T., Hatakeyama T., Kimura J.

Can. J. Microbiol. 35:195-199(1989).

[5] Bandi H.R., Ferrari S., Krieg J., Meyer H.E., Thomas G.

J. Biol. Chem. 268:4530-4533(1993).

15

563. Ribosomal protein S7 signature

Ribosomal protein S7 is one of the proteins from the small ribosomal subunit.

In *Escherichia coli*, S7 is known to bind directly to part of the 3'end of 16S

20 ribosomal RNA. It belongs to a family of ribosomal proteins which, on the basis of sequence similarities [1,2,3], groups: - Eubacterial S7.

- Algal and plant chloroplast S7. - Cyanelle S7. - Archaeobacterial S7.

- Plant mitochondrial S7 - Mammalian S5. - Plant S5.

- *Caenorhabditis elegans* S5 (T05E11.1).

25 The best conserved region located in the N-terminal section of these proteins has been selected as a signature pattern.

-Consensus pattern: [DENSK SEQ ID NO:527)]-x-[LIVMDET SEQ ID NO:528)]-x(3)-

[LIVMFTA SEQ ID NO:386)](2)-x(6)-G-K-[KR]-x(5)-

[LIVMF SEQ ID NO:2)]-[LIVMFC SEQ ID NO:90)]-x(2)-[STAC SEQ ID NO:204)]

30 [1] Klussmann S., Franke P., Bergmann U., Kostka S., Wittmann-Liebold B.

Biol. Chem. Hoppe-Seyler 374:305-312(1993).

[2] Otaka E., Hashimoto T., Mizuta K.

Protein Seq. Data Anal. 5:285-300(1993).

[3] Ignatovich O., Cooper M., Kulesza H.M., Beggs J.D.
Nucleic Acids Res. 23:4616-4619(1995).

5 564. Ribosomal protein S7e signature

A number of eukaryotic ribosomal proteins can be grouped on the basis of sequence similarities [1]. One of these families consists of:

- Mammalian S7.
- Xenopus S8.
- 10 - Insect S7.
- Yeast probable ribosomal protein S7 (N2212).
- Fission yeast probable ribosomal protein S7 (SpAC18G6.13c).

These proteins have about 200 amino acids. A highly conserved stretch of 14 residues which is located in the central section and which is rich in charged residues was selected as a
15 signature pattern.

Consensus pattern: [KR]-L-x-R-E-L-E-K-K-F-[SAP]-x-[KR]-H

[1] Salazar C.E., Mills-Hamm D.M., Kumar V., Collins F.H. Nucleic Acids Res. 21:4147-
20 4147(1993).

565. Ribosomal protein S8 signature

Ribosomal protein S8 is one of the proteins from the small ribosomal subunit.

- 25 In *Escherichia coli*, S8 is known to bind directly to 16S ribosomal RNA. It belongs to a family of ribosomal proteins which, on the basis of sequence similarities [1], groups:
- Eubacterial S8. - Algal and plant chloroplast S8.
 - Cyanelle S8. - Archaeobacterial S8. - *Marchantia polymorpha* mitochondrial S8.
 - Mammalian S15A. - Plant S15A. - Yeast S22 (S24).

30 The best conserved region located in the C-terminal section of these proteins has been selected as a signature pattern.

-Consensus pattern: [GE]-x(2)-[LIV](2)-[STY]-[ST]-x(2)-G-[LIVM SEQ ID NO:4)](2)-x(4)-
[AG]-

[KRHAYI SEQ ID NO:529)]

[1] Otaka E., Hashimoto T., Mizuta K.

Protein Seq. Data Anal. 5:285-300(1993).

5

566. Ribosomal protein S8e signature

A number of eukaryotic and archaeobacterial ribosomal proteins can be grouped on the basis of sequence similarities [1]. One of these families consists of:

- Mammalian S8. - *Caenorhabditis elegans* S8 (F42C5.8). - *Leishmania major* S8.
- 10 - Plant S8. - Yeast S8 (S14) (Rp19). - Archeobacterial S8e.

These proteins have either about 220 amino acids (in eukaryotes) or about 125 amino acids (in archeobacteria). A conserved stretch which is located in the N-terminal section and which is rich in positively charged residues has been selected as a signature pattern.

15 -Consensus pattern: [KR]-x(2)-[ST]-G-[GA]-x(5)-[HR]-[KG]-[KR]-x-K-x-E-[LM]-G

[1] Engemann S., Herfurth E., Briesemeister U., Wittmann-Liebold B.

J. Protein Chem. 14:189-195(1995).

20 567. Ribosomal protein S9 signature

Ribosomal protein S9 is one of the proteins from the small ribosomal subunit.

It belongs to a family of ribosomal proteins which, on the basis of sequence similarities [1,2], groups: - Eubacterial S9. - Algal chloroplast S9.

- Cyanelle S9. - Archaeobacterial S9. - Mammalian S16. - Plant S16.
- 25 - Yeast mitochondrial ribosomal S9.

A conserved region containing many charged residues and located in the central section of these proteins has been selected as a signature pattern.

-Consensus pattern: G-G-G-x(2)-[GSA]-Q-x(2)-[SA]-x(3)-[GSA]-x-[GSTAV SEQ ID NO:420)]-[KR]-

30 [GSAL SEQ ID NO:530)]-[LIF]

[1] Chan Y.-L., Paz V., Olvera J., Wool I.G. FEBS Lett. 263:85-88(1990).

[2] Otaka E., Hashimoto T., Mizuta K.

Protein Seq. Data Anal. 5:285-300(1993).

568. Ribulose-phosphate 3-epimerase family signatures

Ribulose-phosphate 3-epimerase (EC 5.1.3.1) (also known as pentose-5-phosphate

5 3-epimerase or PPE) is the enzyme that converts D-ribulose 5-phosphate into
D-xylulose 5-phosphate in Calvin's reductive pentose phosphate cycle. In
Alcaligenes eutrophus two copies of the gene coding for PPE are known [1],
one is chromosomally encoded (cbbEC), the other one is on a plasmid (cbbEP).
PPE has been found in a wide range of bacteria, archebacteria, fungi and
10 plants. The sequence of PPE is highly related to:

- Escherichia coli D-allulose-6-phosphate 3-epimerase (gene alsE).
- Escherichia coli protein sgcE.
- Mycoplasma genitalium hypothetical protein MG112.

All these proteins have from 209 to 241 amino acid residues.

15 Two conserved regions which are located respectively in the N-terminal and in the
central part of these proteins have been selected as signature patterns.

-Consensus pattern: [LIVMF SEQ ID NO:2)]-H-[LIVMFY SEQ ID NO:18)]-D-[LIVM SEQ
ID NO:4)]-x-D-x(1,2)-[FY]-[LIVM SEQ ID NO:4)]-x-N-x-
[STAV SEQ ID NO:105)]

20 -Consensus pattern: [LIVMA SEQ ID NO:30)]-x-[LIVM SEQ ID NO:4)]-M-[ST]-[VS]-x-P-
x(3)-G-Q-x-F-x(6)-[NK]-
[LIVMC SEQ ID NO:142)]

[1] Kusian B., Yoo J.G., Bednarski R., Bowien B.

J. Bacteriol. 174:7337-7344(1992).

25

569. (Ricin B lectin) Similarity to lectin domain of ricin beta-chain, 3 copies.

This family consists of a triplicated domain involved in

30 cell agglutination in ricin.

570. (Rotamase) PpiC-type peptidyl-prolyl cis-trans isomerase signature

Peptidyl-prolyl cis-trans isomerase (EC 5.2.1.8) (PPIase or rotamase) is an enzyme that accelerates protein folding by catalyzing the cis-trans isomerization of proline imidic peptide bonds in oligopeptides [1]. Most characterized PPIases belong to two families, the cyclophilin-type (see <PDOC00154>) and the FKBP-type (see <PDOC00426>). Recently a third family has been discovered [2,3]. So far, the only biochemically characterized member of this family is the *Escherichia coli* protein parvulin (gene *ppiC*), a small (92 residues) cytoplasmic enzyme that prefers amino acid residues with hydrophobic side chains like leucine and phenylalanine in the P1 position of the peptides substrates. *PpiC* is evolutionary related to a number of proteins that are also probably PPIases:

- *Escherichia coli* and *Haemophilus influenzae* *ppiD*. *PpiD* is a PPIase which contains a periplasmic *ppiC*-like domain anchored to the inner membrane and which seems to be involved in the folding of outer membrane proteins.
- *Escherichia coli* *surA*. *SurA* is a periplasmic protein that contains two *ppiC*-like domains.
- Nitrogen-assimilating bacteria protein *nifM* which is involved in the activation and stabilization of the iron-component (*nifH*) of nitrogenase.
- *Bacillus subtilis* protein *prsA*, a membrane-bound lipoprotein involved in protein export.
- *Lactococcus* and *Lactobacillus* protease maturation protein *prtM*, a membrane-bound lipoprotein involved in the maturation of a secreted serine proteinase.
- Yeast protein *ESS1/PTF1* (processing/termination factor 1).
- *Drosophila* protein *dodo* (gene *dod*).
- Mammalian protein *PIN1*,
- *Campylobacter jejuni* cell binding factor 2 (*CBF2*), a secreted antigen.
- *Bacillus subtilis* hypothetical protein *yacD*.
- *Helicobacter pylori* hypothetical protein *HP0175*.
- A hypothetical slime mold protein.

A conserved region that contains a serine which could play a role in the catalytic mechanism of these enzymes has been selected as a signature pattern.

-Consensus pattern: F-[GSADEI SEQ ID NO:531)]-x-[LVAQ SEQ ID NO:532)]-A-x(3)-[ST]-x(3,4)-[STQ]-x(3,5)-[GER]-G-x-[LIVM SEQ ID NO:4)]-[GS]

[1] Fischer G., Schmid F.X.

Biochemistry 29:2205-2212(1990).

[2] Rudd K.E., Sofia H.J., Koonin E.V., Plunkett G. III, Lazar S.,

Rouviere P.E. Trends Biochem. Sci. 20:14-15(1995).

5 [3] Rahfeld J.-U., Ruecknagel K.P., Schelbert B., Ludwig B., Hacker J.,

Mann K., Fischer G. FEBS Lett. 352:180-184(1994).

571. (RrnaAD) Ribosomal RNA adenine dimethylases signature

10 A number of enzymes responsible for the dimethylation of adenosines in
ribosomal RNAs (EC 2.1.1.48) have been found [1,2] to be evolutionary related.

These enzymes are:

- Bacterial 16S rRNA dimethylase (gene ksgA), which acts in the biogenesis
of ribosomes by catalyzing the dimethylation of two adjacent adenosines in
15 the loop of a conserved hairpin near the 3'-end of 16S rRNA. Inactivation
of ksgA leads to resistance to the aminoglycoside antibiotic kasugamycin.

- Yeast 18S rRNA dimethylase (gene DIM1), which is functionally similar to
ksgA and that dimethylates twin adenosines in the 3'-end of 18S rRNA.

20 - Bacterial 'erm' methylases. These enzymes confer resistance to macrolide-
lincosamide-streptogramin B (MLS) antibiotics - such as erythromycin - by
dimethylating the adenine residue at position 2058 of 23S rRNA thus
resulting in a reduced affinity between ribosomes and the MLS antibiotics.

- Caenorhabditis elegans hypothetical protein EO2H1.1.

25 The best conserved regions in these enzymes is located in the N-terminal
section and corresponds to a region that is probably involved in S-adenosyl
methionine (SAM) binding.

-Consensus pattern: [LIVM SEQ ID NO:4)]-[LIVMFY SEQ ID NO:18)]-[DE]-x-G-[STAPV
SEQ ID NO:304)]-G-x-[GA]-x-[LIVMF SEQ ID NO:2)]-[ST]-

30 x(2)-[LIVM SEQ ID NO:4)]-x(6)-[LIVMY SEQ ID NO:141)]-x-[STAGV SEQ ID
NO:451)]-[LIVMFYHC SEQ ID NO:533)]-E-x-D

[1] van Gemen B., van Knippenberg P.H.

(In) Nucleic acid methylation, Clawson G.A., Willis D.B., Weissbach A.,

Jones P.A., Eds., pp.19-36, Alan R. Liss Inc, New-York, (1990).

[2] Lafontaine D., Delcour J., Glasser A.L., Desgres J., Vandenhaute J.
J. Mol. Biol. 241:492-497(1994).

5 572. (RuBisCO small) Ribulose bisphosphate carboxylase, small chain. 206 members

573. ATP/GTP-binding site motif A (P-loop) (ras)

From sequence comparisons and crystallographic data analysis it has been shown
10 [1,2,3,4,5,6] that an appreciable proportion of proteins that bind ATP or GTP share a number
of more or less conserved sequence motifs. The best conserved of these motifs is a glycine-
rich region, which typically forms a flexible loop between a beta-strand and an alpha-helix.
This loop interacts with one of the phosphate groups of the nucleotide. This sequence motif is
generally referred to as the 'A' consensus sequence [1] or the 'P-loop' [5]. There are numerous
15 ATP- or GTP-binding proteins in which the P-loop is found. A number of protein families for
which the relevance of the presence of such a motif has been noted are listed below: - ATP
synthase alpha and beta subunits. - Myosin heavy chains. - Kinesin heavy chains and kinesin-
like proteins. - Dynamins and dynamin-like proteins - Guanylate kinase - Thymidine kinase (-
Thymidylate kinase. - Shikimate kinase. - Nitrogenase iron protein family (nifH/frxC) - ATP-
20 binding proteins involved in 'active transport' (ABC transporters) [7] - DNA and RNA
helicases [8,9,10]. - GTP-binding elongation factors (EF-Tu, EF-1alpha, EF-G, EF-2, etc.). -
Ras family of GTP-binding proteins (Ras, Rho, Rab, Ral, Ypt1, SEC4, etc.). - Nuclear protein
ran. - ADP-ribosylation factors family - Bacterial dnaA protein - Bacterial recA protein -
Bacterial recF protein - Guanine nucleotide-binding proteins alpha subunits (Gi, Gs, Gt, G0,
25 etc.). - DNA mismatch repair proteins mutS family - Bacterial type II secretion system
protein E. Not all ATP- or GTP-binding proteins are picked-up by this motif. A number of
proteins escape detection because the structure of their ATP-binding site is completely
different from that of the P-loop. Examples of such proteins are the E1-E2 ATPases or the
glycolytic kinases. In other ATP- or GTP-binding proteins the flexible loop exists in a
30 slightly different form; this is the case for tubulins or protein kinases. A special mention must
be reserved for adenylate kinase, in which there is a single deviation from the P-loop pattern:
in the last position Gly is found instead of Ser or Thr.

Consensus pattern: [AG]-x(4)-G-K-[ST]

In addition to the proteins listed above, the 'A' motif is also found in a number of other proteins. Most of these proteins probably bind a nucleotide, but others are definitively not ATP- or GTP-binding (as for example chymotrypsin, or human ferritin light chain).

[1] Walker J.E., Saraste M., Runswick M.J., Gay N.J. EMBO J. 1:945-951(1982).[2] Moller W., Amons R. FEBS Lett. 186:1-7(1985).[3] Fry D.C., Kuby S.A., Mildvan A.S. Proc. Natl. Acad. Sci. U.S.A. 83:907-911(1986).[4] Dever T.E., Glynias M.J., Merrick W.C. Proc. Natl. Acad. Sci. U.S.A. 84:1814-1818(1987).[5] Saraste M., Sibbald P.R., Wittinghofer A. Trends Biochem. Sci. 15:430-434(1990).[6] Koonin E.V. J. Mol. Biol. 229:1165-1174(1993).[7] Higgins C.F., Hyde S.C., Mimmack M.M., Gileadi U., Gill D.R., Gallagher M.P. J. Bioenerg. Biomembr. 22:571-592(1990).[8] Hodgman T.C. Nature 333:22-23(1988) and Nature 333:578-578(1988) (Errata).[9] Linder P., Lasko P., Ashburner M., Leroy P., Nielsen P.J., Nishi K., Schnier J., Slonimski P.P. Nature 337:121-122(1989).[10] Gorbalenya A.E., Koonin E.V., Donchenko A.P., Blinov V.M. Nucleic Acids Res. 17:4713-4730(1989).

15 GTP-binding nuclear protein ran signature (ras)

Ran (or TC4) is a small abundant nuclear protein that binds and hydrolyzes GTP and which has been implicated in a large number of processes including nucleocytoplasmic transport, RNA synthesis, processing and export and cell cycle checkpoint control [1,2]. Ran is generally included in the RAS 'superfamily' of small GTP-binding proteins [3], but it is only slightly related to the other RAS proteins. It also differs from RAS proteins in that it lacks cysteine residues at its C- terminal and is therefore not subject to prenylation. Instead ran has an acidic C-terminus. It is, however similar to RAS family members in requiring a specific guanine nucleotide exchange factor (GEF) and a specific GTPase activating protein (GAP) as stimulators of overall GTPase activity. The region of the GTP-binding B motif which, in ran, is perfectly conserved has been selected as a signature pattern.

Consensus pattern: D-T-A-G-Q-E-K-[LF]-G-G-L-R-[DE]-G-Y-Y- Proteins belonging to this family also contain a copy of the ATP/GTP- binding motif 'A' (P-loop).

[1] Scheffzek K., Klebe C., Fritz-Wolf K., Kabsch W., Wittinghofer A. Nature 374:378-381(1995).[2] Rush M.G., Drivas G., d'Eustachio P. BioEssays 18:103-112(1996).[3] Valencia A., Chardin P., Wittinghofer A., Sander C. Biochemistry 30:4637-4648(1991).

The bacterial recA protein [1,2,3,E1] is essential for homologous recombination and recombinational repair of DNA damage. RecA has many activities: it filaments, it binds to single- and double-stranded DNA, it binds and hydrolyzes ATP, it is also a recombinase and, finally, it interacts with lexA causing its activation and leading to its autocatalytic cleavage.

RecA is a protein of about 350 amino-acid residues. Its sequence is very well conserved [3,4,5,E1] among eubacterial species. It is also found in the chloroplast of plants [6]. The best conserved region, a nonapeptide located in the middle of the sequence which is part of the monomer-monomer interface in a recA filament has been selected as a signature pattern,.

Consensus pattern: A-L-[KR]-[IF]-[FY]-[STA]-[STAD SEQ ID NO:427)]-[LIVMQ SEQ ID NO:534)]-R-

[1] Smith K.C., Wang T.-C. V. BioEssays 10:12-16(1989).[2] Lloyd A.T., Sharp P.M. J. Mol. Evol. 37:399-407(1993).[3] Roca A.I., Cox M.M. Prog. Nucleic Acids Res. Mol. Biol. 56:129-223(1997).[4] Karlin S., Weinstock G.M., Brendel V. J. Bacteriol. 177:6881-6893(1995).[5] Eisen J.A. J. Mol. Evol. 41:1105-1123(1995).[6] Cerutti H.D., Osman M., Grandoni P., Jagendorf A.T. Proc. Natl. Acad. Sci. U.S.A. 89:8068-8072(1992).[E1] <http://www.tigr.org/~jeisen/RecA/RecA.html>

575. Response regulator receiver domain

This domain receives the signal from the sensor partner inComment: bacterial two-component systems. It is usually found N-terminalComment: to a DNA binding effector domain.

[1] Pao GM, Saier MH; J Mol Evol 1995;40:136-154.

576. Ribonucleotide reductase large subunit signature

*Ribonucleotide reductase (EC 1.17.4.1) [1,2] catalyzes the reductive synthesis of deoxyribonucleotides from their corresponding ribonucleotides. It provides the precursors necessary for DNA synthesis. Ribonucleotide reductase is an oligomeric enzyme composed of a large subunit (700 to 1000 residues) and a small subunit (300 to 400 residues). There are regions of similarities in the sequence of the large chain from prokaryotes, eukaryotes and viruses. One of these regions has been selected as a signature pattern.

Consensus pattern: W-x(2)-[LF]-x(6,7)-G-[LIVM SEQ ID NO:4)]-[FYRA SEQ ID NO:535)]-[NH]-x(3)-[STAQLIVM SEQ ID NO:536)]- [ASC]-x(2)-[PA]-

[1] Nillson O., Lundqvist T., Hahne S., Sjoberg B.-M. Biochem. Soc. Trans. 16:91-94(1988).[2] Reichard P. Science 260:1773-1777(1993).

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577. Ribonuclease T2 family histidine active sites

The fungal ribonucleases T2 from *Aspergillus oryzae*, M from *Aspergillus saitoi* and Rh from *Rhizopus niveus* are structurally and functionally related 30 Kd glycoproteins [1] that cleave the 3'-5' internucleotide linkage of RNA via a nucleotide 2',3'-cyclic phosphate intermediates (EC 3.1.27.1). A number of other RNases have been found to be evolutionary related to these fungal enzymes: - Self-incompatibility [2] in flowering plants is often controlled by a single gene (S-gene) that has several alleles. This gene prevents fertilization by self-pollen or by pollen bearing either of the two S- alleles expressed in the style. The self-incompatibility glycoprotein from several higher plants of the solanaceae family has been shown [2,3] to be a ribonuclease. - Phosphate-starvation induced RNases LE and LX from tomato [4]. These two enzymes are probably involved in a phosphate-starvation rescue system. - *Escherichia coli* periplasmic RNase I (EC 3.1.27.6) (gene *rna*) [5]. - *Aeromonas hydrophila* periplasmic RNase. - *Haemophilus influenzae* hypothetical protein HI0526. Two histidine residues have been shown [6,7] to be involved in the catalytic mechanism of RNase T2 and Rh. These residues and the region around them are highly conserved in all the sequence described above. Two signature patterns have been developed, one for each of the two active-site histidines. The second pattern also contains a cysteine which is known to be involved in a disulfide bond.

Consensus pattern: [FYWL SEQ ID NO:293)]-x-[LIVM SEQ ID NO:4)]-H-G-L-W-P [H is an active site residue]

Consensus pattern: [LIVMF SEQ ID NO:2)]-x(2)-[HDGTY SEQ ID NO:537)]-[EQ]-[FYW]-x-[KR]-H-G-x-C [H is an active site residue] [C is involved in a disulfide bond]

[1] Watanabe H., Naitoh A., Suyama Y., Inokuchi N., Shimada H., Koyama T., Ohgi K., Irie M. J. Biochem. 108:303-310(1990).[2] Haring V., Gray J.E., McClure B.A., Anderson M.A., Clarke A.E. Science 250:937-941(1990).[3] McClure B.A., Haring V., Ebert P.R., Anderson M.A., Simpson R.J., Sakiyama F., Clarke A.E. Nature 342:95957(1989).[4] Loeffler A., Glund K., Irie M. Eur. J. Biochem. 214:627-633(1993).[5] Meador J. III, Kennell D. Gene

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95:1-7(1990).[6] Kawata Y., Sakiyama F., Hayashi F., Kyogoku Y. Eur. J. Biochem.
187:255-262(1990).[7] Kurihara H., Mitsui Y., Ohgi K., Irie M., Mizuno H., Nakamura K.T.
FEBS Lett. 306:189-192(1992).

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578. Ribonucleotide reductase large subunit signature. Ribonucleotide reductase (EC
1.17.4.1) [1,2] catalyzes the reductive synthesis of deoxyribonucleotides from their
corresponding ribonucleotides. It provides the precursors necessary for DNA synthesis.
Ribonucleotide reductase is an oligomeric enzyme composed of a large subunit (700 to 1000
residues) and a small subunit (300 to 400 residues). There are regions of similarities in the
sequence of the large chain from prokaryotes, eukaryotes and viruses. One of these regions
has been developed as a signature pattern.

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Consensus pattern: W-x(2)-[LF]-x(6,7)-G-[LIVM SEQ ID NO:4)]-[FYRA SEQ ID
NO:535)]-[NH]-x(3)-[STAQLIVM SEQ ID NO:536)]- [ASC]-x(2)-[PA]-

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[1] Nillson O., Lundqvist T., Hahne S., Sjoberg B.-M. Biochem. Soc. Trans. 16:91-
94(1988).[2] Reichard P. Science 260:1773-1777(1993).

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579. RNase H

RNase H digests the RNA strand of an RNA/DNA hybrid. Important enzyme in retroviral
replication cycle, and often found as a domain associated with reverse transcriptases.
Structure is a mixed alpha+beta fold with three a/b/a layers.

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580. Eukaryotic putative RNA-binding region RNP-1 signature (rrm)

Many eukaryotic proteins that are known or supposed to bind single-stranded RNA contain
one or more copies of a putative RNA-binding domain of about 90 amino acids [1,2]. This
region has been found in the following proteins: ** Heterogeneous nuclear
ribonucleoproteins ** - hnRNP A1 (helix destabilizing protein) (twice). - hnRNP A2/B1
(twice). - hnRNP C (C1/C2) (once). - hnRNP E (UP2) (at least once). - hnRNP G (once). **
Small nuclear ribonucleoproteins ** - U1 snRNP 70 Kd (once). - U1 snRNP A (once). - U2

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snRNP B" (once). ** Pre-RNA and mRNA associated proteins ** - Protein synthesis initiation factor 4B (eIF-4B) [3], a protein essential for the binding of mRNA to ribosomes (once). - Nucleolin (4 times). - Yeast single-stranded nucleic acid-binding protein (gene SSB1) (once). - Yeast protein NSR1 (twice). NSR1 is involved in pre-rRNA processing; it specifically binds nuclear localization sequences. - Poly(A) binding protein (PABP) (4 times). ** Others ** - Drosophila sex determination protein Sex-lethal (Sxl) (twice). - Drosophila sex determination protein Transformer-2 (Tra-2) (once). - Drosophila 'elav' protein (3 times), which is probably involved in the RNA metabolism of neurons. - Human paraneoplastic encephalomyelitis antigen HuD (3 times) [4], which is highly similar to elav and which may play a role in neuron-specific RNA processing. - Drosophila 'bicoid' protein (once) [5], a segment-polarity homeobox protein that may also bind to specific mRNAs. - La antigen (once), a protein which may play a role in the transcription of RNA polymerase III. - The 60 Kd Ro protein (once), a putative RNP complex protein. - A maize protein induced by abscisic acid in response to water stress, which seems to be a RNA-binding protein. - Three tobacco proteins, located in the chloroplast [6], which may be involved in splicing and/or processing of chloroplast RNAs (twice). - X16 [7], a mammalian protein which may be involved in RNA processing in relation with cellular proliferation and/or maturation. - Insulin-induced growth response protein CI-4 from rat (twice). - Nucleolysins TIA-1 and TIAR (3 times) [8] which possesses nucleolytic activity against cytotoxic lymphocyte target cells. may be involved in apoptosis. - Yeast RNA15 protein, which plays a role in mRNA stability and/or poly-(A) tail length [9]. Inside the putative RNA-binding domain there are two regions which are highly conserved. The first one is a hydrophobic segment of six residues (which is called the RNP-2 motif), the second one is an octapeptide motif (which is called RNP-1 or RNP-CS). The position of both motifs in the domain is shown in the following schematic representation:

xxxxxxxx#####xx#####xxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxx
RNP-2 RNP-1

The RNP-1 motif has been used as a signature pattern for this type of domain.

Consensus pattern: [RK]-G-{EDRKHPCG}-[AGSCI SEQ ID NO:539)]-[FY]-[LIVA SEQ ID NO:219)]-x-[FYLM SEQ ID NO:38)] In most cases the residue in position 3 of the pattern is either Tyr or Phe.

[1] Bandziulis R.J., Swanson M.S., Dreyfuss G. *Genes Dev.* 3:431-437(1989).[2] Dreyfuss G., Swanson M.S., Pinol-Roma S. *Trends Biochem. Sci.* 13:86-91(1988).[3] Milburn S.C., Hershey J.W.B., Davies M.V., Kelleher K., Kaufman R.J. *EMBO J.* 9:2783-2790(1990).[4] Szabo A., Dalmau J., Manley G., Rosenfeld M., Wong E., Henson J., Posner J.B., Furneaux H.M. *Cell* 67:325-333(1991).[5] Rebagliati M. *Cell* 58:231-232(1989).[6] Li Y., Sugiura M. *EMBO J.* 9:3059-3066(1990).[7] Ayane M., Preuss U., Koehler G., Nielsen P.J. *Nucleic Acids Res.* 19:1273-1278(1991).[8] Kawakami A., Tian Q., Duan X., Streuli M., Schlossman S.F., Anderson P. *Proc. Natl. Acad. Sci. U.S.A.* 89:8681-8685(1992).[9] Minvielle-Sebastia L., Winsor B., Bonneaud N., Lacroute F. *Mol. Cell. Biol.* 11:3075-3087(1991).

581. Rubredoxin signature

Rubredoxins [1] are small electron-transfer prokaryotic proteins. They contain an iron atom which is ligated by four cysteine residues. Rubredoxins are, in some cases, functionally interchangeable with ferredoxins.

A conserved region that includes two of the cysteine residues that bind the iron atom has been selected as a pattern for these proteins.

Consensus pattern: [LIVM SEQ ID NO:4]-x(3)-W-x-C-P-x-C-[AGD] [The two C's bind the iron atom]

In *Pseudomonas oleovorans* rubredoxin 2 (gene *alkG*) [2], this pattern is found twice because *alkG* has two rubredoxin domains.

Rubrerhythrin [3], a protein with inorganic pyrophosphatase activity from *Desulfovibrio vulgaris* possesses a C-terminal rubredoxin-like domain, but this domain is too divergent to be detected by the above pattern.

[1] Berg J.M., Holm R.H.(In) *Iron-sulfur proteins*, Spiro T.G., Ed., pp1-66, Wiley, New-York, (1982). [2] Kok M., Oldenhuis R., der Linden M.P.G., Meulenberg C.H.C., Kingma J., Witholt B., *J. Biol. Chem.* 264:5442-5451(1989). [3] van Beeumen J.J., van Driessche G., Liu M.-Y., Le Gall J., *J. Biol. Chem.* 266:20645-20653(1991).

582. (rvp) Eukaryotic and viral aspartyl proteases active site

Aspartyl proteases, also known as acid proteases, (EC 3.4.23.-) are a widely distributed family of proteolytic enzymes [1,2,3] known to exist invertebrates, fungi, plants, retroviruses and some plant viruses. Aspartate proteases of eukaryotes are monomeric enzymes which consist of two domains. Each domain contains an active site centered on a catalytic aspartyl residue. The two domains most probably evolved from the duplication of an ancestral gene encoding a primordial domain. Currently known eukaryotic aspartyl proteases are: -

Vertebrate gastric pepsins A and C (also known as gastricsin). - Vertebrate chymosin (rennin), involved in digestion and used for making cheese. - Vertebrate lysosomal cathepsins D (EC 3.4.23.5) and E (EC 3.4.23.34). - Mammalian renin (EC 3.4.23.15) whose function is to generate angiotensin I from angiotensinogen in the plasma. - Fungal proteases such as aspergillopepsin A (EC 3.4.23.18), candidapepsin (EC 3.4.23.24), mucoropepsin (EC 3.4.23.23) (mucor rennin), endothiapepsin (EC 3.4.23.22), polyporopepsin (EC 3.4.23.29), and rhizopuspepsin (EC 3.4.23.21). - Yeast saccharopepsin (EC 3.4.23.25) (proteinase A) (gene PEP4). PEP4 is implicated in posttranslational regulation of vacuolar hydrolases. - Yeast barrier pepsin (EC 3.4.23.35) (gene BAR1); a protease that cleaves alpha-factor and thus acts as an antagonist of the mating pheromone. - Fission yeast *ssa1* which is involved in degrading or processing the mating pheromones. Most retroviruses and some plant viruses, such as badnaviruses, encode for an aspartyl protease which is a homodimer of a chain of about 95 to 125 amino acids. In most retroviruses, the protease is encoded as a segment of a polyprotein which is cleaved during the maturation process of the virus. It is generally part of the pol polyprotein and, more rarely, of the gag polyprotein. Conservation of the sequence around the two aspartates of eukaryotic aspartyl proteases and around the single active site of the viral proteases allows us to develop a single signature pattern for both groups of protease. Consensus pattern: [LIVMFGAC SEQ ID NO:106]-[LIVMTADN SEQ ID NO:107)]-[LIVFSA SEQ ID NO:108)]-D-[ST]-G-[STAV SEQ ID NO:105)]-[STAPDENQ SEQ ID NO:109)]-x-[LIVMFSTNC SEQ ID NO:110)]-x-[LIVMFGTA SEQ ID NO:111)] [D is the active site residue] -

[1] Foltmann B. *Essays Biochem.* 17:52-84(1981). [2] Davies D.R. *Annu. Rev. Biophys. Chem.* 19:189-215(1990). [3] Rao J.K.M., Erickson J.W., Wlodawer A. *Biochemistry* 30:4663-4671(1991). [4] Rawlings N.D., Barrett A.J. *Meth. Enzymol.* 248:105-120(1995).

583. (rvt) Reverse transcriptase (RNA-dependent DNA polymerase)

A reverse transcriptase gene is usually indicative of a mobile element such as a retrotransposon or retrovirus. Reverse transcriptases occur in a variety of mobile elements, including retrotransposons, retroviruses, group II introns, bacterial msDNAs, hepadnaviruses, and caulimoviruses. Number of members: 1233

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[1] Medline: 91006031. Origin and evolution of retroelements based upon their reverse transcriptase sequences. Xiong Y, Eickbush TH; EMBO J 1990;9:3353-3362.

10 584. (S-AdoMet synt) S-adenosylmethionine synthetase signatures

S-adenosylmethionine synthetase (EC 2.5.1.6) is the enzyme that catalyzes the formation of S-adenosylmethionine (AdoMet) from methionine and ATP [1]. AdoMet is an important methyl donor for transmethylation and is also the propylamino donor in polyamine biosynthesis. In bacteria there is a single isoform of AdoMet synthetase (gene metK), there are two in budding yeast (genes SAM1 and SAM2) and in mammals while in plants there is generally a multigene family. The sequence of AdoMet synthetase is highly conserved throughout isozymes and species. Two signature patterns have been selected for this type of enzyme; the first is a hexapeptide which seems to be involved in ATP-binding; the second is an almost perfectly conserved glycine-rich nonapeptide.

20 Consensus pattern: G-A-G-D-Q-G-x(3)-G-[FYH]-Sequences known to belong to this class detected by the pattern:

Consensus pattern: G-[GA]-G-[ASC]-F-S-x-K-[DE]

[1] Horikawa S., Sasuga J., Shimizu K., Ozasa H., Tsukada K. J. Biol. Chem. 265:13683-13686(1990).

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585. S1 RNA binding domain

The S1 domain occurs in a wide range of RNACComment: associated proteins. It is structurally similarComment: to cold shock protein which binds nucleic acids.Comment: The S1 domain has an OB-fold structure.

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[1] Bycroft M, Hubbard TJ, Proctor M, Freund SM, Murzin AG; Cell 1997;88:235-242.

586. SAICAR synthetase signatures

Phosphoribosylaminoimidazole-succinocarboxamide synthase (EC 6.3.2.6)

(SAICARSynthetase) catalyzes the seventh step in the de novo purine biosynthetic pathway; the ATP-dependent conversion of 5'-phosphoribosyl-5-aminoimidazole-4-carboxylic acid and aspartic acid to SAICAR [1]. In bacteria (gene *purC*), fungi (gene *ADE1*) and plants, SAICAR synthetase is a monofunctional protein; in higher vertebrates it is the N-terminal domain of a bifunctional enzyme that also catalyze phosphoribosylaminoimidazole carboxylase (AIRC) activity. Two conserved regions in the central section of this enzyme have been selected as signature patterns for SAICAR synthetase.

Consensus pattern: [LIVMF SEQ ID NO:2)](2)-P-[LIVM SEQ ID NO:4)]-E-x-[LIVM SEQ ID NO:4)]-[LIVMCA SEQ ID NO:149)]-R-x(3)-[TA]-G-S-

Consensus pattern: [LIVM SEQ ID NO:4)]-[LIVMA SEQ ID NO:30)]-D-x-K-[LIVMFY SEQ ID NO:18)]-E-F-G

[1] Zalkin H., Dixon J.E. *Prog. Nucleic Acid Res. Mol. Biol.* 42:259-287(1992).

587. (SCP) Extracellular proteins SCP/Tpx-1/Ag5/PR-1/Sc7 signatures

A variety of extracellular proteins from eukaryotes have been found to be evolutionary related: - Rodent sperm-coating glycoprotein (SCP), also known as acidic epididymal

glycoprotein (AEG) . This protein is thought to be involved in sperm maturation [1]. It is a protein of about 220 residues and probably contains eight disulfide bonds. - Mammalian

testis-specific protein Tpx-1 [2]. Tpx-1 is highly related to SCP's. - Mammalian glioma pathogenesis-related protein (GliPR). - Lizard helothermine, a toxin that blocks ryanodine

receptors. - Venom allergen 5 (Ag5) from vespid wasps and venom allergen 3 (Ag3) from fire ants. These proteins are potent allergens and are the main cause of allergic reactions to

stings from insects of the hymenoptera family [3]. Ag5/3 are proteins of about 200 residues and contain four disulfide bonds. - Plant pathogenesis proteins of the PR-1 family [4]. These

proteins are synthesized during pathogen infection or other stress-related responses. They are proteins of about 130 to 140 residues and probably contain three disulfide bonds. - Proteins

Sc7 and Sc14 from the basidiomycete fungus *Schizophyllum commune*. These extracellular proteins are loosely associated with fruit body hyphal walls [5]. Sc7/14 are proteins of about

180 residues and probably contain two disulfide bonds. - *Ancylostoma* secreted protein from dog hookworm. - Yeast hypothetical proteins YJL078c, YJL079c and YKR013w. The exact

function of these proteins is not yet known. Two conserved regions located in their C-terminal half have been selected as signature patterns. The second signature contains a cysteine which is known to be involved in a disulfide bond in Ag5.

Consensus pattern: [GDER SEQ ID NO:540)]-H-[FYWH SEQ ID NO:272)]-T-Q-[LIVM
5 SEQ ID NO:4)](2)-W-x(2)-[STN]

Consensus pattern: [LIVMFYH SEQ ID NO:541)]-[LIVMFY SEQ ID NO:18)]-x-C-
[NQRHS SEQ ID NO:542)]-Y-x-[PARH SEQ ID NO:543)]-x-[GL]-N- [LIVMFYWDN SEQ
ID NO:544)] [C is involved in a disulfide bond]

[1] Mizuki N., Kasahara M. Mol. Cell. Endocrinol. 89:25-32(1992).[2] Kasahara M.,
10 Gutknecht J., Brew K., Spurr N., Goodfellow P.N. Genomics 5:527-534(1989).[3] Lu G.,
Villalba M., Coscia M.R., Hoffman D.R., King T.P. J. Immunol. 150:2823-2830(1993).[4]
Dixon D.C., Cutt J.R., Klessig D.F. EMBO J. 10:1317-1324(1991).[5] Schuren F.H.J.,
Asgeirsdottir S.A., Kothe E.M., Scheer J.M.J., Wessels J.G.H. J. Gen. Microbiol. 139:2083-
2090(1993).

588. SET domain

SET domains appear to be protein-protein interactionComment: domains. It has been
demonstrated that SET domainsComment: mediate interactions with a family of proteins
20 thatComment: display similarity with dual-specificity phosphatasesComment: (dsPTPases)
[2].

[1] Tripoulas N, LaJeunesse D, Gildea J, Shearn A; Genetics 1996;143:913-928. [2] Cui X,
De Vivo I, Slany R, Miyamoto A, Firestein R, Cleary, ML; Nat Genet 1998;18:331-337.

25 589. Src homology 3 (SH3) domain profile

The Src homology 3 (SH3) domain is a small protein domain of about 60 amino-acid residues
first identified as a conserved sequence in the non-catalytic part of several cytoplasmic
protein tyrosine kinases (e.g. Src, Abl, Lck) [1]. Since then, it has been found in a great
30 variety of other intracellular or membrane-associated proteins [2,3,4,5]. The SH3 domain has
a characteristic fold which consists of five or six beta-strands arranged as two tightly packed
anti-parallel beta sheets. The linker regions may contain short helices [6]. The function of the
SH3 domain is not well understood. The current opinion is that they mediate assembly of

specific protein complexes via binding to proline-rich peptides [7]. In general SH3 domains are found as single copies in a given protein, but there is a significant number of protein with two SH3 domains and a few with 3 or 4 copies. So far, SH3 domains have been identified in the following proteins: - Many vertebrate, invertebrate and retroviral cytoplasmic (non-receptor) protein tyrosine kinases. In particular in the Src, Abl, Bkt, Csk and ZAP70 families of kinases. - Mammalian phosphatidylinositol-specific phospholipase C-gamma-1 and -2. - Mammalian phosphatidyl inositol 3-kinase regulatory p85 subunit. - Mammalian Ras GTPase-activating protein (GAP). - Adaptor proteins mediating binding of guanine nucleotide exchange factors to growth factor receptors: vertebrate GRB2, *Caenorhabditis elegans* sem-5 and *Drosophila* DRK. All of which have two SH3 domains. - Mammalian Vav oncoprotein, a guanine nucleotide exchange factor of the CDC24 family. - Some guanine-nucleotide releasing factors of the CDC25 family: yeast CDC25, yeast SCD25, fission yeast ste6. - MAGUK proteins. These proteins consist of at least three types of domains: one or more copies of the DHR domain, a SH3 domain and a C-terminal guanylate kinase domain. Members of this family are: *Drosophila* lethal(1) discs large-1 tumor suppressor protein (gene Dlg1), mammalian tight junction protein ZO-1, vertebrate erythrocyte membrane protein p55, *Caenorhabditis elegans* protein lin-2, rat protein CASK and mammalian synaptic proteins SAP90/PSD-95, CHAPSIN-110/PSD-93, SAP97/DLG1 and SAP102. - Miscellaneous proteins interacting with vertebrate receptor protein tyrosine kinases: mammalian cytoplasmic protein Nck (3 copies), oncoprotein Crk (2 copies). - Chicken Src substrate p80/85 protein (cortactin) and the similar human hemopoietic lineage cell specific protein Hs1. - Mammalian dihydropyridine-sensitive L-type calcium channel beta (regulatory) subunit including the related human myasthenic syndrome antigen B (MSYB). - Mammalian neutrophil cytosolic activators of NADPH oxidase: p47 (NCF-1), p67 (NCF-2), and a potential homolog from *Caenorhabditis elegans* (B0303.7). NCF-1 and -2 have two copies of the SH3 domain, while B0303.7 has four. - Some myosin heavy chains from amoebae, slime molds and yeast (gene MYO3). - Vertebrate and *Drosophila* spectrin and fodrin alpha-chain. - Human amphiphysin. - Yeast actin-binding protein ABP1. - Yeast actin-binding protein SLA1 (3 copies). - Yeast protein BEM1 and the fission yeast homolog scd2 (or ral3) (2 copies). - Yeast BEM1-binding proteins BOI2 (BEB1) and BOB1 (BOI1). - Yeast fusion protein FUS1. - Yeast protein RSV167. - Yeast protein SSU81. - Yeast hypothetical proteins YAR014c (1 copy), YFR024c (1 copy), YHL002w (1 copy), YHR016c (1 copy), YJL020C (1 copy), YHR114w (2 copies) and the fission yeast homolog SpAC12C2.05c. -

Caenorhabditis elegans hypothetical proteins F42H10.3. The profile developed to detect SH3 domains is based on a structural alignment consisting of 5 gap-free blocks and 4 linker regions totaling 62 match positions.

[1] Mayer B.J., Hamaguchi M., Hanafusa H. *Nature* 332:272-275(1988).[2] Musacchio A., Gibson T., Lehto V.P., Saraste M. *FEBS Lett.* 307:55-61(1992).[3] Pawson T., Schlessinger J. *Curr. Biol.* 3:434-442(1993).[4] Mayer B.J., Baltimore D. *Trends Cell Biol.* 3:8-13(1993).[5] Pawson T. *Nature* 373:573-580(1995).[6] Kuriyan J., Cowburn D. *Curr. Opin. Struct. Biol.* 3:828-837(1993).[7] Morton C.J., Campbell I.D. *Curr. Biol.* 4:615-617(1994).

590. Serine hydroxymethyltransferase pyridoxal-phosphate attachment site (SHMT)
Serine hydroxymethyltransferase (EC 2.1.2.1) (SHMT) [1] catalyzes the transfer of the hydroxymethyl group of serine to tetrahydrofolate to form 5,10-methylenetetrahydrofolate and glycine. In vertebrates, it exists in acytoplasmic and a mitochondrial form whereas only one form is found in prokaryotes. Serine hydroxymethyltransferase is a pyridoxal-phosphate containing enzyme. The pyridoxal-P group is attached to a lysine residue around which the sequence is highly conserved in all forms of the enzyme.

Consensus pattern: [DEH]-[LIVMFY SEQ ID NO:18)]-x-[STMV SEQ ID NO:545)]-[GST]-[ST](2)-H-K-[ST]-[LF]-x-G- [PAC]-[RQ]-[GSA]-[GA] [K is the pyridoxal-P attachment site]

[1] Usha R., Savithri H.S., Rao N.A. *Biochim. Biophys. Acta* 1204:75-83(1994).

591. SIS domain

SIS (Sugar ISomerase) domains are found in many phosphosugar isomerases and phosphosugar binding proteins.

[1] Teplyakov A, Obmolova G, Badet-Denisot MA, Badet B, Polikarpov I; *Structure* 1998;6:1047-1055.

592. (SKI) Shikimate kinase signature

Shikimate kinase (EC 2.7.1.71) catalyzes the fifth step in the biosynthesis from chorismate of the aromatic amino acids (the shikimate pathway) in bacteria (gene *aroK* or *aroL*), plants and

in fungi (where it is part of a multifunctional enzyme which catalyzes five consecutive steps in this pathway). Shikimate kinase is a small protein of about 200 residues. A conserved region that contains a run of three glycines has been selected as a signature pattern.

Consensus pattern: [KR]-x(2)-E-x(3)-[LIVMF SEQ ID NO:2)]-x(8,12)-[LIVMF SEQ ID NO:2)](2)-[SA]-x-G(3)-x-[LIVMF SEQ ID NO:2)]. Proteins belonging to this family also contain a copy of the ATP/GTP-binding motif 'A' (P-loop).

593. SNAP-25 family

SNAP-25 (synaptosome-associated protein 25 kDa) proteins are components of SNARE complexes. Members of this family contain a cluster of cysteine residues that can be palmitoylated for membrane attachment [2].

[1] Brennwald P, Kearns B, Champion K, Keranen S, Bankaitis V, Novick P; Cell 1994;79:245-258. [2] Risinger C, Blomqvist AG, Lundell I, Lambertsson A, Nassel D, Pieribone VA, Brodin L, Larhammar D; J Biol Chem 1993;268:24408-24414.

594. SNF2 and others N-terminal domain

This domain is found in proteins involved in a variety of processes including transcription regulation (e.g., SNF2, STH1, brahma, MOT1), DNA repair (e.g., ERCC6, RAD16, RAD5), DNA recombination (e.g., RAD54), and chromatin unwinding (e.g., ISWI) as well as a variety of other proteins with little functional information (e.g., Iodestar, ETL1).

595. Staphylococcal nuclease homologues (Snase)

Present in all three domains of cellular life. Four copies in the transcriptional coactivator p100. These, however, appear to lack the active site residues of Staphylococcal nuclease. Positions 14 (Asp-21), 34 (Arg-35), 39 (Asp-40), 42 (Glu-43) and Comment: 110 (Arg-87) [SNase numbering in parentheses] are thought to be involved in substrate-binding and catalysis.

[1] Ponting CP; Protein Sci 1997;6:459-463. [2] Callebaut I, Mornon JP; Biochem J 1997;321:125-132.

5 596. SPRY domainA

SPRY Domain is named from SP1a and the RYanodine Receptor. Domain of unknown function. Distant homologues are domains in Comment: butyrophilin/marenostrin/pyrin homologues.

[1] Ponting C, Schultz J, Bork P; Trends Biochem Sci 1997;22:193-194.

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597. (SQS PSY) Squalene and phytoene synthases signatures

Two different polyisoprene synthases have been shown [1,2,3] to share a number of regions of sequence similarities: - Squalene synthase (EC 2.5.1.21) (farnesyl-diphosphate

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farnesyltransferase) (SQS), which catalyzes the conversion of two molecules of farnesyl diphosphate (FPP) into squalene. It is the first committed step in the cholesterol biosynthetic pathway. The reaction carried out by SQS is catalyzed in two separate steps: the first is a head-to-head condensation of the two molecules of FPP to form presqualene diphosphate; this intermediate is then rearranged in a NADP-dependent reduction, to form squalene. SQS

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is found in eukaryotes. In yeast it is encoded by the ERG9 gene, in mammals by the FDFT1 gene. SQS seems to be membrane-bound. - Phytoene synthase (EC 2.5.1.-) (PSY), which catalyzes the conversion of two molecules of geranylgeranyl diphosphate (GGPP) into phytoene. It is the second step in the biosynthesis of carotenoids from isopentenyl

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head-to-head condensation of the two molecules of GGPP to form prephytoene diphosphate; this intermediate is then rearranged to form phytoene. PSY is found in all organisms that synthesize carotenoids: plants and photosynthetic bacteria as well as some non-

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photosynthetic bacteria and fungi. In bacteria PSY is encoded by the gene crtB. In plants PSY is localized in the chloroplast. As it can be seen from the description above, both SQS and PSY share a number of functional similarities which are also reflected at the level of their primary structure. In particular three well conserved regions are shared by SQS and PSY; they could be involved in substrate binding and/or the catalytic mechanism. Signature patterns

have been developed for the second and third conserved regions; they are localized in the central part of these enzymes.

Consensus pattern: Y-[CSAM SEQ ID NO:546)]-x(2)-[VSG]-A-[GSA]-[LIVAT SEQ ID NO:374)]-[IV]-G-x(2)-[LMSC SEQ ID NO:547)]- x(2)-[LIV]

Consensus pattern: [LIVM SEQ ID NO:4)]-G-x(3)-Q-x(2,3)-N-[IF]-x-R-D-[LIVMFY SEQ ID NO:18)]-x(2)-[DE]- x(4,7)-R-x-[FY]-x-P-

[1] Summers C., Karst F., Charles A.D. Gene 136:185-192(1993).[2] Robinson G.W., Tsay Y.H., Kienzle B.K., Smith-Monroy C.A., Bishop R.W. Mol. Cell. Biol. 13:2706-

2727(1993).[3] Roemer S., Hugueney P., Bouvier F., Camara B., Kuntz M. Biochem.

Biophys. Res. Commun. 196:1414-1421(1993).

598. SRP54-type proteins GTP-binding domain signature

The signal recognition particle (SRP) is an oligomeric complex that mediates targeting and insertion of the signal sequence of exported proteins into the membrane of the endoplasmic reticulum. SRP consists of a 7S RNA and six protein subunits. One of these subunits, the 54 Kd protein (SRP54), is a GTP-binding protein that interacts with the signal sequence when it emerges from the ribosome. The N-terminal 300 residues of SRP54 include the GTP-binding site (G-domain) and are evolutionary related to similar domains in other proteins which are listed below [1]. - Escherichia coli and Bacillus subtilis ffh protein (P48), a protein which seems to be the prokaryotic counterpart of SRP54. Ffh is associated with a 4.5S RNA in the prokaryotic SRP complex. - Signal recognition particle receptor alpha subunit (docking protein), an integral membrane GTP-binding protein which ensures, in conjunction with SRP, the correct targeting of nascent secretory proteins to the endoplasmic reticulum membrane.

The G-domain is located at the C-terminal extremity of the protein. - Bacterial ftsY protein, a protein which is believed to play a similar role to that of the docking protein in eukaryotes.

The G-domain is located at the C-terminal extremity of the protein. - The pilA protein from Neisseria gonorrhoeae which seems to be the homolog of ftsY. - A protein from the archaeobacteria Sulfolobus solfataricus. This protein is also believed to be a docking protein.

The G-domain is also at the C- terminus. - Bacterial flagellar biosynthesis protein flhF. The best conserved regions in those domains are the sequence motifs that are part of the GTP-binding site, but as those regions are not specific to these proteins, they were not used as a

signature pattern. Instead, a conserved region located at the C-terminal end of the domain was selected.

Consensus pattern: P-[LIVM SEQ ID NO:4)]-x-[FYI]-[LIVMAT SEQ ID NO:162)]-[GS]-x-[GS]-[EQ]-x(4)-[LIVMF SEQ ID NO:2)]

5 [1] Althoff S., Selinger D., Wise J.A. Nucleic Acids Res. 22:1933-1947(1994).

599. (STphosphatase) Serine/threonine specific protein phosphatases signature

10 Serine/threonine specific protein phosphatases (EC 3.1.3.16) (PP) [1,2,3] are enzymes that catalyze the removal of a phosphate group attached to a serine or evolutionary related. - Protein phosphatase-1 (PP1) is an enzyme of broad specificity. It is inhibited by two thermostable proteins, inhibitor-1 and -2. In mammals, there are two closely related isoforms of PP-1: PP-1alpha and PP-1beta, produced by alternative splicing of the same gene. In *Emericella nidulans*, PP-1 (gene bimG) plays an important role in mitosis control by
15 reversing the action of the nimA kinase. In yeast, PP-1 (gene SIT4) is involved in dephosphorylating the large subunit of RNA polymerase II. - Protein phosphatase-2A (PP2A) is also an enzyme of broad specificity. PP2A is a trimeric enzyme that consist of a core composed of a catalytic subunit associated with a 65 Kd regulatory subunit and a third variable subunit. In mammals, there are two closely related isoforms of the catalytic subunit
20 of PP2A: PP2A-alpha and PP2A-beta, encoded by separate genes. - Protein phosphatase-2B (PP2B or calcineurin), a calcium-dependent enzyme whose activity is stimulated by calmodulin. It is composed of two subunits: the catalytic A-subunit and the calcium-binding B-subunit. The specificity of PP2B is restricted. In addition to the above-mentioned enzymes, some additional serine/threoninespecific protein phosphatases have been characterized and
25 are listed below. - Mammalian phosphatase-X (PP-X), and *Drosophila* phosphatase-V (PP-V) which are closely related but yet distinct from PP2A. - Yeast phosphatase PPH3, which is similar to PP2A, but with different enzymatic properties. - *Drosophila* phosphatase-Y (PP-Y), and yeast phosphatases Z1 and Z2 (genes PPZ1 and PPZ2) which are closely related but yet distinct from PP1. - *Drosophila* retinal degeneration protein C (gene rdgC), a calcium-binding
30 phosphatase required to prevent light-induced retinal degeneration. - Phages Lambda and Phi-80 ORF-221 which have been shown to have phosphatase activity and are related to mammalian PP's. The best conserved regions in these proteins is a perfectly conserved pentapeptide that can be used as a signature pattern.

Consensus pattern: [LIVM SEQ ID NO:4)]-R-G-N-H-E-

[1] Cohen P. Annu. Rev. Biochem. 58:453-508(1989).[2] Cohen P., Cohen P.T.W. J. Biol. Chem. 264:21435-21438(1989).[3] Cohen P.T.W., Brewis N.D., Hughes V., Mann D.J. FEBS Lett. 268:355-359(1990).

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600. Translation initiation factor SUI1 signature

In budding yeast (*Saccharomyces cerevisiae*), SUI1 is a translation initiation factor that functions in concert with eIF-2 and the initiator tRNA-Met in directing the ribosome to the proper start site of translation [1]. SUI1 is a protein of 108 residues. Close homologs of SUI1 have been found [2] in mammals, insects and plants. SUI1 is also evolutionary related to hypothetical proteins from *Escherichia coli* (yciH), *Haemophilus influenzae* (HI1225) and *Methanococcus vannielii*. A conserved region in the C-terminal section has been selected as a signature pattern.

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Consensus pattern: [LIVM SEQ ID NO:4)]-[EQ]-[LIVM SEQ ID NO:4)]-Q-G-[DEN]-[KHQ]-[KRV]

[1] Yoon H., Donahue T.F. Mol. Cell. Biol. 12:248-260(1992).[2] Fields C.A., Adams M.D. Biochem. Biophys. Res. Commun. 198:288-291(1994).

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601. (S T dehydratase) Serine/threonine dehydratases pyridoxal-phosphate attachment site
Serine and threonine dehydratases [1,2] are functionally and structurally related pyridoxal-phosphate dependent enzymes: - L-serine dehydratase (EC 4.2.1.13) and D-serine dehydratase (EC 4.2.1.14) catalyze the dehydration of L-serine (respectively D-serine) into ammonia and pyruvate. - Threonine dehydratase (EC 4.2.1.16) (TDH) catalyzes the dehydration of threonine into alpha-ketobutarate and ammonia. In *Escherichia coli* and other microorganisms, two classes of TDH are known to exist. One is involved in the biosynthesis of isoleucine, the other in hydroxamino acid catabolism. Threonine synthase (EC 4.2.99.2) is also a pyridoxal-phosphate enzyme, it catalyzes the transformation of homoserine-phosphate into threonine. It has been shown [3] that threonine synthase is distantly related to the serine/threonine dehydratases. In all these enzymes, the pyridoxal-phosphate group is attached to a lysine residue. The sequence around this residue is

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sufficiently conserved to allow the derivation of a pattern specific to serine/threonine dehydratases and threonine synthases.

Consensus pattern: [DESH SEQ ID NO:548)]-x(4,5)-[STVG SEQ ID NO:549)]-x-[AS]-
[FYI]-K-[DLIFSA SEQ ID NO:550)]-[RVMF SEQ ID NO:551)]-[GA]- [LIVMGA SEQ ID
5 NO:175)] [The K is the pyridoxal-P attachment site]

[1] Ogawa H., Gomi T., Konishi K., Date T., Naakashima H., Nose K., Matsuda Y., Peraino
C., Pitot H.C., Fujioka M. J. Biol. Chem. 264:15818-15823(1989).[2] Datta P., Goss T.J.,
Omnaas J.R., Patil R.V. Proc. Natl. Acad. Sci. U.S.A. 84:393-397(1987).[3] Parsot C.
EMBO J. 5:3013-3019(1986).[4] Grabowski R., Hofmeister A.E.M., Buckel W. Trends
10 Biochem. Sci. 18:297-300(1993).

Cysteine synthase/cystathionine beta-synthase P-phosphate attachment site

Cysteine synthase (CSase) is the pyridoxal-phosphate dependent enzyme responsible [1] for
the formation of cysteine from O-acetyl-serine and hydrogen sulfide with the concomitant
15 release of acetic acid. In bacteria such as Escherichia coli, two forms of the enzyme are
known (genes cysK and cysM). In plants there are also two forms, one located in the
cytoplasm and the other in chloroplasts. Cystathionine beta-synthase [2] catalyzes the first
irreversible step in homocysteine transsulfuration; the conjugation of homocysteine and serine
forming cystathionine. Like CSase it is a pyridoxal-phosphate dependent enzyme. The two
20 types of enzymes are evolutionary related. The pyridoxal-phosphate group of CSases has been
shown to be attached to a lysine residue which is located in the N-terminal section of these
enzymes; the sequence around this residue is highly conserved and can be used as a signature
pattern to detect this class of enzymes.

Consensus pattern: K-x-E-x(3)-[PA]-[STAGC SEQ ID NO:45)]-x-S-[IVAP SEQ ID
25 NO:552)]-K-x-R-x-[STAG SEQ ID NO:20)]-x(2)- [LIVM SEQ ID NO:4)] [The 2nd K is the
pyridoxal-P attachment site]

[1] Saito K., Kurosawa M., Murakoshi I. FEBS Lett. 328:111-114(1993).[2] Swaroop M.,
Bradley K., Ohura T., Tahara T., Roper M.D., Rosenberg L.E., Kraus J.P. J. Biol. Chem.
267:11455-11461(1992).

602. S locus glycop

S-locus glycoprotein family. In Brassicaceae, self-incompatible plants have a self/non-self
 Comment: recognition system. This is sporophytically controlled by Comment: multiple
 alleles at a single locus (S). S-locus glycoproteins, Comment: as well as S-receptor kinases,
 are in linkage with the S-alleles [1]. Number of members: 128

- 5 [1] Evolutionary aspects of the S-related genes of the Brassica self-incompatibility system:
 synonymous and nonsynonymous base substitutions. Hinata K, Watanabe M, Yamakawa S,
 Satta Y, Isogai A; Genetics 1995;140:1099-1104. [2] Polymorphism of the S-locus
 glycoprotein gene (SLG) and the S-locus related gene (SLR1) in *Raphanus sativus* L. and
 self-incompatible ornamental plants in the Brassicaceae. Sakamoto K, Kusaba M, Nishio T;
 10 Mol Gen Genet 1998;258:397-403.

603. (sdh cyt) Succinate dehydrogenase cytochrome b subunit signatures

- 15 Succinate dehydrogenase (SDH) is a membrane-bound complex of two main components: a
 membrane-extrinsic component composed of an FAD-binding flavoprotein and an iron-sulfur
 protein, and a hydrophobic component composed of a cytochrome B and a membrane anchor
 protein. The cytochrome b component is a mono heme transmembrane protein [1,2,3]
 belonging to a family that groups: - Cytochrome b-556 from bacterial SDH (gene *sdhC*). -
 Cytochrome b560 from the mammalian mitochondrial SDH complex. - Cytochrome b560
 20 subunit encoded in the mitochondrial genome of some algae and in the plant *Marchantia*
polymorpha. - Cytochrome b from yeast mitochondrial SDH complex (gene *SDH3* or *CYB3*).
 - Protein cyt-1 from *Caenorhabditis*. These cytochromes are proteins of about 130 residues
 that comprise three transmembrane regions. There are two conserved histidines which may
 be involved in binding the heme group. Two signature patterns have been developed that
 25 include these histidine residues.

Consensus pattern: R-P-[LIVMT SEQ ID NO:1)]-x(3)-[LIVM SEQ ID NO:4)]-x(6)-
 [LIVMWPK SEQ ID NO:553)]-x(4)-S-x(2)-H-R-x- [ST] [H could be a heme ligand]

Consensus pattern: H-x(3)-[GA]-[LIVMT SEQ ID NO:1)]-R-[HF]-[LIVMF SEQ ID NO:2)]-
 x-[FYWM SEQ ID NO:137)]-D-x-[GVA] [H could be a heme ligand]

- 30 [1] Yu L., Wei Y.-Y., Usui S., Yu C.-A. J. Biol. Chem. 267:24508-24515(1992).[2]
 Abraham P.R., Mulder A., Van't Riet J., Raue H.A. Mol. Gen. Genet. 242:708-716(1994).[3]
 Leblanc C., Boyen C., Richard O., Bonnard G., Grienemberger J.M., Kloareg B. J. Mol. Biol.
 250:484-495(1995).

604. Sec1 family

- [1] The Sec1 family: a novel family of proteins involved in synaptic transmission and general secretion. Halachmi N, Lev Z; J Neurochem 1996;66:889-897.

Number of members: 40

605. Protein secE/sec61-gamma signature

- In bacteria, the secE protein plays a role in protein export; it is one of the components - with secY and secA - of the preprotein translocase. In eukaryotes, the evolutionary related protein sec61-gamma plays a role in protein translocation through the endoplasmic reticulum; it is part of a trimeric complex that also consist of sec61-alpha and beta [1]. Both secE and sec61-gamma are small proteins of about 60 to 90 amino acids that contain a single transmembrane region at their C-terminal extremity (Escherichia colisecE is an exception, in that it possess an extra N-terminal segment of 60 residues that contains two additional transmembrane domains). The sequence of secE/sec61-gamma is not extremely well conserved, however it is possible to derive a signature pattern centered on a conserved proline located 10 residues before the beginning of the transmembrane domain.

- Consensus pattern: [LIVMFY SEQ ID NO:18)]-x(2)-[DENQGA SEQ ID NO:554)]-x(4)-[LIVMFTA SEQ ID NO:386)]-x-[KRV]-x(2)-[KW]-P- x(3)-[SEQ]-x(7)-[LIVT SEQ ID NO:165)]-[LIVGA SEQ ID NO:555)]-[LIVFGAST SEQ ID NO:556)]
- [1] Hartmann E., Sommer T., Prehn S., Goerlich D., Jentsch S., Rapoport T.A. Nature 367:654-657(1994).

606. 11-S plant seed storage proteins signature

- Plant seed storage proteins, whose principal function appears to be the major nitrogen source for the developing plant, can be classified, on the basis of their structure, into different families. 11-S are non-glycosylated proteins which form hexameric structures [1,2]. Each of the subunits in the hexamer is itself composed of an acidic and a basic chain derived from a single precursor and linked by a disulfide bond. This structure is shown in the following representation. +-----+ |

xxxxxxxxxxCxxxxxxxxxxxxxxxxxxxxxxxxxxNGxCxxxxxxxxxxxxxxxxxxxxxxxxxx ***** <--
 ----Acidic-subunit-----><----Basic-subunit-----> <-----About-480-to-500-

residues----->'C': conserved cysteine involved in a disulfide bond.'*': position of the
 pattern. Proteins that belong to the 11-S family are: pea and broad bean legumins, rape
 cruciferin, rice glutelins, cotton beta-globulins, soybean glycinins, pumpkin 11-S globulin,
 oat globulin, sunflower helianthinin G3, etc. The region that includes the conserved cleavage
 site between the acidic and basic subunits (Asn-Gly) and a proximal cysteine residue which is
 involved in the interchain disulfide bond have been used as a signature pattern for this family
 of proteins.

Consensus pattern: N-G-x-[DE](2)-x-[LIVMF SEQ ID NO:2)]-C-[ST]-x(11,12)-[PAG]-D [C
 is involved in a disulfide bond

[1] Hayashi M., Mori H., Nishimura M., Akazawa T., Hara-Nishimura I. Eur. J. Biochem.
 172:627-632(1988).[2] Shotwell M.A., Afonso C., Davies E., Chesnut R.S., Larkins B.A.
 Plant Physiol. 87:698-704(1988).

607. 7S seed storage protein

7S globulin is one of the main storage proteins of most angiosperms and
 gymnosperms. The 7S storage proteins are homotrimers.

Number of members: 67

[1] The three-dimensional structure of canavalin from jack bean (*Canavalia*
ensiformis). Ko TP, Ng JD, McPherson A; Plant Physiol 1993;101:729-744.

608. Aspartate-semialdehyde dehydrogenase signature

Aspartate-semialdehyde dehydrogenase (ASD) catalyzes the second step in the common
 biosynthetic pathway leading from Asp to diaminopimelate and Lys, to Met, and to Thr; the
 NADP-dependent reductive dephosphorylation of L-aspartyl phosphate to L-aspartate-
 semialdehyde. In bacteria and fungi, ASD is a protein of about 40 Kd (340 to 370 residues)
 whose sequence is not extremely well conserved [1]. A conserved cysteine residue has been
 implicated as important for the catalytic activity [2]. The region of conservation around the
 active site residue is too small to be used as signature pattern. Another more conserved

region, located in the last third of the sequence, and which contains both a conserved cysteine as well as an histidine has been used instead.

Consensus pattern: [LIVM SEQ ID NO:4)]-[SADN SEQ ID NO:71)]-x(2)-C-x-R-[LIVM SEQ ID NO:4)]-x(4)-[GSC]-H-[STA

- 5 [1] Baril C., Richaud C., Fourni E., Baranton G., Saint Girons I. J. Gen. Microbiol. 138:47-53(1992).[2] Karsten W.E., Viola R.E. Biochim. Biophys. Acta 1121:234-238(1992).

N-acetyl-gamma-glutamyl-phosphate reductase active site

- 10 N-acetyl-gamma-glutamyl-phosphate reductase (EC 1.2.1.38) (AGPR) [1,2] is the enzyme that catalyzes the third step in the biosynthesis of arginine from glutamate, the NADP-dependent reduction of N-acetyl-5-glutamyl phosphate into N-acetylglutamate 5-semialdehyde. In bacteria it is a monofunctional protein of 35 to 38 Kd (gene argC) while in fungi it is part of a bifunctional mitochondrial enzyme (gene ARG5,6, arg11 or arg-6) which contains a N-terminal acetylglutamate kinase (EC 2.7.2.8) domain and a C-terminal AGPR
- 15 domain. In the Escherichia coli enzyme, a cysteine has been shown to be implicated in the catalytic activity, the region around this residue is well conserved and can be used as a signature pattern.

Consensus pattern: [LIVM SEQ ID NO:4)]-[GSA]-x-P-G-C-[FY]-[AVP]-T-[GA]-x(3)-[GTAC SEQ ID NO:557)]-[LIVM SEQ ID NO:4)]- x-P [C is the active site residue]

- 20 [1] Ludovice M., Martin J.F., Carrachas P., Liras P. J. Bacteriol. 174:4606-4613(1992).[2] Gessert S.F., Kim J.H., Nargang F.E., Weiss R.L. J. Biol. Chem. 269:8189-8203(1994).

609. Sialyltransferase family,

- 25 Number of members: 18

610. SpoU rRNA Methylase family

This family of proteins probably use S-AdoMet. Number of members: 58

- 30 [1] SpoU protein of Escherichia coli belongs to a new family of putative rRNA methylases. Koonin EV, Rudd KE; Nucleic Acids Res 1993;21:5519-5519. [2] The spoU gene of escherichia coli , the fourth gene of the spoT operon, is essential for tRNA (Gm18) 2'

methyltransferase activity. Persson BC, Jager G, Gustafsson C; Nucleic Acids Res 1997;25:4093-4097.

5 611. Stathmin family signatures

Stathmin [1] (from the Greek 'stathmos' which means relay), is an ubiquitous intracellular protein, present in a variety of phosphorylated forms and which serves as a relay for diverse second messenger pathways. Its expression and phosphorylation are regulated throughout development and in response to extracellular signals regulating cell proliferation,
10 differentiation and function. Stathmin is a highly conserved protein of 149 amino acid residues. Structurally, it consists of an N-terminal domain of about 45 residues followed by a 78 residue alpha-helical domain consisting of a heptad repeat coiled coil structure and a C-terminal domain of 25 residues. Protein SCG10 is a neuron-specific, membrane-associated protein that accumulates in the growth cones of developing neurons. It is highly similar in its
15 sequence to stathmin, but differs in that it contains an additional N-terminal hydrophobic segment of 32 residues which is probably responsible for its interaction with membranes. Xenopus protein XB3 is also evolutionary related to stathmin and also contains an additional N-terminal hydrophobic domain [2]. A conserved decapeptide which ends with the first three residues of the coiled coil domain and a second pattern that corresponds to part of the central
20 region of the coiled coil have been selected as signatures for proteins of the stathmin family. Consensus pattern: P-[KRQ]-[KR](2)-[DE]-x-S-L-[EG]-E- Consensus pattern: A-E-K-R-E-H-E-[KR]-E- [1] Sobel A. Trends Biochem. Sci. 16:301-305(1991).[2] Maucuer A., Moreau J., Mechali M., Sobel A. J. Biol. Chem. 268:16420-16429(1993).

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612. SUA5/yciO/yrdC family signature. The following uncharacterized proteins have been shown [1] to share regions of similarities: - Yeast protein SUA5. - Escherichia coli
hypothetical protein yciO and HI1198, the corresponding Haemophilus influenzae protein. -
30 Escherichia coli hypothetical protein yrdC and HI0656, the corresponding Haemophilus influenzae protein. - Bacillus subtilis hypothetical protein ywlC. - Mycobacterium leprae hypothetical protein in rfe-hemK intergenic region. - Methanococcus jannaschii hypothetical protein MJ0062. These are proteins of from 20 to 46 Kd which contain a number of conserved

513

regions in their N-terminal section. They can be picked up in the database by the following pattern.

Consensus pattern: [LIVMTA SEQ ID NO:311)](3)-[LIVMFYC SEQ ID NO:6)]-[PG]-T-
5 [DE]-[STA]-x-[FY]-[GA]- [LIVM SEQ ID NO:4)]-[GS]-

[1] Bairoch A., Rudd K.E., Robison K. Unpublished observations (1995).

10 613. Sucrose synthase

Sucrose synthases catalyse the synthesis of sucrose from UDP-glucose and fructose. This family includes the bulk of the sucrose synthase protein. However the carboxyl terminal region of the sucrose synthases belongs to the glycosyl transferase family Glycos transf 1.

15 614. Sulfotransferase proteins

Number of members: 59

20 615. Synaptophysin / synaptoporin signature

Synaptophysin and synaptoporin [1] are structurally related proteins, found in the membrane of synaptic vesicles, which may function as ionic or solute channels. These two glycoproteins seem to span the membrane four times. Both their N- and C-termini sequences seem to be cytoplasmically located. As a signature pattern for this family of proteins, a highly conserved
25 region located in the beginning of the first intravesicular loop just after the first transmembrane domain has been selected. This region contains a cysteine residue that may be involved in a disulfide bond.

Consensus pattern: L-S-V-[DE]-C-x-N-K-T [C may be involved in a disulfide bond

[1] Knaus P., Marqueze-Pouey B., Scherer H., Betz H. Neuron 5:453-462(1990).

30 616. Syndecans signature

Syndecans [1,2] (from the greek syndein; to bind together) are a family of transmembrane heparan sulfate proteoglycans which are implicated in the binding of extracellular matrix components and growth factors. Syndecans bind a variety of molecules via their heparan sulfate chains and can act as receptors or as co-receptors. Structurally, these proteins consist of four separate domains: a) A signal sequence; b) An extracellular domain (ectodomain) of variable length and whose sequence is not evolutionary conserved in the various forms of syndecans. The ectodomain contains the sites of attachment of the heparan sulfate glycosaminoglycan side chains; c) A transmembrane region; d) A highly conserved cytoplasmic domain of about 30 to 35 residues which could interact with cytoskeletal proteins. The proteins known to belong to this family are: - Syndecan 1. - Syndecan 2 or fibroglycan. - Syndecan 3 or neuroglycan or N-syndecan. - Syndecan 4 or amphiglycan or ryudocan. - Drosophila syndecan. - Caenorhabditis elegans probable syndecan (F57C7.3). The signature pattern that has been developed for syndecans starts with the last residue of the transmembrane region and includes the first 10 residues of the cytoplasmic domain. This region, which contains four basic residues, could act as a stop transfer site.

Consensus pattern: [FY]-R-[IM]-[KR]-K(2)-D-E-G-S-Y

[1] Bernfield M., Kokenyesi R., Kato M., Hinkes M.T., Spring J., Gallo R.L., Lose E.J. Annu. Rev. Cell Biol. 8:365-393(1992).[2] David G. FASEB J. 7:1023-1030(1993).

617. Syntaxin / epimorphin family signature

The following proteins have been shown to be evolutionary related [1,2,3]: - Epimorphin (or syntaxin 2), a mammalian mesenchymal protein which plays an essential role in epithelial morphogenesis. - Syntaxin 1A (also known as antigen HPC-1) and syntaxin 1B which are synaptic proteins which may be involved in docking of synaptic vesicles at presynaptic active zones. - Syntaxin 3. - Syntaxin 4, which is potentially involved in docking of synaptic vesicles at presynaptic active zones. - Syntaxin 5, which mediates endoplasmic reticulum to golgi transport. - Syntaxin 6, which is involved in intracellular vesicle trafficking. - Syntaxin 7. - Yeast PEP12 (or VPS6) which is required for the transport of proteases to the vacuole. - Yeast SED5 which is required for the fusion of transport vesicles with the Golgi complex. - Yeast SSO1 and SSO2 which are required for vesicle fusion with the plasma membrane. - Yeast VAM3, which is required for vacuolar assembly. - Arabidopsis thaliana protein KNOLLE which may be involved in cytokinesis. - Caenorhabditis elegans hypothetical

proteins F35C8.4, F48F7.2, F55A11.2 and T01B11.3. The above proteins share the following characteristics: a size ranging from 30 Kd to 40 Kd; a C-terminal extremity which is highly hydrophobic and is probably involved in anchoring the protein to the membrane; a central, well conserved region, which seems to be in a coiled-coil conformation. The pattern specific for this family is based on the most conserved region of the coiled coil domain.

Consensus pattern: [RQ]-x(3)-[LIVMA SEQ ID NO:30)]-x(2)-[LIVM SEQ ID NO:4)]-[ESH]-x(2)-[LIVMT SEQ ID NO:1)]-x-[DEVMS SEQ ID NO:263)]-[LIVM SEQ ID NO:4)]-x(2)-[LIVM SEQ ID NO:4)]-[FS]-x(2)-[LIVM SEQ ID NO:4)]-x(3)-[LIVT SEQ ID NO:165)]-x(2)-Q-[GADEQ SEQ ID NO:558)]-x(2)-[LIVM SEQ ID NO:4)]-[DNQT SEQ ID NO:559)]-x-[LIVMF SEQ ID NO:2)]-[DESV SEQ ID NO:560)]-x(2)-[LIVM SEQ ID NO:4)]

[1] Bennett M.K., Garcia-Ararras J.E., Elferink L.A., Peterson K., Fleming A.M., Hazuka C.D., Scheller R.H. *Cell* 74:863-873(1993). [2] Spring J., Kato M., Bernfield M. *Trends Biochem. Sci.* 18:124-125(1993). [3] Pelham H.R.B. *Cell* 73:425-426(1993).

618. Sm protein

The U1, U2, U4/U6, and U5 small nuclear ribonucleoprotein particles (snRNPs) involved in pre-mRNA splicing contain seven Sm proteins (B/B', D1, D2, D3, E, F and G) in common, which assemble around the Sm site present in four of the major spliceosomal small nuclear RNAs. These proteins contain a common sequence motif in two segments, Sm1 and Sm2, separated by a short variable linker.

[1] Hermann H, Fabrizio P, Raker VA, Foulaki K, Hornig H, Brahms H, Luhrmann R *EMBO J* 1995;14:2076-2088. [2] Kambach C, Walke S, Young R, Avis JM, de la Fortelle E, Raker VA, Luhrmann R, Li J, Nagai K; *Cell* 1999;96:375-387.

619. Skp1 family

[1] Stebbins CE, Kaelin WG Jr, Pavletich NP; *Science* 1999;284:455-461.

620. Protein secY signatures

The eubacterial secY protein [1] plays an important role in protein export. It interacts with the signal sequences of secretory proteins as well as with two other components of the protein translocation system: secA and secE. SecY is an integral plasma membrane protein of 419 to 492 amino acid residues that apparently contains ten transmembrane segments. Such a structure probably confers to secY a 'translocator' function, providing a channel for periplasmic and outer-membrane precursor proteins. Homologs of secY are found in archaeobacteria [2]. SecY is also encoded in the chloroplast genome of some algae [3] where it could be involved in a prokaryotic-like protein export system across the two membranes of the chloroplast endoplasmic reticulum (CER) which is present in chromophyte and cryptophyte algae. Two signature patterns have been developed for secY proteins. The first corresponds to the second transmembrane region, which is the most conserved section of these proteins. The second spans the C-terminal part of the fourth transmembrane region, a short intracellular loop, and the N-terminal part of the fifth transmembrane region.

Consensus pattern: [GST]-[LIVMF SEQ ID NO:2]](2)-x-[LIVM SEQ ID NO:4]]-G-[LIVM SEQ ID NO:4]]-x-P-[LIVMFY SEQ ID NO:18]](2)-x-[AS]-[GSTQ SEQ ID NO:561]]-[LIVMFAT SEQ ID NO:562]](3)-Q-[LIVMFA SEQ ID NO:81]](2)

Consensus pattern: [LIVMFYW SEQ ID NO:26]](2)-x-[DE]-x-[LIVMF SEQ ID NO:2]]-[STN]-x(2)-G-[LIVMF SEQ ID NO:2]]-[GST]-[NST]-G-x-[GST]-[LIVMF SEQ ID NO:2]](3)

[1] Ito K. Mol. Microbiol. 6:2423-2428(1992).[2] Auer J., Spicker G., Boeck A. Biochimie 73:683-688(1991).[3] Douglas S.E. FEBS Lett. 298:93-96(1992).

621. (Seed protein) Small hydrophilic plant seed proteins signature. The following small hydrophilic plant seed proteins are structurally related: - Arabidopsis thaliana proteins GEA1 and GEA6. - Cotton late embryogenesis abundant (LEA) protein D-19. - Carrot EMB-1 protein. - Barley LEA proteins B19.1A, B19.1B, B19.3 and B19.4. - Maize late embryogenesis abundant protein Emb564. - Radish late seed maturation protein p8B6. - Rice embryonic abundant protein Empl. - Sunflower 10 Kd late embryogenesis abundant protein (DS10). - Wheat Em proteins. These proteins contains from 83 to 153 amino acid residues

and may play a role[1,2] in equipping the seed for survival, maintaining a minimal level of hydration in the dry organism and preventing the denaturation of cytoplasmic components. They may also play a role during imbibition by controlling water uptake. As a signature pattern, the best conserved region in the sequence of these proteins has been developed, it is a glycine-rich nonapeptide located in the N-terminal section.-

Consensus pattern: G-[EQ]-T-V-V-P-G-G-T-

[1] Dure L. III, Crouch M., Harada J., Ho T.-H. D., Mundy J., Quatrano R., Thomas T., Sung Z.R. Plant Mol. Biol. 12:475-486(1989).[2] Gaubier P., Raynal M., Hull G., Huestis G.M., Grellet F., Arenas C., Pages M., Delseny M. Mol. Gen. Genet. 238:409-418(1993).

622. Serine carboxypeptidases, active sites

All known carboxypeptidases are either metallo carboxypeptidases or serinecarboxypeptidases. The catalytic activity of the serine carboxypeptidases, like that of the trypsin family serine proteases, is provided by a charge relay system involving an aspartic acid residue hydrogen-bonded to a histidine, which is itself hydrogen-bonded to a serine [1]. Proteins known to be serine carboxypeptidases are: - Barley and wheat serine carboxypeptidases I, II, and III [2]. - Yeast carboxypeptidase Y (YSCY) (gene PRC1), a vacuolar protease involved in degrading small peptides. - Yeast KEX1 protease, involved in killer toxin and alpha-factor precursor processing. - Fission yeast sxa2, a probable carboxypeptidase involved in degrading or processing mating pheromones [3]. - Penicillium janthinellum carboxypeptidase S1 [4]. - Aspergillus niger carboxypeptidase pepF. - Aspergillus satoi carboxypeptidase cpdS. - Vertebrate protective protein / cathepsin A [5], a lysosomal protein which is not only a carboxypeptidase but also essential for the activity of both beta-galactosidase and neuraminidase. - Mosquito vitellogenic carboxypeptidase (VCP) [6]. - Naegleria fowleri virulence-related protein Nf314 [7]. - Yeast hypothetical protein YBR139w. - Caenorhabditis elegans hypothetical proteins C08H9.1, F13D12.6, F32A5.3, F41C3.5 and K10B2.2. This family also includes: - Sorghum (s)-hydroxymandelonitrile lyase (hydroxynitrile lyase) (HNL) [8], an enzyme involved in plant cyanogenesis. The sequences surrounding the active site serine and histidine residues are highly conserved in all these serine carboxypeptidases.

Consensus pattern: [LIVM SEQ ID NO:4)]-x-[GTA]-E-S-Y-[AG]-[GS] [S is the active site residue]

Consensus pattern: [LIVF SEQ ID NO:127)]-x(2)-[LIVSTA SEQ ID NO:563)]-x-[IVPST SEQ ID NO:564)]-x-[GSDNQL SEQ ID NO:565)]-[SAGV SEQ ID NO:25)]-[SG]-H-x-[IVAQ SEQ ID NO:566)]-P-x(3)-[PSA] [H is the active site residue]

[1] Liao D.I., Remington S.J. J. Biol. Chem. 265:6528-6531(1990).[2] Sorensen S.B., Svendsen I., Breddam K. Carlsberg Res. Commun. 54:193-202(1989).[3] Imai Y., Yamamoto M. Mol. Cell. Biol. 12:1827-1834(1992).[4] Svendsen I., Hofmann T., Endrizzi J., Remington J., Breddam K. FEBS Lett. 333:39-43(1993).[5] Galjart N.J., Morreau H., Willemsen R., Gillemans N., Bonten E.J., d'Azzo A. J. Biol. Chem. 266:14754-14762(1991).[6] Cho W.L., Deitsch K.W., Raikhel A.S. Proc. Natl. Acad. Sci. U.S.A. 88:10821-10824(1991).[7] Hu W.N., Kopachik W., Band R.N. Infect. Immun. 60:2418-2424(1992).[8] Wajant H., Mundry K.W., Pfitzenmaier K. Plant Mol. Biol. 26:735-746(1994).[9] Rawlings N.D., Barrett A.J. Meth. Enzymol. 244:19-61(1994).[E1]

623. Serpins signature. Serpins (SERine Proteinase INhibitors) [1,2,3,4] are a group of structurally related proteins. They are high molecular weight (400 to 500 amino acids), extracellular, irreversible serine protease inhibitors with a well defined structural-functional characteristic: a reactive region that acts as a 'bait' for an appropriate serine protease. This region is found in the C-terminal part of these proteins. Proteins which are known to belong to the serpin family are listed below (references are only provided for recently determined sequences): - Alpha-1 protease inhibitor (alpha-1-antitrypsin, contrapsin). - Alpha-1-antichymotrypsin, - Antithrombin III. - Alpha-2-antiplasmin. - Heparin cofactor II. - Complement C1 inhibitor. - Plasminogen activator inhibitors 1 (PAI-1) and 2 (PAI-2). - Glia derived nexin (GDN) (Protease nexin I). - Protein C inhibitor. - Rat hepatocytes SPI-1, SPI-2 and SPI-3 inhibitors. - Human squamous cell carcinoma antigen (SCCA) which may act in the modulation of the host immune response against tumor cells. - A lepidopteran protease inhibitor. - Leukocyte elastase inhibitor which, in contrast to other serpins, is an intracellular protein. - Neuroserpin [5], a neuronal inhibitor of plasminogen activators and plasmin. - Cowpox virus crmA [6], an inhibitor of the thiol protease interleukin-1B converting enzyme (ICE). CrmA is the only serpin known to inhibit a non-serine proteinase. - Some orthopoxviruses probable protease inhibitors, which may be

involved in the regulation of the blood clotting cascade and/or of the complement cascade in the mammalian host. On the basis of strong sequence similarities, a number of proteins with no known inhibitory activity are said to belong to this family: - Birds ovalbumin and the related genes X and Y proteins. - Angiotensinogen; the precursor of the angiotensin active peptide. - Barley protein Z; the major endosperm albumin. - Corticosteroid binding globulin (CBG). - Thyroxine-binding globulin (TBG). - Sheep uterine milk protein (UTMP) and pig uteroferrin-associated protein (UFAP). - Hsp47, an endoplasmic reticulum heat-shock protein that binds strongly to collagen and could act as a chaperone in the collagen biosynthetic pathway [7]. - Maspin, which seems to function as a tumor suppressor [5]. - Pigment epithelium-derived factor precursor (PEDF), a protein with a strong neutrophilic activity [8]. - Ep45, an estrogen-regulated protein from *Xenopus* [9]. A signature pattern has been developed for this family of proteins, centered on a well conserved Pro-Phe sequence which is found ten to fifteen residues on the C-terminal side of the reactive bond

Consensus pattern: [LIVMFY SEQ ID NO:18)]-x-[LIVMFYAC SEQ ID NO:97)]-[DNQ]-[RKHQ S SEQ ID NO:567)]-[PST]-F-[LIVMFY SEQ ID NO:18)]- [LIVMFYC SEQ ID NO:6)]-x-[LIVMFAH SEQ ID NO:568)]-

[1] Carrell R., Travis J. Trends Biochem. Sci. 10:20-24(1985).[2] Carrell R., Pemberton P.A., Boswell D.R. Cold Spring Harbor Symp. Quant. Biol. 52:527-535(1987).[3] Huber R., Carrell R.W. Biochemistry 28:8951-8966(1989).[4] Remold-O'Donneel E. FEBS Lett. 315:105-108(1993).[5] Osterwalder T., Contartese J., Stoeckli E.T., Kuhn T.B., Sonderegger P. EMBO J. 15:2944-2953(1996).[6] Komiyama T., Ray C.A., Pickup D.J., Howard A.D., Thornberry N.A., Peterson E.P., Salvesen G. J. Biol. Chem. 269:19331-19337(1994).[7] Clarke E., Sandwal B.D. Biochim. Biophys. Acta 1129:246-248(1992).[8] Zou Z., Anisowicz A., Neveu M., Rafidi K., Sheng S., Sager R., Hendrix M.J., Seftor E., Thor A. Science 263:526-529(1994).[9] Steele F.R., Chader G.J., Johnson L.V., Tombran-Tink J. Proc. Natl. Acad. Sci. U.S.A. 90:1526-1530(1993).[10] Holland L.J., Suksang C., Wall A.A., Roberts L.R., Moser D.R., Bhattacharya A. J. Biol. Chem. 267:7053-7059(1992).

Some bacterial regulatory proteins activate the expression of genes from promoters recognized by core RNA polymerase associated with the alternative sigma-54 factor. These have a conserved domain of about 230 residues involved in the ATP-dependent [1,2] interaction with sigma-54. This domain has been found in the proteins listed below:

- *acoR* from *Alcaligenes eutrophus*, an activator of the acetoin catabolism operon *acoXABC*.
- *algB* from *Pseudomonas aeruginosa*, an activator of alginate biosynthetic gene *algD*.
- *dctD* from *Rhizobium*, an activator of *dctA*, the C4-dicarboxylate transport protein.
- *dhaR* from *Citrobacter freundii*, a regulator of the *dha* operon for glycerol utilization.
- *fhlA* from *Escherichia coli*, an activator of the formate dehydrogenase H and hydrogenase III structural genes.
- *flbD* from *Caulobacter crescentus*, an activator of flagellar genes.
- *hoxA* from *Alcaligenes eutrophus*, an activator of the hydrogenase operon.
- *hrpS* from *Pseudomonas syringae*, an activator of *hprD* as well as other *hrp* loci involved in plant pathogenicity.
- *hupR1* from *Rhodobacter capsulatus*, an activator of the [NiFe] hydrogenase genes *hupSL*.
- *hydG* from *Escherichia coli* and *Salmonella typhimurium*, an activator of the hydrogenase activity.
- *levR* from *Bacillus subtilis*, which regulates the expression of the levanase operon (*levDEFG* and *sacC*).
- *nifA* (as well as *anfA* and *vnfA*) from various bacteria, an activator of the *nif* nitrogen-fixing operon.
- *ntrC*, from various bacteria, an activator of nitrogen assimilatory genes such as that for glutamine synthetase (*glnA*) or of the *nif* operon.
- *pgtA* from *Salmonella typhimurium*, the activator of the inducible phospho- glycerate transport system.
- *pilR* from *Pseudomonas aeruginosa*, an activator of pilin gene transcription.
- *rocR* from *Bacillus subtilis*, an activator of genes for arginine utilization
- *tyrR* from *Escherichia coli*, involved in the transcriptional regulation of aromatic amino-acid biosynthesis and transport.
- *wtsA*, from *Erwinia stewartii*, an activator of plant pathogenicity gene *wtsB*.
- *xylR* from *Pseudomonas putida*, the activator of the *tol* plasmid xylene catabolism operon *xylCAB* and of *xylS*.
- *Escherichia coli* hypothetical protein *yfhA*.
- *Escherichia coli* hypothetical protein *yhgB*.

About half of these proteins (*algB*, *dcdT*, *flbD*, *hoxA*, *hupR1*, *hydG*, *ntrC*, *pgtA* and *pilR*) belong to signal transduction two-component systems [3] and possess a domain that can be phosphorylated by a sensor-kinase protein in their N- terminal section. Almost all of these proteins possess a helix-turn-helix DNA-binding domain in their C-terminal section. The domain which interacts with the sigma-54 factor has an ATPase activity. This may be required to promote a conformational change necessary for the interaction [4]. The domain contains an atypical ATP-binding motif A (P-loop) as well as a form of motif B. The two ATP-binding motifs are located in the N-terminal section of the

domain; signature patterns have been developed for both motifs. Other regions of the domain are also conserved. One of them, located in the C-terminal section, has been selected as a third signature pattern.

Consensus pattern: [LIVMFY SEQ ID NO:18]](3)-x-G-[DEQ]-[STE]-G-[STAV SEQ ID NO:105]]-G-K-x(2)-[LIVMFY SEQ ID NO:18]]

Consensus pattern: [GS]-x-[LIVMF SEQ ID NO:2]]-x(2)-A-[DNEQASH SEQ ID NO:569]]-[GNEK SEQ ID NO:570]]-G-[STIM SEQ ID NO:571]]-[LIVMFY SEQ ID NO:18]](3)-[DE]-[EK]-[LIVM SEQ ID NO:4]]

Consensus pattern: [FYW]-P-[GS]-N-[LIVM SEQ ID NO:4]]-R-[EQ]-L-x-[NHAT SEQ ID NO:572]]

[1] Morrett E., Segovia L. J. Bacteriol. 175:6067-6074(1993).[2] Austin S., Kundrot C., Dixon R. Nucleic Acids Res. 19:2281-2287(1991).[3] Albright L.M., Huala E., Ausubel F.M. Annu. Rev. Genet. 23:311-336(1989).[4] Austin S., Dixon R. EMBO J. 11:2219-2228(1992).

625. Sigma-70 factors family signatures

Sigma factors [1] are bacterial transcription initiation factors that promote the attachment of the core RNA polymerase to specific initiation sites and are then released. They alter the specificity of promoter recognition. Most bacteria express a multiplicity of sigma factors. Two of these factors, sigma-70 (gene rpoD), generally known as the major or primary sigma factor, and sigma-54 (gene rpoN or ntrA) direct the transcription of a wide variety of genes. The other sigma factors, known as alternative sigma factors, are required for the transcription of specific subsets of genes. With regard to sequence similarity, sigma factors can be grouped into two classes: the sigma-54 and sigma-70 families. The sigma-70 family includes, in addition to the primary sigma factor, a wide variety of sigma factors, some of which are listed below: - *Bacillus* sigma factors involved in the control of sporulation-specific genes: sigma-E (sigE or spoIIGB), sigma-F (sigF or spoIIAC), sigma-G (sigG or spoIIIG), sigma-H (sigH or spo0C) and sigma-K (sigK or spoIVCB/spoIIIC). - *Escherichia coli* and related bacteria sigma-32 (gene rpoH or htpR) involved in the expression of heat shock genes. - *Escherichia coli* and related bacteria sigma-27 (gene fliA) involved in the expression of the flagellin gene. - *Escherichia coli* sigma-S (gene rpoS or katF) which seems to be involved in the expression of genes required for protection against external stresses. - *Myxococcus xanthus* sigma-B

(sigB) which is essential for the late-stage differentiation of that bacteria. Alignments of the sigma-70 family permit the identification of four regions of high conservation [2,3]. Each of these four regions can in turn be subdivided into a number of sub-regions. Signature patterns based on the two best-conserved sub-regions have been developed. The first pattern corresponds to sub-region 2.2; the exact function of this sub-region is not known although it could be involved in the binding of the sigma factor to the core RNA polymerase. The second pattern corresponds to sub-region 4.2 which seems to harbor a DNA-binding 'helix-turn-helix' motif involved in binding the conserved -35 region of promoters recognized by the major sigma factors. The second pattern starts one residue before the N-terminal extremity of the HTH region and ends six residues after its C-terminal extremity.

Consensus pattern: [DE]-[LIVMF SEQ ID NO:2]](2)-[HEQS SEQ ID NO:573]]-x-G-x-[LIVMFA SEQ ID NO:81]]-G-L-[LIVMFYE SEQ ID NO:574]]-x-[GSAM SEQ ID NO:575]]-[LIVMAP SEQ ID NO:253]]

Consensus pattern: [STN]-x(2)-[DEQ]-[LIVM SEQ ID NO:4]]-[GAS]-x(4)-[LIVMF SEQ ID NO:2]]-[PSTG SEQ ID NO:576]]-x(3)-[LIVMA SEQ ID NO:30]]-x-[NQR]-[LIVMA SEQ ID NO:30]]-[EQH]-x(3)-[LIVMFW SEQ ID NO:13]]-x(2)-[LIVM SEQ ID NO:4]]

[1] Helmann J.D., Chamberlin M.J. Annu. Rev. Biochem. 57:839-872(1988).[2] Gribskov M., Burgess R.R. Nucleic Acids Res. 14:6745-6763(1986).[3] Lonetto M.A., Gribskov M., Gross C.A. J. Bacteriol. 174:3843-3849(1992).[4] Lonetto M.A., Brown K.L., Rudd K.E., Buttner M.J. Proc. Natl. Acad. Sci. U.S.A. 91:7573-7577(1994).

626. Signal carboxyl-terminal domain. 430 members.

627. Signal peptidases I signatures

Signal peptidases (SPases) [1] (also known as leader peptidases) remove the signal peptides from secretory proteins. In prokaryotes three types of SPases are known: type I (gene lepB) which is responsible for the processing of the majority of exported pre-proteins; type II (gene lsp) which only process lipoproteins, and a third type involved in the processing of pili subunits. SPase I is an integral membrane protein that is anchored in the cytoplasmic membrane by one (in *B. subtilis*) or two (in *E. coli*) N-terminal transmembrane domains with the main part of the protein protruding in the periplasmic space. Two residues have been

shown [2,3] to be essential for the catalytic activity of SPase I: a serine and an lysine. SPase I is evolutionary related to the yeast mitochondrial inner membrane protease subunit 1 and 2 (genes IMP1 and IMP2) which catalyze the removal of signal peptides required for the targeting of proteins from the mitochondrial matrix, across the inner membrane, into the inter-membrane space [4]. In eukaryotes the removal of signal peptides is effected by an oligomeric enzymatic complex composed of at least five subunits: the signal peptidase complex (SPC). The SPC is located in the endoplasmic reticulum membrane. Two components of mammalian SPC, the 18 Kd (SPC18) and the 21 Kd (SPC21) subunits as well as the yeast SEC11 subunit have been shown [5] to share regions of sequence similarity with prokaryotic SPases I and yeast IMP1/IMP2. Three signature patterns for these proteins have been developed. The first signature contains the putative active site serine, the second signature contains the putative active site lysine which is not conserved in the SPC subunits, and the third signature corresponds to a conserved region of unknown biological significance which is located in the C-terminal section of all these proteins.

Consensus pattern: [GS]-x-S-M-x-[PS]-[AT]-[LF] [S is an active site residue]
 Consensus pattern: K-R-[LIVMSTA SEQ ID NO:433]](2)-G-x-[PG]-G-[DE]-x-[LIVM SEQ ID NO:4]]-x-[LIVMFY SEQ ID NO:18]] [K is an active site residue]
 Consensus pattern: [LIVMFYW SEQ ID NO:26]](2)-x(2)-G-D-[NH]-x(3)-[SND]-x(2)-[SG]
 [1] Dalbey R.E., von Heijne G. Trends Biochem. Sci. 17:474-478(1992).[2] Sung M., Dalbey R.E. J. Biol. Chem. 267:13154-13159(1992).[3] Black M.T. J. Bacteriol. 175:4957-4961(1993).[4] Nunnari J., Fox T.D., Walter P. Science 262:1997-2004(1993).[5] van Dijk J.M., de Jong A., Vehmaanpera J., Venema G., Bron S. EMBO J. 11:2819-2828(1992).[6] Rawlings N.D., Barrett A.J. Meth. Enzymol. 244:19-61(1994).[E1]

628. (sodcu) Copper/Zinc superoxide dismutase signatures

Copper/Zinc superoxide dismutase (SODC) [1] is one of the three forms of an enzyme that catalyzes the dismutation of superoxide radicals. SODC binds one atom each of zinc and copper. Various forms of SODC are known: acytoplasmic form in eukaryotes, an additional chloroplast form in plants, an extracellular form in some eukaryotes, and a periplasmic form in prokaryotes. The metal binding sites are conserved in all the known SODC sequences [2]. Two signature patterns have been derived for this family of enzymes: the first one contains

two histidine residues that bind the copper atom; the second one is located in the C-terminal section of SODC and contains a cysteine which is involved in a disulfide bond.

Consensus pattern: [GA]-[IMFAT SEQ ID NO:577)]-H-[LIVF SEQ ID NO:127)]-H-x(2)-[GP]-[SDG]-x-[STAGDE SEQ ID NO:578)] [The two H's are copper ligands]

Consensus pattern: G-[GN]-[SGA]-G-x-R-x-[SGA]-C-x(2)-[IV] [C is involved in a disulfide bond]

[1] Bannister J.V., Bannister W.H., Rotilio G. CRC Crit. Rev. Biochem. 22:111-154(1987).
[2] Smith M.W., Doolittle R.F. J. Mol. Evol. 34:175-184(1992).

629. (sodfe) Manganese and iron superoxide dismutases signature

Manganese superoxide dismutase (SODM) [1] is one of the three forms of an enzyme that catalyzes the dismutation of superoxide radicals. The four ligands of the manganese atom are conserved in all the known SODM sequences. These metal ligands are also conserved in the related iron form of superoxide dismutases [2,3]. A short conserved region which includes two of the four ligands: an aspartate and a histidine has been selected as a signature.

Consensus pattern: D-x-W-E-H-[STA]-[FY](2) [D and H are manganese/iron ligands]

[1] Bannister J.V., Bannister W.H., Rotilio G. CRC Crit. Rev. Biochem. 22:111-154(1987).
[2] Parker M.W., Blake C.C.F. FEBS Lett. 229:377-382(1988). [3] Smith M.W., Doolittle R.F. J. Mol. Evol. 34:175-184(1992).

630. Spectrin repeat

Spectrin repeats are found in several proteins involved in cytoskeletal structure. These include spectrin, alpha-actinin and dystrophin. The sequence repeat used in this family is taken from the structural repeat in reference [2]. The spectrin repeat forms a three helix bundle. The second helix is interrupted by proline in some sequences.

Number of members: 898

[1] Actin-binding proteins. 1: Spectrin super family. Hartwig JH; Protein Profile 1995;2:732-732. [2] Crystal structure of the repetitive segments of spectrin. Yan Y, Winograd E, Viel A, Cronin T, Harrison SC, Branton D; Science 1993;262:2027-2030.

631. (subtilase) Streptomyces subtilisin-type inhibitors signature

Bacteria of the Streptomyces family produce a family of proteinase inhibitors[1] characterized by their strong activity toward subtilisin. They are collectively known as SSI's: Streptomyces Subtilisin Inhibitors. Some SSI's also inhibit trypsin or chymotrypsin. In their mature secreted form, SSI's are proteins of about 110 residues with two conserved disulfide bonds. +-----+ +-----+ |||

xxxxxxxxxxxxxxxxCxxxxxxxxCxxxxxxxxCx#xxxxxxxxxxxxxxxxCxxxxxx *****'C': conserved cysteine involved in a disulfide bond. '#': active site residue. '*': position of the pattern.

Consensus pattern: C-x-P-x(2,3)-G-x-H-P-x(4)-A-C-[ATD]-x-L [The two C's are involved in a disulfide bond]

[1] Taguchi S., Kojima S., Terabe M., Miura K.-I., Momose H. Eur. J. Biochem. 220:911-918(1994).

632. Sugar transport proteins signatures

In mammalian cells the uptake of glucose is mediated by a family of closely related transport proteins which are called the glucose transporters [1,2,3]. At least seven of these transporters are currently known to exist (in Human they are encoded by the GLUT1 to GLUT7 genes). These integral membrane proteins are predicted to comprise twelve membrane spanning domains. The glucose transporters show sequence similarities [4,5] with a number of other sugar or metabolite transport proteins listed below (references are only provided for recently determined sequences). - Escherichia coli arabinose-proton symport (araE). - Escherichia coli galactose-proton symport (galP). - Escherichia coli and Klebsiella pneumoniae citrate-proton symport (also known as citrate utilization determinant) (gene cit). - Escherichia coli alpha-ketoglutarate permease (gene kgtP). - Escherichia coli proline/betaine transporter (gene proP) [6]. - Escherichia coli xylose-proton symport (xylE). - Zymomonas mobilis glucose facilitated diffusion protein (gene glf). - Yeast high and low affinity glucose transport proteins (genes SNF3, HXT1 to HXT14). - Yeast galactose transporter (gene GAL2). - Yeast maltose permeases (genes MAL3T and MAL6T). - Yeast myo-inositol transporters (genes ITR1 and ITR2). - Yeast carboxylic acid transporter protein homolog JEN1. - Yeast inorganic phosphate transporter (gene PHO84). - Kluyveromyces

lactis lactose permease (gene LAC12). - *Neurospora crassa* quinate transporter (gene *Qa-y*), and *Emericella nidulans* quinate permease (gene *qutD*). - *Chlorella* hexose carrier (gene *HUP1*). - *Arabidopsis thaliana* glucose transporter (gene *STP1*). - Spinach sucrose transporter. - *Leishmania donovani* transporters D1 and D2. - *Leishmania enriettii* probable transport protein (LTP). - Yeast hypothetical proteins YBR241c, YCR98c and YFL040w. - *Caenorhabditis elegans* hypothetical protein ZK637.1. - *Escherichia coli* hypothetical proteins *yabE*, *ydjE* and *yhjE*. - *Haemophilus influenzae* hypothetical proteins HI0281 and HI0418. - *Bacillus subtilis* hypothetical proteins *ymbC* and *ymbF*. It has been suggested [4] that these transport proteins have evolved from the duplication of an ancestral protein with six transmembrane regions, this hypothesis is based on the conservation of two G-R-[KR] motifs. The first one is located between the second and third transmembrane domains and the second one between transmembrane domains 8 and 9. Two patterns have been developed to detect this family of proteins. The first pattern is based on the G-R-[KR] motif; but because this motif is too short to be specific to this family of proteins, a pattern from a larger region centered on the second copy of this motif was derived. The second pattern is based on a number of conserved residues which are located at the end of the fourth transmembrane segment and in the short loop region between the fourth and fifth segments.

Consensus pattern: [LIVMSTAG SEQ ID NO:44]-[LIVMFSAG SEQ ID NO:579]-x(2)-[LIVMSA SEQ ID NO:187]-[DE]-x-[LIVMFYWA SEQ ID NO:41]-G-R-[RK]-x(4,6)-[GSTA SEQ ID NO:19]

Consensus pattern: [LIVMF SEQ ID NO:2]-x-G-[LIVMFA SEQ ID NO:81]-x(2)-G-x(8)-[LIFY SEQ ID NO:580]-x(2)-[EQ]-x(6)-[RK]

[1] Silverman M. Annu. Rev. Biochem. 60:757-794(1991).[2] Gould G.W., Bell G.I. Trends Biochem. Sci. 15:18-23(1990).[3] Baldwin S.A. Biochim. Biophys. Acta 1154:17-49(1993).[4] Maiden M.C.J., Davis E.O., Baldwin S.A., Moore D.C.M., Henderson P.J.F. Nature 325:641-643(1987).[5] Henderson P.J.F. Curr. Opin. Struct. Biol. 1:590-601(1991).[6] Culham D.E., Lasby B., Marangoni A.G., Milner J.L., Steer B.A., van Nues R.W., Wood J.M. J. Mol. Biol. 229:268-276(1993).

633. Synaptobrevin signature

Synaptobrevin [1] is an intrinsic membrane protein of small synaptic vesicles whose function is not yet known, but which is highly conserved in mammals, electric ray (where its is known

as VAMP-1), *Drosophila* and yeast [2]. In yeast there are two closely related forms of synaptobrevin (genes SNC1 and SNC2) while in mammals there is at least 4 (genes SYB1, SYB2, SYB3 and SYBL1). Structurally synaptobrevin consist of a N-terminal cytoplasmic domain of from 90 to 110 residues, followed by a transmembrane region, and then by a short (from 2 to 22 residues) C-terminal intravesicular domain. As a signature pattern for synaptobrevin, a highly conserved stretch of residues located in the central part of the sequence was selected.

Consensus pattern: N-[LIVM SEQ ID NO:4)]-[DENS SEQ ID NO:405)]-[KL]-V-x-[DEQ]-R-x(2)-[KR]-[LIVM SEQ ID NO:4)]-[STDE SEQ ID NO:581)]- x-[LIVM SEQ ID NO:4)]-x-[DE]-[KR]-[TA]-[DE]

[1] Suedhof T.C., Baumert M., Perin M.S., Jahn R. *Neuron* 2:1475-1481(1989).[2] Gerst J.E., Rodgers L., Riggs M., Wigler M. *Proc. Natl. Acad. Sci. U.S.A.* 89:4338-4342(1992).

634. TBC domain. Identification of a TBC domain in GYP6_YEAST and GYP7_YEAST, which are GTPase activator proteins of yeast Ypt6 and Ypt7, imply that these domains are GTPase activator proteins of Rab-like small GTPases. Number of members: 55

[1] Medline: 96032578. Molecular cloning of a cDNA with a novel domain present in the tre-2 oncogene and the yeast cell cycle regulators BUB2 and cdc16. Richardson PM, Zon LI; Oncogene 1995;11:1139-1148.

[2]Medline: 97398935. A shared domain between a spindle assembly checkpoint protein and Ypt/Rab-specific GTPase-activators. Neuwald AF; Trends Biochem Sci 1997;22:243-244.

635. Transcription factor TFIID repeat signature (TBP)

Transcription factor TFIID (or TATA-binding protein, TBP) [1,2] is a general factor that plays a major role in the activation of eukaryotic genes transcribed by RNA polymerase II.

TFIID binds specifically to the TATA box promoter element which lies close to the position of transcription initiation. There is a remarkable degree of sequence conservation of a C-terminal domain of about 180 residues in TFIID from various eukaryotic sources. This region is necessary and sufficient for TATA box binding. The most significant structural feature of this domain is the presence of two conserved repeats of a 77 amino-acid region. The intramolecular symmetry generates a saddle-shaped structure that sits astride the DNA [3]. Drosophila TRF (TBP-related factor) [4] is a sequence-specific transcription factor that also binds to the TATA box and is highly similar to TFIID. Archaeobacteria also possess a TBP homolog [5]. A signature pattern that spans the last 50 residues of the repeated region has been derived.-

Consensus pattern: Y-x-P-x(2)-[IF]-x(2)-[LIVM SEQ ID NO:4]](2)-x-[KRH]-x(3)-P-[RKQ]-x(3)- L-[LIVM SEQ ID NO:4]-F-x-[STN]-G-[KR]-[LIVM SEQ ID NO:4]-x(3)-G-[TAGL SEQ ID NO:582]]-[KR]-x(7)- [AGC]-x(7)-[LIVM

[1] Hoffmann A., Sinn E., Yamamoto T., Wang J., Roy A., Horikoshi M., Roeder R.G.

Nature 346:387-390(1990).[2] Gash A., Hoffmann A., Horikoshi M., Roeder R.G., Chua N.-

H. Nature 346:390-394(1990).[3] Nikolov D.B., Hu S.-H., Lin J., Gasch A., Hoffmann A.,

Horikoshi M., Chua N.-H., Roeder R.G., Burley S.K. Nature 360:40-46(1992).[4] Crowley

T.E., Hoey T., Liu J.-K., Jan Y.N., Jan L.Y., Tjian R. Nature 361:557-561(1993).[5] Marsh

T.L., Reich C.I., Whitelock R.B., Olsen G.J. Proc. Natl. Acad. Sci. U.S.A. 91:4180-4184(1994).

5 636. Translationally controlled tumor protein signatures (TCTP)

Mammalian translationally controlled tumor protein (TCTP) (or P23) is a protein which has been found to be preferentially synthesized in cells during the early growth phase of some types of tumor [1,2], but which is also expressed in normal cells. The physiological function of TCTP is still not known. It is a hydrophilic protein of 18 to 20 Kd. Close homologs have
10 been found in plants [3], earthworm [4], *Caenorhabditis elegans* (F52H2.11), *Hydra*, budding yeast (YKL056c) [5] and fission yeast (SpAC1F12.02c). Two of the best conserved regions have been selected as signature patterns for TCTP.

Consensus pattern: [IFA]-[GA]-[GAS]-N-[PAK]-S-[GA]-E-[GDE]-[PAGE SEQ ID NO:583)]-[DEQGA SEQ ID NO:584)]

15 Consensus pattern: [FLVH SEQ ID NO:585)]-[FY]-[IVCT SEQ ID NO:586)]-G-E-x-[MA]-x(2,5)-[DEN]-[GAST SEQ ID NO:179)]-x-[LV]-[AV]-x(3)-[FYW]

[1] Boehm H., Beendorf R., Gaestel M., Gross B., Nuernberg P., Kraft R., Otto A., Bielka H. Biochem. Int. 19:277-286(1989).[2] Makrides S., Chitpatima S.T., Bandyopadhyay R., Brawerman G. Nucleic Acids Res. 16:2350-2350(1988).[3] Pay A., Heberle-Bors E., Hirt H.
20 Plant Mol. Biol. 19:501-503(1992).[4] Stuerzenbaum S.R., Kille P., Morgan A.J. Biochim. Biophys. Acta 1398:294-304(1998).[5] Rasmussen S.W. Yeast 10:S63-S68(1994).

637. TFIIS zinc ribbon domain signature

25 Transcription factor S-II (TFIIS) [1] is a eukaryotic protein necessary for efficient RNA polymerase II transcription elongation, past template-encoded pause sites. TFIIS shows DNA-binding activity only in the presence of RNA polymerase II. It is a protein of about 300 amino acids whose sequence is highly conserved in mammals, *Drosophila*, yeast (where it was first known as PPR2, a transcriptional regulator of URA4, and then as DST1, the DNA
30 strand transfer protein alpha [2]) and in the archaeobacteria *Sulfolobus acidocaldarius* [3]. This family also includes the eukaryotic and archebacterial RNA polymerase subunits of the 15 Kd / M family (see <PDOC00790>) as well as the following viral proteins: - Vaccinia virus RNA polymerase 30 Kd subunit (rpo30) [4]. - African swine fever virus protein I243L

[5]. The best conserved region of all these proteins contains four cysteines that bind a zinc ion and fold in a conformation termed a 'zinc ribbon' [6]. Besides these cysteines, there are a number of other conserved residues which can be used to help define a specific pattern for this type of domain.

- 5 Consensus pattern: C-x(2)-C-x(9)-[LIVMQSAR SEQ ID NO:587)]-[QH]-[STQL SEQ ID NO:588)]-[RA]-[SACR SEQ ID NO:589)]-x-[DE]-[DET]-[PGSEA SEQ ID NO:590)]-x(6)-C-x(2,5)-C-x(3)-[FW] [The four C's are zinc ligands]
- [1] Hirashima S., Hirai H., Nakanishi Y., Natori S. J. Biol. Chem. 263:3858-3863(1988).[2] Kipling D., Kearsey S.E. Nature 353:509-509(1991).[3] Langer D., Zillig W. Nucleic Acids Res. 21:2251-2251(1993).[4] Ahn B.-Y., Gershon P.D., Jones E.V., Moss B. Mol. Cell. Biol. 10:5433-5441(1990).[5] Rodriguez J.M., Salas M.L., Vinuela E. Virology 186:40-52(1992).[6] Qian X., Jeon C., Yoon H., Agarwal K., Weiss M.A. Nature 365:277-279(1993).

- 15 638. Tetrahydrofolate dehydrogenase/cyclohydrolase signatures (THF DHG CYH)
- Enzymes that participate in the transfer of one-carbon units are involved in various biosynthetic pathways. In many of these processes the transfers of one-carbon units are mediated by the coenzyme tetrahydrofolate (THF). Various reactions generate one-carbon derivatives of THF which can be interconverted between different oxidation states by
- 20 formyltetrahydrofolate synthetase(EC 6.3.4.3), methylenetetrahydrofolate dehydrogenase (EC 1.5.1.5 or EC 1.5.1.15) and methenyltetrahydrofolate cyclohydrolase (EC 3.5.4.9). The dehydrogenase and cyclohydrolase activities are expressed by a variety of multifunctional enzymes: - Eukaryotic C-1-tetrahydrofolate synthase (C1-THF synthase), which catalyzes all three reactions described above. Two forms of C1-THF synthases are known [1], one is
- 25 located in the mitochondrial matrix, while the second one is cytoplasmic. In both forms the dehydrogenase/cyclohydrolase domain is located in the N-terminal section of the 900 amino acids protein and consists of about 300 amino acid residues. The C1-THF synthases are NADP- dependent. - Eukaryotic mitochondrial bifunctional dehydrogenase/cyclohydrolase [2]. This is an homodimeric NAD-dependent enzyme of about 300 amino acid residues. -
- 30 Bacterial fold [3]. Fold is an homodimeric bifunctional NADP-dependent enzyme of about 290 amino acid residues. The sequence of the dehydrogenase/cyclohydrolase domain is highly conserved in all forms of the enzyme. Two conserved regions have been selected as signature patterns. The first one is located in the N-terminal part of these enzymes and

contains three acidic residues. The second pattern is a highly conserved sequence of 9 amino acids which is located in the C-terminal section.

Consensus pattern: [EQ]-x-[EQK]-[LIVM SEQ ID NO:4)](2)-x(2)-[LIVM SEQ ID NO:4)]-x(2)-[LIVMY SEQ ID NO:141)]-N-x-[DN]- x(5)-[LIVMF SEQ ID NO:2)](3)-Q-L-P-[LV]

5 Consensus pattern: P-G-G-V-G-P-[MF]-T-[IV]

[1] Shannon K.W., Rabinowitz J.C. J. Biol. Chem. 263:7717-7725(1988).[2] Belanger C., Mackenzie R.E. J. Biol. Chem. 264:4837-4843(1989).[3] d'Ari L., Rabinowitz J.C. J. Biol. Chem. 266:23953-23958(1991).

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639. Triosephosphate isomerase active site (TIM)

Triosephosphate isomerase (EC 5.3.1.1) (TIM) [1] is the glycolytic enzyme that catalyzes the reversible interconversion of glyceraldehyde 3-phosphate and dihydroxyacetone phosphate.

TIM plays an important role in several metabolic pathways and is essential for efficient

15

energy production. It is a dimer of identical subunits, each of which is made up of about 250 amino-acid residues. A glutamic acid residue is involved in the catalytic mechanism [2]. The sequence around the active site residue is perfectly conserved in all known TIM's and can be used as a signature pattern for this type of enzyme.

Consensus pattern: [AV]-Y-E-P-[LIVM SEQ ID NO:4)]-W-[SA]-I-G-T-[GK] [E is the active site residue]

20

[1] Lolis E., Alber T., Davenport R.C., Rose D., Hartman F.C., Petsko G.A. Biochemistry 29:6609-6618(1990).[2] Knowles J.R. Nature 350:121-124(1991).

25 640. Thymidine kinase cellular-type signature (TK)

Thymidine kinase (TK) (EC 2.7.1.21) is an ubiquitous enzyme that catalyzes the ATP-

dependent phosphorylation of thymidine. A comparison of TK sequences has shown [1,2,3]

that there are two different families of TK. One family groups together TK from herpes

viruses as well as cellular thymidylate kinases, while the second family currently consists of

30

TK from the following sources: - Vertebrates. - Bacterial. - Bacteriophage T4. - Pox viruses. - African swine fever virus (ASF). - Fish lymphocystis disease virus (FLDV). A conserved region which is located in the C-terminal section of these enzymes has been selected as a signature pattern for this family of TKA.

Consensus pattern: [GA]-x(1,2)-[DE]-x-Y-x-[STAP SEQ ID NO:135)]-x-C-[NKR]-x-[CH]-[LIVMFYWH SEQ ID NO:591)]

[1] Boyle D.B., Coupar B.E.H., Gibbs A.J., Seigman L.J., Both G.W. Virology 156:355-365(1987).[2] Blasco R., Lopez-Otin C., Munoz M., Bockamp E.-O., Simon-Mateo C., Vinuela E. Virology 178:301-304(1990).[3] Robertson G.R., Whalley J.M. Nucleic Acids Res. 16:11303-11317(1988).

641. Thymidine kinase from herpesvirus (TK herpes)

[1]

Medline: 96003730

Crystal structures of the thymidine kinase from herpes simplex virus type-1 in complex with deoxythymidine and ganciclovir.

Brown DG, Visse R, Sandhu G, Davies A, Rizkallah PJ, Melitz C, Summers WC, Sanderson MR;
Nat Struct Biol 1995;2:876-881.

Number of members: 65

642. Nuclear transition protein 2 signatures (TP2)

In mammals, the second stage of spermatogenesis is characterized by the conversion of nucleosomal chromatin to the compact, non-nucleosomal and transcriptionally inactive form found in the sperm nucleus. This condensation is associated with a double-protein transition.

The first transition corresponds to the replacement of histones by several spermatid-specific proteins, also called transition proteins, which are themselves replaced by protamines during the second transition. Nuclear transition protein 2 (TP2) is one of those spermatid-specific proteins. TP2 is a basic, zinc-binding protein [1] of 116 to 137 amino-acid residues.

Structurally, TP2 consists of three distinct parts: a conserved serine-rich N-terminal domain of about 25 residues, a variable central domain of 20 to 50 residues which contains cysteine residues, and a conserved C-terminal domain of about 70 residues rich in lysines and

arginines. Two signature patterns for TP2 have been developed: one located in the N-terminal domain, the other in the C-terminal.

533

Consensus pattern: H-x(3)-H-S-[NS]-S-x-P-Q-S

Consensus pattern: K-x-R-K-x(2)-E-G-K-x(2)-K-[KR]-K

[1] Baskaran R., Rao M.R.S. Biochem. Biophys. Res. Commun. 179:1491-1499(1991).

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643. Thiamine pyrophosphate enzymes signature (TTP enzymes)

A number of enzymes require thiamine pyrophosphate (TPP) (vitamin B1) as a cofactor. It has been shown [1] that some of these enzymes are structurally related. These related TPP enzymes are: - Pyruvate oxidase (POX) (EC 1.2.3.3) Reaction catalyzed: pyruvate +

10

orthophosphate + O(2) + H(2)O = acetyl phosphate + CO(2) + H(2)O(2). - Pyruvate decarboxylase (PDC) (EC 4.1.1.1) Reaction catalyzed: pyruvate = acetaldehyde + CO(2). -

Indolepyruvate decarboxylase (EC 4.1.1.74) [2] Reaction catalyzed: indole-3-pyruvate = indole-3-acetaldehyde + CO(2). - Acetolactate synthase (ALS) (EC 4.1.3.18) Reaction

15

catalyzed: 2 pyruvate = acetolactate + CO(2). - Benzoylformate decarboxylase (BFD) (EC 4.1.1.7) [3] Reaction catalyzed: benzoylformate = benzaldehyde + CO(2). A conserved region which is located in their C-terminal section has been selected as a signature pattern for these enzymes.

Consensus pattern: [LIVMF SEQ ID NO:2)]-[GSA]-x(5)-P-x(4)-[LIVMFYW SEQ ID NO:26)]-x-[LIVMF SEQ ID NO:2)]-x-G-D-[GSA]- [GSAC SEQ ID NO:93)]

20

[1] Green J.B.A. FEBS Lett. 246:1-5(1989).[2] Koga J., Adachi T., Hidaka H. Mol. Gen. Genet. 226:10-16(1991).[3] Tsou A.Y., Ransom S.C., Gerlt J.A., Buechter D.D., Babbitt P.C., Kenyon G.L. Biochemistry 29:9856-9862(1990).

25

644. TPR Domain

[1]

Medline: 95397415

Tetratricopeptide repeat interactions: to TPR or not to TPR?

Lamb JR, Tugendreich S, Hieter P;

30

Trends Biochem Sci 1995;20:257-259.

[2]Medline: 98151343

The structure of the tetratricopeptide repeats of protein phosphatase 5: implications for TPR-mediated protein-protein

interactions.

Das AK, Cohen PW, Barford D;

EMBO J 1998;17:1192-1199.

Number of members: 621

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645. Uroporphyrin-III C-methyltransferase signatures (TP methylase)

Uroporphyrin-III C-methyltransferase (EC 2.1.1.107) (SUMT) [1,2] catalyzes the transfer of two methyl groups from S-adenosyl-L-methionine to the C-2 and C-7 atoms of

10 uroporphyrinogen III to yield precorrin-2 via the intermediate formation of precorrin-1.

SUMT is the first enzyme specific to the cobalamin pathway and precorrin-2 is a common intermediate in the biosynthesis of corrinoids such as vitamin B12, siroheme and coenzyme F430. The sequences of SUMT from a variety of eubacterial and archaebacterial species are currently available. In species such as *Bacillus megaterium* (gene *cobA*), *Pseudomonas*

15 *denitrificans* (*cobA*) or *Methanobacterium ivanovii* (gene *corA*) SUMT is a protein of about 25 to 30 Kd. In *Escherichia coli* and related bacteria, the *cysG* protein, which is involved in the biosynthesis of siroheme, is a multifunctional protein composed of a N-terminal domain, probably involved in transforming precorrin-2 into siroheme, and a C-terminal domain which has SUMT activity. The sequence of SUMT is related to that of a number of *P. denitrificans*
20 and *Salmonella typhimurium* enzymes involved in the biosynthesis of cobalamin which also seem to be SAM-dependent methyltransferases [3,4]. The similarity is especially strong with two of these enzymes: *cobI/cbiL* which encodes S-adenosyl-L-methionine--precorrin-2 methyltransferase and *cobM/cbiF* whose exact function is not known. Two signature patterns have been developed for these enzymes. The first corresponds to a well conserved region in
25 the N-terminal extremity (called region 1 in [1,3]) and the second to a less conserved region located in the central part of these proteins (this pattern spans what are called regions 2 and 3 in [1,3]).

Consensus pattern: [LIVM SEQ ID NO:4)]-[GS]-[STAL SEQ ID NO:471)]-G-P-G-x(3)-
[LIVMFY SEQ ID NO:18)]-[LIVM SEQ ID NO:4)]-T-[LIVM SEQ ID NO:4)]- [KRHQG
30 SEQ ID NO:592)]-[AG]

Consensus pattern: V-x(2)-[LI]-x(2)-G-D-x(3)-[FYW]-[GS]-x(8)-[LIVF SEQ ID NO:127)]-
x(5,6)- [LIVMFYWPAC SEQ ID NO:593)]-x-[LIVMY SEQ ID NO:141)]-x-P-G

[1] Blanche F., Robin C., Couder M., Faucher D., Cauchois L., Cameron B., Crouzet J. J. Bacteriol. 173:4637-4645(1991).[2] Robin C., Blanche F., Cauchois L., Cameron B., Couder M., Crouzet J. J. Bacteriol. 173:4893-4896(1991).[3] Crouzet J., Cameron B., Cauchois L., Rigault S., Rouyez M.-C., Blanche F., Thibaut D., Debussche L. J. Bacteriol. 172:5980-5990(1990).[4] Roth J.R., Lawrence J.G., Rubenfield M., Kieffer-Higgins S., Church G.M. J. Bacteriol. 175:3303-3316(1993).[5] Mattheakis L.C., Shen W.H., Collier R.J. Mol. Cell. Biol. 12:4026-4037(1992).

10 646. Tudor domain

Domain of unknown function present in several RNA-binding proteins. copies in the Drosophila Tudor protein. Slight ambiguities in the alignment.Number of members: 18
[1]Medline: 97200561 Tudor domains in proteins that interact with RNA. Ponting CP; Trends Biochem Sci 1997;22:51-52. [2]Medline: 97157029 The human EBNA-2 coactivator p100: multidomain organization and relationship to the staphylococcal nuclease fold and to the tudor protein involved in Drosophila melanogaster development. Callebaut I, Mornon JP; Biochem J 1997;321:125-132.

20 647. Terpene synthase family

It has been suggested that this gene family be designated tps (for terpene synthase) [1]. It has been split into six subgroups on the basis of phylogeny, called tpsa-tpsf.
tpsa includes vetispiradiene synthase Swiss:Q39979, 5-epi-aristolochene synthase, Swiss:Q40577 and (+)-delta-cadinene synthase Swiss:P93665.
tpsb includes (-)-limonene synthase, Swiss:Q40322.
tpsc includes kaurene synthase A, Swiss:O04408.
tpsd includes taxadiene synthase, Swiss:Q41594, pinene synthase, Swiss:O24475 and myrcene synthase, Swiss:O24474.
tpse includes kaurene synthase B.
tpsf includes linalool synthase.

Number of members: 51

[1]

Medline: 97413772

Monoterpene synthases from grand fir (*Abies grandis*). cDNA
isolation, characterization, and functional expression of
myrcene synthase, (-)-(4S)-limonene synthase, and
(-)-(1S,5S)-pinene synthase.

Bohlmann J, Steele CL, Croteau R;
J Biol Chem 1997;272:21784-21792.

648. ThiF family

This family contains a repeated domain in ubiquitin
activating enzyme E1 and members of the bacterial
ThiF/MoeB/HesA family. Number of members: 87

649. Thioester dehydrase

Members of this family are involved in fatty acid biosynthesis.
Number of members: 19

[1]

Medline: 96398612

Structure of a dehydratase-isomerase from the bacterial
pathway for biosynthesis of unsaturated fatty acids: two
catalytic activities in one active site.

Leesong M, Henderson BS, Gillig JR, Schwab JM, Smith JL;
Structure 1996;4:253-264.

Database Reference: SCOP; 1mka; fa; [SCOP-USA][CATH-PDBSUM]

Database reference: PFAMB; PB058036;

650. Tub family signatures

The mouse tubby mutation is the cause of maturity-onset obesity, insulin resistance and
sensory deficits. This mutation maps to a gene, tub [1,2], which codes for a protein that

belongs to a family which currently consists of the following members: - Mammalian tub, an hydrophilic protein of about 500 residues, which could be involved in the hypothalamic regulation of body weight. - Human protein TULP1 [3] which may be involved in retinis pigmentosa 14, a retinal degeneration disease. - Mouse protein p4-6 whose function is not known. - *Caenorhabditis elegans* hypothetical protein F10B5.4. - Several fragmentary sequences from plants, *Drosophila* and human ESTs. While the N-terminal part of these protein is not conserved in length nor in the sequence, the C-terminal 250 residues are highly conserved. Therefore, two regions were selected in the C-terminal part as signature patterns. The second region is located at the C-terminal extremity and contains a penultimate cysteine residue that could be critical to the normal functioning of these proteins.

Consensus pattern: F-[KHQ]-G-R-V-[ST]-x-A-S-V-K-N-F-Q

Consensus pattern: A-F-[AG]-I-[SAC]-[LIVM SEQ ID NO:4)]-[ST]-S-F-x-[GST]-K-x-A-C-E

[1] Kleyn P.W., Fan W., Kovats S.G., Lee J.L., Pulido J.C., Wu Y., Berkemeier L.R.,

Misumi D.J., Holmgren L., Charlat O., Woolf E.A., Tayber O., Brody T., Shu P., Hawkins F., Kennedy B., Baldini L., Ebeling C., Alperin G.D., Deeds J., Lakey N.D., Culpepper J., Chen H., Gluecksmann-Kuis M.A., Carlson G.A., Duyk G.M., Moore K.J. Cell 85:281-290(1996).

[2] Noben-Trauth K., Naggert J.K., North M.A., Nishina P.M. *Nature* 380:534-538(1996).[3]

North M.A., Naggert J.K., Yan Y., Noben-Trauth K., Nishina P.M. *Proc. Natl. Acad. Sci.*

U.S.A. 94:3128-3133(1997).

651. Eukaryotic DNA topoisomerase I active site

DNA topoisomerase I (EC 5.99.1.2) [1,2,3,4,E1] is one of the two types of enzyme that catalyze the interconversion of topological DNA isomers. Type I topoisomerases act by catalyzing the transient breakage of DNA, one strand at a time, and the subsequent rejoining of the strands. When a eukaryotic type I topoisomerase breaks a DNA backbone bond, it simultaneously forms a protein-DNA link where the hydroxyl group of a tyrosine residue is joined to a 3'-phosphate on DNA, at one end of the enzyme-severed DNA strand. In eukaryotes and pox virus topoisomerases I, there are a number of conserved residues in the region around the active site tyrosine.

Consensus pattern: [DEN]-x(6)-[GS]-[IT]-S-K-x(2)-Y-[LIVM SEQ ID NO:4)]-x(3)-[LIVM SEQ ID NO:4)] [Y is the active site tyrosine]

[1] Sternglanz R. Curr. Opin. Cell Biol. 1:533-535(1990).[2] Sharma A., Mondragon A. Curr. Opin. Struct. Biol. 5:39-47(1995).[3] Lynn R.M., Bjornsti M.-A., Caron P.R., Wang J.C. Proc. Natl. Acad. Sci. U.S.A. 86:3559-3563(1989).[4] Roca J. Trends Biochem. Sci. 20:156-160(1995).[E1]

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652. Transaldolase signatures

Transaldolase (EC 2.2.1.2) catalyzes the reversible transfer of a three-carbonketol unit from sedoheptulose 7-phosphate to glyceraldehyde 3-phosphate to form erythrose 4-phosphate and fructose 6-phosphate. This enzyme, together with transketolase, provides a link between the glycolytic and pentose-phosphate pathways. Transaldolase is an enzyme of about 34 Kd whose sequence has been well conserved throughout evolution. A lysine has been implicated [1]in the catalytic mechanism of the enzyme; it acts as a nucleophilic group that attacks the carbonyl group of fructose-6-phosphate. Transaldolase is evolutionary related [2] to a bacterial protein of about 20Kd (known as talC in Escherichia coli), whose exact function is not yet known. Two signature patterns have been developed for these proteins. The first, located in the N-terminal section, contains a perfectly conserved pentapeptide; these cond, includes the active site lysine.

Consensus pattern: [DG]-[IVSA SEQ ID NO:594)]-T-[ST]-N-P-[STA]-[LIVMF SEQ ID NO:2)](2)

Consensus pattern: [LIVM SEQ ID NO:4)]-x-[LIVM SEQ ID NO:4)]-K-[LIVM SEQ ID NO:4)]-[PAS]-x-[ST]-x-[DENQPAS SEQ ID NO:595)]-G- [LIVM SEQ ID NO:4)]-x-[AGV]-x-[QEKIRST SEQ ID NO:596)]-x-[LIVM SEQ ID NO:4)] [K is the active site residue]

[1] Miosga T., Schaaff-Gerstenschlaeger I., Franken E., Zimmermann F.K. Yeast 9:1241-1249(1993).[2] Reizer J., Reizer A., Saier M.H. Jr. Microbiology 141:961-971(1995).

653. (Transpeptidase) Penicillin binding protein transpeptidase domain

30

The active site serine (residue 337 in Swiss:P14677) is conserved in all members of this family.

[1] Pares S, Mouz N, Petillot Y, Hakenbeck R, Dideberg O *Nat Struct Biol* 1996;3:284-289.

654. Trehalase signatures

5 Trehalase (EC 3.2.1.28) is the enzyme responsible for the degradation of the disaccharide alpha, alpha-trehalose yielding two glucose subunits [1]. It is an enzyme found in a wide variety of organisms and whose sequence has been highly conserved throughout evolution. Two of the most highly conserved regions have been selected as signature patterns. The first pattern is located in the central section, the second one is in the C-terminal region.

10 Consensus pattern: P-G-G-R-F-x-E-x-Y-x-W-D-x-Y

Consensus pattern: Q-W-D-x-P-x-[GA]-W-[PAS]-P

[1] Kopp M., Mueller H., Holzer H. *J. Biol. Chem.* 268:4766-4774(1993).[2] Henrissat B., Bairoch A. *Biochem. J.* 293:781-788(1993).[E1]

15

655. Trehalose-6-phosphate synthase domain

OtsA (Trehalose-6-phosphate synthase) is homologous to regions in the subunits of yeast trehalose-6-phosphate synthase/phosphate complex, [1].

[1] Kaasen I, McDougall J, Strom AR; *Gene* 1994;145:9-15.

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656. Tropomyosins signature

Tropomyosins [1,2] are family of closely related proteins present in muscle and non-muscle cells. In striated muscle, tropomyosin mediate the interactions between the troponin complex and actin so as to regulate muscle contraction. The role of tropomyosin in smooth muscle and non-muscle tissues is not clear. Tropomyosin is an alpha-helical protein that forms a coiled-coil dimer. Muscle isoforms of tropomyosin are characterized by having 284 amino acid residues and a highly conserved N-terminal region, whereas non-muscle forms are generally smaller and are heterogeneous in their N-terminal region. The signature pattern for tropomyosins is based on a very conserved region in the C-terminal section of tropomyosins and which is present in both muscle and non-muscle forms.

25

30

Consensus pattern: L-K-E-A-E-x-R-A-E

[1] Smilie L.B. Trends Biochem. Sci. 4:151-155(1979).[2] McLeod A.R. BioEssays 6:208-212(1986).

5 657. Troponin

Troponin (Tn) contains three subunits, Ca²⁺ binding (TnC), inhibitory (TnI), and tropomyosin binding (TnT). this Pfam contains members of the TnT subunit.

10 Troponin is a complex of three proteins, Ca²⁺ binding (TnC), inhibitory (TnI), and tropomyosin binding (TnT).

The troponin complex regulates Ca⁺⁺ induced muscle contraction.

This family includes troponin T and troponin I. Troponin I binds to actin and troponin T binds to tropomyosin.

Number of members: 81 [1]

15 Medline: 87144593

Structure of co-crystals of tropomyosin and troponin.

White SP, Cohen C, Phillips GN Jr;

Nature 1987;325:826-828. [2]

Medline: 95155315

20 A direct regulatory role for troponin T and a dual role for troponin C in the Ca²⁺ regulation of muscle contraction.

Potter JD, Sheng Z, Pan BS, Zhao J;

J Biol Chem 1995;270:2557-2562.

[3]Medline: 95324796

25 The troponin complex and regulation of muscle contraction.

Farah CS, Reinach FC;

FASEB J 1995;9:755-767.

30 658. (Tryp mucin) Mucin-like glycoprotein

This family of trypanosomal proteins resemble vertebrate mucins. The protein consists of three regions. The N and C termini are conserved between all members of the family,

whereas the central region is not well conserved and contains a large number of threonine residues which can be glycosylated [1].

Indirect evidence suggested that these genes might encode the core protein of parasite mucins, glycoproteins that were proposed to be involved in the interaction with, and invasion of, mammalian host cells.

[1] Di Noia JM, Sanchez DO, Frasch AC; J Biol Chem 1995;270:24146-24149.

[2] Di Noia JM, D'Orso I, Aslund L, Sanchez DO, Frasch AC; J Biol Chem 1998;273:10843-10850.

659. Aminoacyl-transfer RNA synthetases class-I signature (tRNA synt 1)

Aminoacyl-tRNA synthetases (EC 6.1.1.-) [1] are a group of enzymes which activate amino acids and transfer them to specific tRNA molecules as the first step in protein biosynthesis. In prokaryotic organisms there are at least twenty different types of aminoacyl-tRNA synthetases, one for each different amino acid. In eukaryotes there are generally two aminoacyl-tRNA synthetases for each different amino acid: one cytosolic form and a mitochondrial form. While all these enzymes have a common function, they are widely diverse in terms of subunit size and of quaternary structure. A few years ago it was found [2] that several aminoacyl-tRNA synthetases share a region of similarity in their N-terminal section, in particular the consensus tetrapeptide His-Ile-Gly-His ('HIGH') is very well conserved. The 'HIGH' region has been shown [3] to be part of the adenylate binding site. The 'HIGH' signature has been found in the aminoacyl-tRNA synthetases specific for arginine, cysteine, glutamic acid, glutamine, isoleucine, leucine, methionine, tyrosine, tryptophan, and valine. These aminoacyl-tRNA synthetases are referred to as class-I synthetases [4,5,6] and seem to share the same tertiary structure based on a Rossmann fold. Consensus pattern: P-x(0,2)-[GSTAN SEQ ID NO:296)]-[DENQGAPK SEQ ID NO:597)]-x-[LIVMFPP SEQ ID NO:598)]-[HT]-[LIVMYAC SEQ ID NO:599)]-G- [HNTG SEQ ID NO:600)]-[LIVMFYSTAGPC SEQ ID NO:601)]

[1] Schimmel P. Annu. Rev. Biochem. 56:125-158(1987).[2] Webster T., Tsai H., Kula M., Mackie G.A., Schimmel P. Science 226:1315-1317(1984).[3] Brick P., Bhat T.N., Blow D.M. J. Mol. Biol. 208:83-98(1988).[4] Delarue M., Moras D. BioEssays 15:675-

687(1993).[5] Schimmel P. Trends Biochem. Sci. 16:1-3(1991).[6] Nagel G.M., Doolittle R.F. Proc. Natl. Acad. Sci. U.S.A. 88:8121-8125(1991).

5 660. Aminoacyl-transfer RNA synthetases class-I signature (tRNA synt 1b)

Aminoacyl-tRNA synthetases (EC 6.1.1.-) [1] are a group of enzymes which activate amino acids and transfer them to specific tRNA molecules as the first step in protein biosynthesis. In prokaryotic organisms there are at least twenty different types of aminoacyl-tRNA synthetases, one for each different amino acid. In eukaryotes there are generally two aminoacyl-tRNA synthetases for each different amino acid: one cytosolic form and a mitochondrial form. While all these enzymes have a common function, they are widely diverse in terms of subunit size and of quaternary structure. A few years ago it was found [2] that several aminoacyl-tRNA synthetases share a region of similarity in their N-terminal section, in particular the consensus tetrapeptide His-Ile-Gly-His ('HIGH') is very well conserved. The 'HIGH' region has been shown [3] to be part of the adenylate binding site. The 'HIGH' signature has been found in the aminoacyl-tRNA synthetases specific for arginine, cysteine, glutamic acid, glutamine, isoleucine, leucine, methionine, tyrosine, tryptophan, and valine. These aminoacyl-tRNA synthetases are referred to as class-I synthetases [4,5,6] and seem to share the same tertiary structure based on a Rossmann fold.

20 Consensus pattern: P-x(0,2)-[GSTAN SEQ ID NO:296)]-[DENQGAPK SEQ ID NO:597)]-x-[LIVMFP SEQ ID NO:598)]-[HT]-[LIVMYAC SEQ ID NO:599)]-G- [HNTG SEQ ID NO:600)]-[LIVMFYSTAGPC

[1] Schimmel P. Annu. Rev. Biochem. 56:125-158(1987).[2] Webster T., Tsai H., Kula M., Mackie G.A., Schimmel P. Science 226:1315-1317(1984).[3] Brick P., Bhat T.N., Blow D.M. J. Mol. Biol. 208:83-98(1988).[4] Delarue M., Moras D. BioEssays 15:675-687(1993).[5] Schimmel P. Trends Biochem. Sci. 16:1-3(1991).[6] Nagel G.M., Doolittle R.F. Proc. Natl. Acad. Sci. U.S.A. 88:8121-8125(1991).

30 661. (tRNA-synt 1C) tRNA synthetases class I (E and Q)

Other tRNA synthetase sub-families are too dissimilar to be included.

This family includes only glutamyl and glutaminyl tRNA synthetases.

In some organisms, a single glutamyl-tRNA synthetase aminoacylates both tRNA(Glu) and tRNA(Gln).

[1] Rath VL, Silvian LF, Beijer B, Sproat BS, Steitz TA; Structure 1998;6:439-449.

5

662. (tRNA-synt 1d) tRNA synthetases class I (R)

Other tRNA synthetase sub-families are too dissimilar to be included.

10 This family includes only arginyl tRNA synthetase.

663. Aminoacyl-transfer RNA synthetases class-II signatures (tRNA synt 2)

15 Aminoacyl-tRNA synthetases (EC 6.1.1.-) [1] are a group of enzymes which activate amino acids and transfer them to specific tRNA molecules as the first step in protein biosynthesis. In prokaryotic organisms there are at least twenty different types of aminoacyl-tRNA synthetases, one for each different amino acid. In eukaryotes there are generally two aminoacyl-tRNA synthetases for each different amino acid: one cytosolic form and a mitochondrial form. While all these enzymes have a common function, they are widely
20 diverse in terms of subunit size and of quaternary structure. The synthetases specific for alanine, asparagine, aspartic acid, glycine, histidine, lysine, phenylalanine, proline, serine, and threonine are referred to as class-II synthetases [2 to 6] and probably have a common folding pattern in their catalytic domain for the binding of ATP and amino acid which is different to the Rossmann fold observed for the class I synthetases [7]. Class-II tRNA
25 synthetases do not share a high degree of similarity, however at least three conserved regions are present [2,5,8]. Signature patterns have been derived from two of these regions.

Consensus pattern: [FYH]-R-x-[DE]-x(4,12)-[RH]-x(3)-F-x(3)-[DE]

Consensus pattern: [GSTALVF SEQ ID NO:42]-{DENQHRKP SEQ ID NO:43}-[GSTA SEQ ID NO:19]-[LIVMF SEQ ID NO:2]-[DE]-R-[LIVMF SEQ ID NO:2])-x-

30 [LIVMSTAG SEQ ID NO:44]-[LIVMFY SEQ ID NO:18]]

[1] Schimmel P. Annu. Rev. Biochem. 56:125-158(1987).[2] Delarue M., Moras D.

BioEssays 15:675-687(1993).[3] Schimmel P. Trends Biochem. Sci. 16:1-3(1991).[4] Nagel

G.M., Doolittle R.F. Proc. Natl. Acad. Sci. U.S.A. 88:8121-8125(1991). [5] Cusack S.,

Haertlein M., Leberman R. *Nucleic Acids Res.* 19:3489-3498(1991).[6] Cusack S. *Biochimie* 75:1077-1081(1993).[7] Cusack S., Berthet-Colominas C., Haertlein M., Nassar N., Leberman R. *Nature* 347:249-255(1990).[8] Leveque F., Plateau P., Dessen P., Blanquet S. *Nucleic Acids Res.* 18:305-312(1990).

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664. Aminoacyl-transfer RNA synthetases class-I signature (tRNA synt 1e)

Aminoacyl-tRNA synthetases (EC 6.1.1.-) [1] are a group of enzymes which activate amino acids and transfer them to specific tRNA molecules as the first step in protein biosynthesis. In prokaryotic organisms there are at least twenty different types of aminoacyl-tRNA synthetases, one for each different amino acid. In eukaryotes there are generally two aminoacyl-tRNA synthetases for each different amino acid: one cytosolic form and a mitochondrial form. While all these enzymes have a common function, they are widely diverse in terms of subunit size and of quaternary structure. A few years ago it was found [2] that several aminoacyl-tRNA synthetases share a region of similarity in their N-terminal section, in particular the consensus tetrapeptide His-Ile-Gly-His ('HIGH') is very well conserved. The 'HIGH' region has been shown [3] to be part of the adenylate binding site. The 'HIGH' signature has been found in the aminoacyl-tRNA synthetases specific for arginine, cysteine, glutamic acid, glutamine, isoleucine, leucine, methionine, tyrosine, tryptophan, and valine. These aminoacyl-tRNA synthetases are referred to as class-I synthetases [4,5,6] and seem to share the same tertiary structure based on a Rossmann fold. Consensus pattern: P-x(0,2)-[GSTAN SEQ ID NO:296)]-[DENQGAPK SEQ ID NO:597)]-x-[LIVMFP SEQ ID NO:598)]-[HT]-[LIVMYAC SEQ ID NO:599)]-G- [HNTG SEQ ID NO:600)]-[LIVMFYSTAGPC

[1] Schimmel P. *Annu. Rev. Biochem.* 56:125-158(1987).[2] Webster T., Tsai H., Kula M., Mackie G.A., Schimmel P. *Science* 226:1315-1317(1984).[3] Brick P., Bhat T.N., Blow D.M. *J. Mol. Biol.* 208:83-98(1988).[4] Delarue M., Moras D. *BioEssays* 15:675-687(1993).[5] Schimmel P. *Trends Biochem. Sci.* 16:1-3(1991).[6] Nagel G.M., Doolittle R.F. *Proc. Natl. Acad. Sci. U.S.A.* 88:8121-8125(1991).

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665. Aminoacyl-transfer RNA synthetases class-II signatures (tRNA synt 2b)

Aminoacyl-tRNA synthetases (EC 6.1.1.-) [1] are a group of enzymes which activate amino acids and transfer them to specific tRNA molecules as the first step in protein biosynthesis. In prokaryotic organisms there are at least twenty different types of aminoacyl-tRNA synthetases, one for each different amino acid. In eukaryotes there are generally two aminoacyl-tRNA synthetases for each different amino acid: one cytosolic form and a mitochondrial form. While all these enzymes have a common function, they are widely diverse in terms of subunit size and of quaternary structure. The synthetases specific for alanine, asparagine, aspartic acid, glycine, histidine, lysine, phenylalanine, proline, serine, and threonine are referred to as class-II synthetases [2 to 6] and probably have a common folding pattern in their catalytic domain for the binding of ATP and amino acid which is different to the Rossmann fold observed for the class I synthetases [7]. Class-II tRNA synthetases do not share a high degree of similarity, however at least three conserved regions are present [2,5,8]. Signature patterns have been derived from two of these regions.

Consensus pattern: [FYH]-R-x-[DE]-x(4,12)-[RH]-x(3)-F-x(3)-[DE

Consensus pattern: [GSTALVF SEQ ID NO:42)]-{DENQHRKP SEQ ID NO:43)}-[GSTA SEQ ID NO:19)]-[LIVMF SEQ ID NO:2)]-[DE]-R-[LIVMF SEQ ID NO:2)]-x-[LIVMSTAG SEQ ID NO:44)]-[LIVMFY SEQ ID NO:18)]

[1] Schimmel P. Annu. Rev. Biochem. 56:125-158(1987).[2] Delarue M., Moras D. BioEssays 15:675-687(1993).[3] Schimmel P. Trends Biochem. Sci. 16:1-3(1991).[4] Nagel G.M., Doolittle R.F. Proc. Natl. Acad. Sci. U.S.A. 88:8121-8125(1991). [5] Cusack S., Haertlein M., Leberman R. Nucleic Acids Res. 19:3489-3498(1991).[6] Cusack S. Biochimie 75:1077-1081(1993).[7] Cusack S., Berthet-Colominas C., Haertlein M., Nassar N., Leberman R. Nature 347:249-255(1990).[8] Leveque F., Plateau P., Dessen P., Blanquet S. Nucleic Acids Res. 18:305-312(1990).

666. Thaumatin family signature

Thaumatococcus daniellii, an African brush. The protein is made of about 200 residues and contains 8 disulfide bonds. A number of proteins have been found to be related to thaumatins. These proteins are listed below (references are only provided for recently determined sequences). - A maize alpha-amylase/trypsin inhibitor. - Two tobacco pathogenesis-related proteins: PR-R major and minor forms, which are induced after

infection with viruses. - Salt-induced protein NP24 from tomato. - Osmotin, a salt-induced protein from tobacco. - Osmotin-like proteins OSML13, OSML15 and OSML81 from potato [2]. - P21, a leaf protein from soybean. - PWIR2, a leaf protein from wheat. - Zeamatin, a maize antifungal protein [3]. The exact biological function of all these proteins is not yet known. A conserved region that includes three cysteine residues known (in thaumatin) to be involved in disulfide bonds has been selected as a signature pattern.

```
+-----+ | +-----+ | | ***** |
||
```

```
xxCxxxxxxxxxxxxxxxxCxxCxxCxxxxxxxxxxxxxxxxCxxCxCxxxCxCxxCCxCxxxCxxxxxC
xxxCx ||||| ||| | +--+ +-+ | +--+ +--+ | +-----+'C': conserved cysteine
involved in a disulfide bond. '*': position of the pattern.
```

Consensus pattern: G-x-[GF]-x-C-x-T-[GA]-D-C-x(1,2)-G-x(2,3)-C

[1] Edens L., Heslinga L., Klok R., Ledebor A.M., Maat J., Toonen M.Y., Visser C., Verrips C.T. Gene 18:1-12(1982). [2] Zhu B., Chen T.H.H., Li P.H. Plant Physiol. 108:929-937(1995). [3] Malehorn D.E., Borgmeyer J.R., Smith C.E., Shah D.M.; Plant Physiol. 106:1471-1481(1994).

667. Thiolases signatures

Two different types of thiolase [1,2,3] are found both in eukaryotes and in prokaryotes: acetoacetyl-CoA thiolase (EC 2.3.1.9) and 3-ketoacyl-CoA thiolase (EC 2.3.1.16). 3-ketoacyl-CoA thiolase (also called thiolase I) has a broad chain-length specificity for its substrates and is involved in degradative pathways such as fatty acid beta-oxidation. Acetoacetyl-CoA thiolase (also called thiolase II) is specific for the thiolysis of acetoacetyl-CoA and involved in biosynthetic pathways such as poly beta-hydroxybutyrate synthesis or steroid biogenesis. In eukaryotes, there are two forms of 3-ketoacyl-CoA thiolase: one located in the mitochondrion and the other in peroxisomes. There are two conserved cysteine residues important for thiolase activity. The first located in the N-terminal section of the enzymes is involved in the formation of an acyl-enzyme intermediate; the second located at the C-terminal extremity is the active site base involved in deprotonation in the condensation reaction. Mammalian nonspecific lipid-transfer protein (nsL-TP) (also known as sterol carrier protein 2) is a protein which seems to exist in two different forms: a 14 Kd protein (SCP-2) and a larger 58 Kd protein (SCP-x). The former is found in the cytoplasm or the mitochondria and is involved in

lipid transport; the latter is found in peroxisomes. The C-terminal part of SCP-x is identical to SCP-2 while the N-terminal portion is evolutionary related to thiolases[4]. Three signature patterns have been developed for this family of proteins, two of which are based on the regions around the biologically important cysteines. The third is based on a highly conserved region in the C-terminal part of these proteins.

Consensus pattern: [LIVM SEQ ID NO:4)]-[NST]-x(2)-C-[SAGLI SEQ ID NO:602)]-[ST]-[SAG]-[LIVMFYNS SEQ ID NO:603)]-x- [STAG SEQ ID NO:20)]-[LIVM SEQ ID NO:4)]-x(6)-[LIVM SEQ ID NO:4)] [C is involved in formation of acyl-enzyme intermediate]

Consensus pattern: N-x(2)-G-G-x-[LIVM SEQ ID NO:4)]-[SA]-x-G-H-P-x-[GA]-x-[ST]-G

Consensus pattern: [AG]-[LIVMA SEQ ID NO:30)]-[STAGCLIVM SEQ ID NO:604)]-[STAG SEQ ID NO:20)]-[LIVMA SEQ ID NO:30)]-C-x-[AG]-x-[AG]-x- [AG]-x-[SAG] [C is the active site residue]

[1] Peoples O.P., Sinskey A.J. J. Biol. Chem. 264:15293-15297(1989).[2] Yang S.-Y., Yang X.-Y.H., Healy-Louie G., Schulz H., Elzinga M. J. Biol. Chem. 265:10424-10429(1990).[3] Igual J.C., Gonzalez-Bosch C., Dopazo J., Perez-Ortin J.E. J. Mol. Evol. 35:147-155(1992).[4] Baker M.E., Billheimer J.T., Strauss J.F. III DNA Cell Biol. 10:695-698(1991).

668. Thioredoxin family active site

Thioredoxins [1 to 4] are small proteins of approximately one hundred amino-acid residues which participate in various redox reactions via the reversible oxidation of an active center disulfide bond. They exist in either a reduced form or an oxidized form where the two cysteine residues are linked in an intramolecular disulfide bond. Thioredoxin is present in prokaryotes and eukaryotes and the sequence around the redox-active disulfide bond is wellconserved. Bacteriophage T4 also encodes for a thioredoxin but its primary structure is not homologous to bacterial, plant and vertebrate thioredoxins. A number of eukaryotic proteins contain domains evolutionary related tothioredoxin, all of them seem to be protein disulphide isomerases (PDI). PDI(EC 5.3.4.1) [5,6,7] is an endoplasmic reticulum enzyme that catalyzes the rearrangement of disulfide bonds in various proteins. The various forms of PDI which are currently known are: - PDI major isozyme; a multifunctional protein that also function as the beta subunit of prolyl 4-hydroxylase (EC 1.14.11.2), as a component of oligosaccharyl transferase (EC 2.4.1.119), as thyroxine deiodinase (EC 3.8. 1.4), as glutathione-insulin transhydrogenase (EC 1.8.4.2) and as a thyroid hormone-binding protein !

- ERp60 (ER-60; 58 Kd microsomal protein). ERp60 was originally thought to be a phosphoinositide-specific phospholipase C isozyme and later to be a protease. - ERp72. - P5. All PDI contains two or three (ERp72) copies of the thioredoxin domain. Bacterial proteins that act as thiol:disulfide interchange proteins that allows disulfide bond formation in some periplasmic proteins also contain a thioredoxin domain. These proteins are: -

5 Escherichia coli dsbA (or prfA) and its orthologs in Vibrio cholerae (tcpG) and Haemophilus influenzae (por). - Escherichia coli dsbC (or xpRA) and its orthologs in Erwinia chrysanthemi and Haemophilus influenzae. - Escherichia coli dsbD (or dipZ) and its Haemophilus influenzae ortholog. - Escherichia coli dsbE (or ccmG) and orthologs in Haemophilus

10 influenzae, Rhodobacter capsulatus (helX), Rhizobiaceae (cycY and tlpA). Consensus pattern: [LIVMF SEQ ID NO:2)]-[LIVMSTA SEQ ID NO:433)]-x-[LIVMFYC SEQ ID NO:6)]-[FYWSTHE SEQ ID NO:605)]-x(2)-[FYWGTN SEQ ID NO:606)]-C-[GATPLVE SEQ ID NO:607)]-[PHYWSTA SEQ ID NO:608)]-C-x(6)-[LIVMFYWT SEQ ID NO:47)] [The two C's form the redox-active bond]

15 [1] Holmgren A. Annu. Rev. Biochem. 54:237-271(1985).[2] Gleason F.K., Holmgren A. FEMS Microbiol. Rev. 54:271-297(1988).[3] Holmgren A. J. Biol. Chem. 264:13963-13966(1989).[4] Eklund H., Gleason F.K., Holmgren A. Proteins 11:13-28(1991).[5] Freedman R.B., Hawkins H.C., Murrant S.J., Reid L. Biochem. Soc. Trans. 16:96-99(1988).[6] Kivirikko K.I., Myllyla R., Pihlajaniemi T. FASEB J. 3:1609-1617(1989).[7] Freedman

20 R.B., Hirst T.R., Tuite M.F. Trends Biochem. Sci. 19:331-336(1994).

669. (Transcript fac2) Transcription factor TFIIB repeat signature

In eukaryotes the initiation of transcription of protein encoding genes by polymerase II is

25 modulated by general and specific transcription factors. The general transcription factors operate through common promoters elements (such as the TATA box). At least seven different proteins associates to form the general transcription factors: TFIIA, -IIB, -IID, -IIE, -IIF, -IIG, and -IIH[1]. Transcription factor IIB (TFIIB) plays a central role in the transcription of class II genes, it associates with a complex of TFIID-IIA bound to DNA (DA

30 complex) to form a ternary complex TFIID-IIA-IBB (DAB complex) which is then recognized by RNA polymerase II [2,3]. TFIIB is a protein of about 315 to 340 amino acid residues which contains, in its C-terminal part an imperfect repeat of a domain of about 75 residues. This repeat could contribute an element of symmetry to the folded protein. The

following proteins have been shown to be evolutionary related to TFIIB: - An archaeobacterial TFIIB homolog. In *Pyrococcus woesei* a previously undetected open reading frame has been shown [4] to be highly related to TFIIB. - Fungal transcription factor IIIB 70 Kd subunit (gene PCF4/TDS4/BRF1) [5]. This protein is a general activator of RNA polymerase III transcription and plays a role analogous to that of TFIIB in pol III transcription. The central section of the repeated domain, which is the most conserved part of that domain has been selected as a signature pattern.

Consensus pattern: G-[KR]-x(3)-[STAGN SEQ ID NO:24)]-x-[LIVMYA SEQ ID NO:609)]-[GSTA SEQ ID NO:19)](2)-[CSAV SEQ ID NO:155)]-[LIVM SEQ ID NO:4)]- [LIVMFY SEQ ID NO:18)]-[LIVMA SEQ ID NO:30)]-[GSA]-[STAC

[1] Weinmann R. Gene Expr. 2:81-91(1992).[2] Hawley D. Trends Biochem. Sci. 16:317-318(1991).[3] Ha I., Lane W.S., Reinberg D. Nature 352:689-695(1991).[4] Ouzounis C., Sander C. Cell 71:189-190(1992).[5] Khoo B., Brophy B., Jackson S.P. Genes Dev. 8:2879-2890(1994).

670. (transcript fact) MADS-box domain signature and profile

A number of transcription factors contain a conserved domain of 56 amino-acid residues, sometimes known as the MADS-box domain [E1]. They are listed below: - Serum response factor (SRF) [1], a mammalian transcription factor that binds to the Serum Response Element (SRE). This is a short sequence of dyad symmetry located 300 bp to the 5' end of the transcription initiation site of genes such as c-fos. - Mammalian myocyte-specific enhancer factors 2A to 2D (MEF2A to MEF2D). These proteins are transcription factor which binds specifically to the MEF2 element present in the regulatory regions of many muscle-specific genes. - *Drosophila* myocyte-specific enhancer factor 2 (MEF2). - Yeast GRM/PRTF protein (gene MCM1) [2], a transcriptional regulator of mating-type-specific genes. - Yeast arginine metabolism regulation protein I (gene ARGR1 or ARG80). - Yeast transcription factor RLM1. - Yeast transcription factor SMP1. - *Arabidopsis thaliana* agamous protein (AG) [3], a probable transcription factor involved in regulating genes that determines stamen and carpel development in wild-type flowers. Mutations in the AG gene result in the replacement of the stamens by petals and the carpels by a new flower. - *Arabidopsis thaliana* homeotic proteins Apetala1 (AP1), Apetala3 (AP3) and Pistillata (PI) which act locally to specify the identity of the floral meristem and to determine sepal and petal development [4]. - *Antirrhinum majus*

and tobacco homeotic protein *deficiens* (DEFA) and *globosa* (GLO) [5]. Both proteins are transcription factors involved in the genetic control of flower development. Mutations in DEFA or GLO cause the transformation of petals into sepals and of stamens into carpels. - *Arabidopsis thaliana* putative transcription factors AGL1 to AGL6 [6]. - *Antirrhinum majus* morphogenetic protein DEF H33 (*squamosa*). In SRF, the conserved domain has been shown [1] to be involved in DNA-binding and dimerization. A pattern that spans the complete length of the domain has been derived. The profile also spans the length of the MADS-box.

Consensus pattern: R-x-[RK]-x(5)-I-x-[DNGSK SEQ ID NO:610]-x(3)-[KR]-x(2)-T-[FY]-x-[RK](3)-x(2)-[LIVM SEQ ID NO:4]-x-K(2)-A-x-E-[LIVM SEQ ID NO:4]-[STA]-x-L-x(4)-[LIVM SEQ ID NO:4]-x-[LIVM SEQ ID NO:4](3)-x(6)-[LIVMF SEQ ID NO:2]-x(2)-[FY]

[1] Norman C., Runswick M., Pollock R., Treisman R. *Cell* 55:989-1003(1988).[2] Passmore S., Maine G.T., Elble R., Christ C., Tye B.-K. *J. Mol. Biol.* 204:593-606(1988).[3] Yanofsky M., Ma H., Bowman J., Drews G., Feldmann K.A., Meyerowitz E.M. *Nature* 346:35-39(1990).[4] Goto K., Meyerowitz E.M. *Genes Dev.* 8:1548-1560(1994).[5] Troebner W., Ramirez L., Motte P., Hue I., Huijser P., Loennig W.-E., Saedler H., Sommer H., Schwartz-Sommer Z. *EMBO J.* 11:4693-4704(1992).[6] Ma H., Yanofsky M.F., Meyerowitz E.M. *Genes Dev.* 5:484-495(1991).[E1]

671. Transketolase signatures

Transketolase (EC 2.2.1.1) (TK) catalyzes the reversible transfer of a two-carbon ketol unit from xylulose 5-phosphate to an aldose receptor, such as ribose 5-phosphate, to form sedoheptulose 7-phosphate and glyceraldehyde 3-phosphate. This enzyme, together with transaldolase, provides a link between the glycolytic and pentose-phosphate pathways. TK requires thiamin pyrophosphate as a cofactor. In most sources where TK has been purified, it is a homodimer of approximately 70 Kd subunits. TK sequences from a variety of eukaryotic and prokaryotic sources [1,2] show that the enzyme has been evolutionarily conserved. In the peroxisomes of methylotrophic yeast *Hansenula polymorpha*, there is a highly related enzyme, dihydroxy-acetone synthase (DHAS) (EC 2.2.1.3) (also known as formaldehyde transketolase), which exhibits a very unusual specificity by including formaldehyde amongst its substrates. 1-deoxyxylulose-5-phosphate synthase (DXP synthase) [3] is an enzyme so far found in bacteria (gene *dxs*) and plants (gene *CLA1*) which catalyzes the thiamin

pyrophosphoate-dependent acyloin condensation reaction between carbon atoms 2 and 3 of pyruvate and glyceraldehyde 3-phosphate to yield 1-deoxy-D- xylulose-5-phosphate (dxp), a precursor in the biosynthetic pathway to isoprenoids, thiamin (vitamin B1), and pyridoxol (vitamin B6). DXP synthase is evolutionary related to TK. Two regions of TK have been selected as signature patterns. The first, located in the N-terminal section, contains a histidine residue which appears to function in proton transfer during catalysis [4]. The second, located in the central section, contains conserved acidic residues that are part of the active cleft and may participate in substrate-binding [4].

Consensus pattern: R-x(3)-[LIVMTA SEQ ID NO:311)]-[DENQSTHKF SEQ ID NO:611)]-x(5,6)-[GSN]-G-H-[PLIVMF SEQ ID NO:612)]- [GSTA SEQ ID NO:19)]-x(2)-[LIMC SEQ ID NO:613)]-[GS

Consensus pattern: G-[DEQGSA SEQ ID NO:614)]-[DN]-G-[PAEQ SEQ ID NO:615)]-[ST]-[HQ]-x-[PAGM SEQ ID NO:616)]-[LIVMYAC SEQ ID NO:599)]- [DEFYW SEQ ID NO:617)]-x(2)-[STAP SEQ ID NO:135)]-x(2)-[RGA]

[1] Abedinia M., Layfield R., Jones S.M., Nixon P.F., Mattick J.S. *Biochem. Biophys. Res. Commun.* 183:1159-1166(1992).[2] Fletcher T.S., Kwee I.L., Nakada T., Largman C., Martin B.M. *Biochemistry* 31:1892-1896(1992).[3] Sprenger G.A., Schorken U., Wiegert T., Grolle S., De Graaf A.A., Taylor S.V., Begley T.P., Bringer-Meyer S., Sahm H. *Proc. Natl. Acad. Sci. U.S.A.* 94:12857-12862(1997).[4] Lindqvist Y., Schneider G., Ermler U., Sundstroem M. *EMBO J.* 11:2373-2379(1992).

672. Transmembrane 4 family signature

Recently a number of eukaryotic cell surface antigens have been found to be evolutionary related [1,2,3]. The proteins known to belong to this family are listed below: - Mammalian antigen CD9 (MIC3); A protein involved in platelet activation and aggregation. - Mammalian leukocyte antigen CD37, expressed on B lymphocytes. - Mammalian leukocyte antigen CD53 (OX-44), which may be involved in growth regulation in hematopoietic cells. - Mammalian lysosomal membrane protein CD63 (melanoma-associated antigen ME491; antigen AD1). - Mammalian antigen CD81 (cell surface protein TAPA-1), which may play an important role in the regulation of lymphoma cell growth. - Mammalian antigen CD82 (protein R2; antigen C33; Kangai 1 (KAI1)), which associates with CD4 or CD8 and delivers costimulatory signals for the TCR/CD3 pathway. - Mammalian antigen CD151 (SFA-1; platelet-endothelial

tetraspan antigen 3 (PETA-3)). - Mammalian cell surface glycoprotein A15 (TALLA-1; MXS1). - Mammalian novel antigen 2 (NAG-2). - Human tumor-associated antigen CO-029.

- *Schistosoma mansoni* and *japonicum* 23 Kd surface antigen (SM23 / SJ23). These proteins share the following characteristics: they all seem to be type III membrane proteins (type III

proteins are integral membrane proteins that contain a N-terminal membrane-anchoring domain which is not cleaved during biosynthesis and which functions both as a translocation signal and as a membrane anchor); they also contain three additional transmembrane regions, at least seven conserved cysteines residues, and are of approximately the same size (218 to 284 residues). These proteins are collectively known as the 'transmembrane 4 super family'

(TM4) because they span the plasma membrane four times. A schematic diagram of the domain structure of these proteins is shown below.

```

+-----+-----+-----+-----+-----+-----+-----+-----+
+-----+-----+-----+ | TMa | Extra | TM2 | Cyt | TM3 | Extracellular | TM4 | Cyt | +-----+
+-----+-----C-----C-----+-----CC-----C-----C---+-----C-----+ *****Cyt : cytoplasmic

```

domain. TMa : transmembrane anchor. TM2 to TM4: transmembrane regions 2 to 4. 'C' :

conserved cysteine. '*' : position of the pattern.

A conserved region that includes two cysteines and seems to be located in a short cytoplasmic loop between two transmembrane domains has been selected as a signature for these proteins.

Consensus pattern: G-x(3)-[LIVMF SEQ ID NO:2]-x(2)-[GSA]-[LIVMF SEQ ID

NO:2)](2)-G-C-x-[GA]-[STA]-x(2)-[EG]-x(2)-[CWN]-[LIVM SEQ ID NO:4)](2)

[1] Levy S., Nguyen V.Q., Andria M.L., Takahashi S. J. Biol. Chem. 266:14597-

14602(1991).[2] Tomlinson M.G., Williams A.F., Wright M.D. Eur. J. Immunol. 23:136-

40(1993).[3] Barclay A.N., Birkeland M.L., Brown M.H., Beyers A.D., Davis S.J., Somoza

C., Williams A.F. The leucocyte antigen factbooks. Academic Press, London / San Diego,

(1993).

673. Tryptophan synthase alpha chain signature

Tryptophan synthase catalyzes the last step in the biosynthesis of tryptophan: the conversion of indoleglycerol phosphate and serine, to tryptophan and glyceraldehyde 3-phosphate [1,2]. It has two functional domains: one for the aldol cleavage of indoleglycerol phosphate to indole and glyceraldehyde 3-phosphate and the other for the synthesis of tryptophan from indole and serine. In bacteria and plants [3], each domain is found on a separate subunit (alpha and beta

chains), while in fungi the two domains are fused together on a single multifunctional protein. A conserved region that contains three conserved acidic residues has been selected as a signature pattern for the alpha chain. The first and the third acidic residues are believed to serve as proton donors/acceptors in the enzyme's catalytic mechanism.

- 5 Consensus pattern: [LIVM SEQ ID NO:4)]-E-[LIVM SEQ ID NO:4)]-G-x(2)-[FYC]-[ST]-[DE]-[PA]-[LIVMY SEQ ID NO:141)]- [AGLI SEQ ID NO:618)]-[DE]-G
 [1] Crawford I.P. Annu. Rev. Microbiol. 43:567-600(1989).[2] Hyde C.C., Miles E.W. Bio/Technology 8:27-32(1990).[3] Berlyn M.B., Last R.L., Fink G.R. Proc. Natl. Acad. Sci. U.S.A. 86:4604-4608(1989).

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674. Tryptophan synthase beta chain pyridoxal-phosphate attachment site

Tryptophan synthase catalyzes the last step in the biosynthesis of tryptophan: the conversion of indoleglycerol phosphate and serine, to tryptophan and glyceraldehyde 3-phosphate [1,2]. It has two functional domains: one for the aldol cleavage of indoleglycerol phosphate to indole and glyceraldehyde 3-phosphate and the other for the synthesis of tryptophan from indole and serine. In bacteria and plants [3], each domain is found on a separate subunit (alpha and beta chains), while in fungi the two domains are fused together on a single multifunctional protein. The beta chain of the enzyme requires pyridoxal-phosphate as a cofactor. The pyridoxal-phosphate group is attached to a lysine residue. The region around this lysine residue also contains two histidine residues which are part of the pyridoxal-phosphate binding site. The signature pattern for the tryptophan synthase beta chain is derived from that conserved region.

-Consensus pattern: [LIVM SEQ ID NO:4)]-x-H-x-G-[STA]-H-K-x-N [K is the pyridoxal-P attachment site]

- 20
 25 [1] Crawford I.P. Annu. Rev. Microbiol. 43:567-600(1989).[2] Hyde C.C., Miles E.W. Bio/Technology 8:27-32(1990).[3] Berlyn M.B., Last R.L., Fink G.R. Proc. Natl. Acad. Sci. U.S.A. 86:4604-4608(1989).

30 675. Serine proteases, trypsin family, active sites

The catalytic activity of the serine proteases from the trypsin family is provided by a charge relay system involving an aspartic acid residue hydrogen-bonded to a histidine, which itself is hydrogen-bonded to a serine. The sequences in the vicinity of the active site serine and

histidine residues are well conserved in this family of proteases [1]. A partial list of proteases known to belong to the trypsin family is shown below. - Acrosin. - Blood coagulation factors VII, IX, X, XI and XII, thrombin, plasminogen, and protein C. - Cathepsin G. -

Chymotrypsins. - Complement components C1r, C1s, C2, and complement factors B, D and

I. - Complement-activating component of RA-reactive factor. - Cytotoxic cell proteases

(granzymes A to H). - Duodenase I. - Elastases 1, 2, 3A, 3B (protease E), leukocyte

(medullasin). - Enterokinase (EC 3.4.21.9) (enteropeptidase). - Hepatocyte growth factor

activator. - Hepsin. - Glandular (tissue) kallikreins (including EGF-binding protein types A,

B, and C, NGF-gamma chain, gamma-renin, prostate specific antigen (PSA) and tonin). -

Plasma kallikrein. - Mast cell proteases (MCP) 1 (chymase) to 8. - Myeloblastin (proteinase

3) (Wegener's autoantigen). - Plasminogen activators (urokinase-type, and tissue-type). -

Trypsins I, II, III, and IV. - Trypsases. - Snake venom proteases such as ancrod, batroxobin,

cerastobin, flavoxobin, and protein C activator. - Collagenase from common cattle grub and

collagenolytic protease from Atlantic sand fiddler crab. - Apolipoprotein(a). - Blood fluke

cercarial protease. - Drosophila trypsin like proteases: alpha, easter, snake-locus. - Drosophila

protease stubble (gene sb). - Major mite fecal allergen Der p III. All the above proteins

belong to family S1 in the classification of peptidases[2,E1] and originate from eukaryotic

species. It should be noted that bacterial proteases that belong to family S2A are similar

enough in the regions of the active site residues that they can be picked up by the same

patterns. These proteases are listed below. - Achromobacter lyticus protease I. - Lysobacter

alpha-lytic protease. - Streptogrisin A and B (Streptomyces proteases A and B). -

Streptomyces griseus glutamyl endopeptidase II. - Streptomyces fradiae proteases 1 and 2.

Consensus pattern: [LIVM SEQ ID NO:4)]-[ST]-A-[STAG SEQ ID NO:20)]-H-C [H is the active site residue]

Consensus pattern: [DNSTAGC SEQ ID NO:619)]-[GSTAPIMVQH SEQ ID NO:620)]-x(2)-

G-[DE]-S-G-[GS]-[SAPHV SEQ ID NO:621)]- [LIVMFYWH SEQ ID NO:591)]-

[LIVMFYSTANQH SEQ ID NO:622)] [S is the active site residue]

[1] Brenner S. Nature 334:528-530(1988).[2] Rawlings N.D., Barrett A.J. Meth. Enzymol. 244:19-61(1994).[E1]

676. (tsp) Thrombospondin type 1 domain

[1] Bork P; FEBS lett 1993;327:125-130.

677. Tubulin subunits alpha, beta, and gamma signature

5 Tubulins [1,2], the major constituent of microtubules are dimeric proteins which consist of two closely related subunits (alpha and beta). Tubulin binds two molecules of GTP at two different sites (N and E). At the E (Exchangeable) site, GTP is hydrolyzed during incorporation into the microtubule. Near the E site is an invariant region rich in glycines which is found in both chains and which is now [3] said to control the access of the nucleotide to its binding site. A signature pattern was developed from this region. With the exception of
10 the simple eukaryotes, most species express a variety of closely related alpha and beta isotypes. In most species there is a third member of the tubulin family: gamma tubulin. Gamma tubulin is found at microtubule organizing centers (MTOC) such as the spindle poles or the centrosome, suggesting that it is involved in the minus-end nucleation of microtubule
15 assembly [4].

Consensus pattern: [SAG]-G-G-T-G-[SA]-G

[1] Cleveland D.W., Sullivan K.F. Annu. Rev. Biochem. 54:331-365(1985).[2] Joshi H.C., Cleveland D.W. Cell Motil. Cytoskeleton 16:159-163(1990).[3] Hesse J., Thierauf M., Ponstingl H. J. Biol. Chem. 262:15472-15475(1987).[4] Joshi H.C. BioEssays 15:637-
20 643(1993).

Tubulin-beta mRNA autoregulation signal

The stability of beta-tubulin mRNAs are autoregulated by their own translation product [1]. Unpolymerized tubulin subunits bind directly (or activate a factor(s) which binds co-
25 translationally) to the nascent N-terminus of beta-tubulin. This binding is transduced through the adjacent ribosomes to activate an RNase that degrades the polysome-bound mRNA. The recognition element has been shown to be the first four amino acids of beta-tubulin: Met-Arg-Glu-Ile. Mutations to this sequence abolish the autoregulation effect (except for the replacement of Glu by Asp); transposition of this sequence to an internal region of a
30 polypeptide also suppresses the autoregulatory effect.

Consensus pattern: <M-R-[DE]-[IL]

[1] Cleveland D.W. Trends Biochem. Sci. 13:339-343(1988).

678. (tRNA-synt 2c) Aminoacyl-transfer RNA synthetases class-II signatures. Aminoacyl-tRNA synthetases (EC 6.1.1.-) [1] are a group of enzymes which activate amino acids and transfer them to specific tRNA molecules as the first step in protein biosynthesis. In prokaryotic organisms there are at least twenty different types of aminoacyl-tRNA synthetases, one for each different amino acid. In eukaryotes there are generally two aminoacyl-tRNA synthetases for each different amino acid: one cytosolic form and a mitochondrial form. While all these enzymes have a common function, they are widely diverse in terms of subunit size and of quaternary structure. The synthetases specific for alanine, asparagine, aspartic acid, glycine, histidine, lysine, phenylalanine, proline, serine, and threonine are referred to as class-II synthetases [2 to 6] and probably have a common folding pattern in their catalytic domain for the binding of ATP and amino acid which is different to the Rossmann fold observed for the class I synthetases [7]. Class-II tRNA synthetases do not share a high degree of similarity, however at least three conserved regions are present [2,5,8]. Signature patterns have been derived from two of these regions.

Consensus pattern: [FYH]-R-x-[DE]-x(4,12)-[RH]-x(3)-F-x(3)-[DE]-

Consensus pattern: [GSTALVF SEQ ID NO:42)]-{DENQHRKP SEQ ID NO:43)}-[GSTA SEQ ID NO:19)]-[LIVMF SEQ ID NO:2)]-[DE]-R-[LIVMF SEQ ID NO:2)]-x-[LIVMSTAG SEQ ID NO:44)]-[LIVMFY SEQ ID NO:18)]-

[1] Schimmel P. Annu. Rev. Biochem. 56:125-158(1987).[2] Delarue M., Moras D. BioEssays 15:675-687(1993).[3] Schimmel P. Trends Biochem. Sci. 16:1-3(1991).[4] Nagel G.M., Doolittle R.F. Proc. Natl. Acad. Sci. U.S.A. 88:8121-8125(1991). [5] Cusack S., Haertlein M., Leberman R. Nucleic Acids Res. 19:3489-3498(1991).[6] Cusack S. Biochimie 75:1077-1081(1993).[7] Cusack S., Berthet-Colominas C., Haertlein M., Nassar N., Leberman R. Nature 347:249-255(1990).[8] Leveque F., Plateau P., Dessen P., Blanquet S. Nucleic Acids Res. 18:305-312(1990).

679. UBA-domain

The UBA-domain (ubiquitin associated domain) is a novel sequence motif found in several proteins having connections to ubiquitin and the ubiquitination pathway. The

structure of the UBA domain consists of a compact three helix bundle [1]. Number of members: 84

[1] Structure of a human DNA repair protein UBA domain that interacts with HIV-1 Vpr. Dieckmann T, Withers-Ward ES, Jarosinski MA, Liu CF, Chen IS, Feigon J; Nat Struct Biol 1998;5:1042-1047.

680. UBX domain

Domain present in ubiquitin-regulatory proteins. Present in FAF1 and Shp1p. Number of members: 19

[1] The UBA domain: a sequence motif present in multiple enzyme classes of the ubiquitination pathway. Hofmann K, Bucher P; Trends Biochem Sci 1996;21:172-173.

681. (UCH) Ubiquitin carboxyl-terminal hydrolases family 1 cysteine active site

Ubiquitin carboxyl-terminal hydrolases (UCH) (deubiquitinating enzymes) [1,2] are thiol proteases that recognize and hydrolyze the peptide bond at the C-terminal glycine of ubiquitin. These enzymes are involved in the processing of poly-ubiquitin precursors as well as that of ubiquitinated proteins. There are two distinct families of UCH. The first class consist of enzymes of about 25 Kd and is currently represented by: - Mammalian isozymes L1 and L3. - Yeast YUH1. - Drosophila Uch. One of the active site residues of class-I UCH [3] is a cysteine. A signature pattern has been derived from the region around that residue.

Consensus pattern: Q-x(3)-N-[SA]-C-G-x(3)-[LIVM SEQ ID NO:4]](2)-H-[SA]-[LIVM SEQ ID NO:4]]-[SA] [C is the active site residue

[1] Jentsch S., Seufert W., Hauser H.-P. Biochim. Biophys. Acta 1089:127-139(1991).[2] D'andrea A., Pellman D. Crit. Rev. Biochem. Mol. Biol. 33:337-352(1998).[3] Johnston S.C., Larsen C.N., Cook W.J., Wilkinson K.D., Hill C.P. EMBO J. 16:3787-3796(1997).[4] Rawlings N.D., Barrett A.J. Meth. Enzymol. 244:461-486(1994).

682. Ubiquitin carboxyl-terminal hydrolases family 2 signatures (UCH-1)

Ubiquitin carboxyl-terminal hydrolases (UCH) (deubiquitinating enzymes) [1,2] are thiol proteases that recognize and hydrolyze the peptide bond at the C-terminal glycine of

ubiquitin. These enzymes are involved in the processing of poly-ubiquitin precursors as well as that of ubiquitinated proteins. There are two distinct families of UCH. The second class consist of largeproteins (800 to 2000 residues) and is currently represented by: - Yeast UBP1, UBP2, UBP3, UBP4 (or DOA4/SSV7), UBP5, UBP7, UBP9, UBP10, UBP11, UBP12, UBP13, UBP14, UBP15 and UBP16. - Human tre-2. - Human isopeptidase T. - Human isopeptidase T-3. - Mammalian Ode-1. - Mammalian Unp. - Mouse Dub-1. - Drosophila fat facets protein (gene faf). - Mammalian faf homolog. - Drosophila D-Ubp-64E. - *Caenorhabditis elegans* hypothetical protein R10E11.3. - *Caenorhabditis elegans* hypothetical protein K02C4.3. These proteins only share two regions of similarity. The first region contains a conserved cysteine which is probably implicated in the catalytic mechanism. The second region contains two conserved histidines residues, one of which is also probably implicated in the catalytic mechanism. Signature patterns for both conserved regions have been developed.

Consensus pattern: G-[LIVMFY SEQ ID NO:18)]-x(1,3)-[AGC]-[NASM SEQ ID NO:623)]-x-C-[FYW]-[LIVMC SEQ ID NO:142)]-[NST]- [SACV SEQ ID NO:391)]-x-[LIVMS SEQ ID NO:429)]-Q [C is the putative active site residue]

Consensus pattern: Y-x-L-x-[SAG]-[LIVMFT SEQ ID NO:282)]-x(2)-H-x-G-x(4,5)-G-H-Y [The two H's are putative active site residues]

[1] Jentsch S., Seufert W., Hauser H.-P. *Biochim. Biophys. Acta* 1089:127-139(1991).[2]

D'andrea A., Pellman D. *Crit. Rev. Biochem. Mol. Biol.* 33:337-352(1998).[3] Rawlings N.D., Barrett A.J. *Meth. Enzymol.* 244:461-486(1994).

683. Ubiquitin carboxyl-terminal hydrolases family 2 signatures (UCH-2)

Ubiquitin carboxyl-terminal hydrolases (UCH) (deubiquitinating enzymes) [1,2] are thiol proteases that recognize and hydrolyze the peptide bond at the C-terminal glycine of ubiquitin. These enzymes are involved in the processing of poly-ubiquitin precursors as well as that of ubiquitinated proteins. There are two distinct families of UCH. The second class consist of largeproteins (800 to 2000 residues) and is currently represented by: - Yeast UBP1, UBP2, UBP3, UBP4 (or DOA4/SSV7), UBP5, UBP7, UBP9, UBP10, UBP11, UBP12, UBP13, UBP14, UBP15 and UBP16. - Human tre-2. - Human isopeptidase T. - Human isopeptidase T-3. - Mammalian Ode-1. - Mammalian Unp. - Mouse Dub-1. - Drosophila fat facets protein (gene faf). - Mammalian faf homolog. - Drosophila D-Ubp-64E. -

Caenorhabditis elegans hypothetical protein R10E11.3. - Caenorhabditis elegans hypothetical protein K02C4.3. These proteins only share two regions of similarity. The first region contains a conserved cysteine which is probably implicated in the catalytic mechanism. The second region contains two conserved histidines residues, one of which is also probably implicated in the catalytic mechanism. Signature patterns for both conserved regions have been developed.

Consensus pattern: G-[LIVMFY SEQ ID NO:18)]-x(1,3)-[AGC]-[NASM SEQ ID NO:623)]-x-C-[FYW]-[LIVMC SEQ ID NO:142)]-[NST]-[SACV SEQ ID NO:391)]-x-[LIVMS SEQ ID NO:429)]-Q [C is the putative active site residue]

Consensus pattern: Y-x-L-x-[SAG]-[LIVMFT SEQ ID NO:282)]-x(2)-H-x-G-x(4,5)-G-H-Y [The two H's are putative active site residues]

[1] Jentsch S., Seufert W., Hauser H.-P. Biochim. Biophys. Acta 1089:127-139(1991).[2] D'andrea A., Pellman D. Crit. Rev. Biochem. Mol. Biol. 33:337-352(1998).[3] Rawlings N.D., Barrett A.J. Meth. Enzymol. 244:461-486(1994).

684. UDP-glycosyltransferases signature

UDP glycosyltransferases (UGT) are a superfamily of enzymes that catalyzes the addition of the glycosyl group from a UTP-sugar to a small hydrophobic molecule. This family currently consist of: - Mammalian UDP-glucuronosyl transferases (UDPGT) [1,2]. A large family of membrane-bound microsomal enzymes which catalyze the transfer of glucuronic acid to a wide variety of exogenous and endogenous lipophilic substrates. These enzymes are of major importance in the detoxification and subsequent elimination of xenobiotics such as drugs and carcinogens. - A large number of putative UDPGT from Caenorhabditis elegans. -

Mammalian 2-hydroxyacylsphingosine 1-beta-galactosyltransferase [3] (also known as UDP-galactose-ceramide galactosyltransferase). This enzyme catalyzes the transfer of galactose to ceramide, a key enzymatic step in the biosynthesis of galactocerebrosides, which are abundant sphingolipids of the myelin membrane of the central nervous system and peripheral nervous system. - Plants flavonol O(3)-glucosyltransferase. An enzyme [4] that catalyzes the transfer of glucose from UDP-glucose to a flavanol. This reaction is essential and one of the last steps in anthocyanin pigment biosynthesis. - Baculoviruses ecdysteroid UDP-glucosyltransferase (EC 2.4.1.-) [5] (egt). This enzyme catalyzes the transfer of glucose from UDP-glucose to ecdysteroids which are insect molting hormones. The expression of egt in the

insect host interferes with the normal insect development by blocking the molting process. - Prokaryotic zeaxanthin glucosyl transferase (gene crtX), an enzyme involved in carotenoid biosynthesis and that catalyses the glycosylation reaction which converts zeaxanthin to zeaxanthin-beta- diglucoside. - Streptomyces macrolide glycosyltransferases [6]. These enzymes specifically inactivates macrolide antibiotics via 2'-O-glycosylation using UDP-glucose. These enzymes share a conserved domain of about 50 amino acid residues located in their C-terminal section and from which a pattern has been extracted to detect them.

Consensus pattern: [FW]-x(2)-Q-x(2)-[LIVMYA SEQ ID NO:609]-[LIMV SEQ ID NO:34)]-x(4,6)-[LVGAC SEQ ID NO:624)]-[LVFYA SEQ ID NO:625)]- [LIVMF SEQ ID NO:2)]-[STAGCM SEQ ID NO:626)]-[HNQ)]-[STAGC SEQ ID NO:45)]-G-x(2)-[STAG SEQ ID NO:20)]-x(3)-[STAGL SEQ ID NO:627)]- [LIVMFA SEQ ID NO:81)]-x(4)-[PQR)]-[LIVMT SEQ ID NO:1)]-x(3)-[PA]-x(3)-[DES)]-[QEHN SEQ ID NO:628)]

[1] Dutton G.J. (In) Glucoronidation of drugs and other compounds, Dutton G.J., Ed., pp 1-78, CRC Press, Boca Raton, (1980).[2] Burchell B., Nebert D.W., Nelson D.R., Bock K.W., Iyanagi T., Jansen P.L., Lancet D., Mulder G.J., Chowdhury J.R., Siest G., Tephly T.R., Mackenzie P.I. DNA Cell Biol. 10:487-494(1991).[3] Schulte S., Stoffel W. Proc. Natl. Acad. Sci. U.S.A. 90:10265-10269(1993).[4] Furtek D., Schiefelbein J.W., Johnston F., Nelson O.E. Jr. Plant Mol. Biol. 11:473-481(1988).[5] O'Reilly D.R., Miller L.K. Science 245:1110-1112(1989).[6] Hernandez C., Olano C., Mendez C., Salas J.A. Gene 134:139-140(1993).

685. UDP-glucose/GDP-mannose dehydrogenase family

The UDP-glucose/GDP-mannose dehydrogenases are a small group of enzymes which possesses the ability to catalyze the NAD-dependent 2-fold oxidation of an alcohol to an acid without the release of an aldehyde intermediate [2]. Number of members: 55

[1] Purification and characterization of guanosine diphospho-D-mannose dehydrogenase. A key enzyme in the biosynthesis of alginate by *Pseudomonas aeruginosa*. Roychoudhury S, May TB, Gill JF, Singh SK, Feingold DS, Chakrabarty AM; J Biol Chem 1989;264:9380-9385. [2] Properties and kinetic analysis of UDP-glucose dehydrogenase from group A streptococci. Irreversible inhibition by UDP-chloroacetol. Campbell RE, Sala RF, van de Rijn I, Tanner ME; J Biol Chem 1997;272:3416-3422.

686. Uracil-DNA glycosylase signature

Uracil-DNA glycosylase (EC 3.2.2.-) (UNG) [1] is a DNA repair enzyme that excises uracil residues from DNA by cleaving the N-glycosylic bond. Uracil in DNA can arise as a result of misincorporation of dUMP residues by DNA polymerase or deamination of cytosine. The sequence of uracil-DNA glycosylase is extremely well conserved [2] in bacteria and eukaryotes as well as in herpes viruses. More distantly related uracil-DNA glycosylases are also found in poxviruses [3]. In eukaryotic cells, UNG activity is found in both the nucleus and the mitochondria. Human UNG1 protein is transported to both the mitochondria and the nucleus [4]. The N-terminal 77 amino acids of UNG1 seem to be required for mitochondrial localization [4], but the presence of a mitochondrial transit peptide has not been directly demonstrated. As a signature for this type of enzyme, the most N-terminal conserved region has been selected. This region contains an aspartic acid residue which has been proposed, based on X-ray structures [5,6] to act as a general base in the catalytic mechanism.

Consensus pattern: [KR]-[LIV]-[LIVC SEQ ID NO:629)]-[LIVM SEQ ID NO:4)]-x-G-[QI]-D-P-Y [D is the active site residue]-

[1] Sancar A., Sancar G.B. *Annu. Rev. Biochem.* 57:29-67(1988).[2] Olsen L.C., Aasland R., Wittwer C.U., Krokan H.E., Helland D.E. *EMBO J.* 8:3121-3125 (1989).[3] Upton C., Stuart D.T., McFadden G. *Proc. Natl. Acad. Sci. U.S.A.* 90:4518-4522(1993).[4] Slupphaug G., Markussen F.-H., Olsen L.C., Aasland R., Aarsaether N., Bakke O., Krokan H.E., Helland D.E. *Nucleic Acids Res.* 21:2579-2584(1993).[5] Savva R., McAuley-Hecht K., Brown T., Pearl L. *Nature* 373:487-493(1995).[6] Mol C.D., Arvai A.S., Slupphaug G., Kavli B., Alseth I., Krokan H.E., Tainer J.A. *Cell* 80:869-878(1995).[7] Muller S.J., Caradonna S. *Biochim. Biophys. Acta* 1088:197-207(1991).[8] Meyer-Siegler K., Mauro D.J., Seal G., Wurzer J., Deriel J.K., Sirover M.A. *Proc. Natl. Acad. Sci. U.S.A.* 88:8460-8464(1991).[9] Muller S.J., Caradonna S. *J. Biol. Chem.* 268:1310-1319(1993).[10] Barnes D.E., Lindahl T., Sedgwick B. *Curr. Opin. Cell Biol.* 5:424-433(1993).

687. Uncharacterized protein family UPF0001 signature

The following uncharacterized proteins have been shown [1] to share regions of similarities: - Yeast chromosome II hypothetical protein YBL036c. - *Caenorhabditis elegans* hypothetical protein F09E5.8. - *Bacillus subtilis* hypothetical protein ylmE. - *Escherichia coli* hypothetical

protein yggS and HI0090, the corresponding *Haemophilus influenzae* protein. - *Helicobacter pylori* hypothetical protein HP0395. - *Mycobacterium tuberculosis* hypothetical protein MtCY270.20. - *Synechocystis* strain PCC 6803 hypothetical protein slr0556. - *A. Pseudomonas aeruginosa* hypothetical protein in pilT 5' region. - *A. Vibrio alginolyticus* hypothetical protein in pilT 5' region. These are proteins of from 25 to 30 Kd which contain a number of conserved regions. The best conserved region which is located in the first third of these proteins has been selected as a signature pattern.

Consensus pattern: [FW]-H-[FM]-[IV]-G-x-[LIV]-Q-x-[NKR]-K-x(3)-[LIV]

[1] Bairoch A., Rudd K.E. Unpublished observations (1996).

688. Uncharacterized protein family UPF0003 signature

The following uncharacterized proteins have been shown [1] to share regions of similarities: - *Escherichia coli* protein aefA. - *Escherichia coli* hypothetical protein yggB. - *Escherichia coli* hypothetical protein yjeP and HI0195.1, the corresponding *Haemophilus influenzae* protein. - *Escherichia coli* hypothetical protein ynaI. - *Bacillus subtilis* hypothetical protein yhdY. - *Helicobacter pylori* hypothetical protein HP0415. - *Synechocystis* strain PCC 6803 hypothetical protein slr0639. - *Archaeoglobus fulgidus* hypothetical protein AF1546. - *Methanococcus jannaschii* hypothetical protein MJ0170. - *Methanococcus jannaschii* hypothetical protein MJ1143. The size of these proteins range from 30 to 120 Kd. They all contain a number of transmembrane regions. The best conserved region which is located in and just after the last potential transmembrane region has been selected as a signature pattern,.

Consensus pattern: G-[STIF SEQ ID NO:630)]-V-x(2)-[LIVM SEQ ID NO:4)]-x(6)-[LIVMF SEQ ID NO:2)]-x(3)-[DQ]-x(3)-[LIV]- x-[LIV]-P-N-x(2)-[LIVMF SEQ ID NO:2)]-[LIVFSTA SEQ ID NO:205)]-x(5)-N

[1] Bairoch A. Unpublished observations (1997).

689. Uncharacterized protein family UPF0004 signature

The following uncharacterized proteins have been shown [1] to share regions of similarities: - *Escherichia coli* hypothetical protein yliG. - *Escherichia coli* hypothetical protein yleA and HI0019, the corresponding *Haemophilus influenzae* protein. - *Bacillus subtilis* hypothetical

protein yqeV. - *Helicobacter pylori* hypothetical protein HP0269. - *Helicobacter pylori* hypothetical protein HP0285. - *Mycoplasma iowae* hypothetical protein in 16S RNA 5'region. - *Mycobacterium leprae* hypothetical protein B2235_C2_195. - *Pseudomonas aeruginosa* hypothetical protein in hemL 3'region. - *Synechocystis* strain PCC 6803

- 5 hypothetical protein slr0082. - *Synechocystis* strain PCC 6803 hypothetical protein slr0996. - *Methanococcus jannaschii* hypothetical protein MJ0865. - *Methanococcus jannaschii* hypothetical protein MJ0867. - *Caenorhabditis elegans* hypothetical protein F25B5.5. The size of these proteins range from 47 to 61 Kd. They contain six conserved cysteines, three of which are clustered in a region that can be used as a signature pattern.

- 10 Consensus pattern: [LIVM SEQ ID NO:4)]-x-[LIVMT SEQ ID NO:1)]-x(2)-G-C-x(3)-C-[STAN SEQ ID NO:250)]-[FY]-C-x-[LIVM SEQ ID NO:4)]- x(4)-G
[1] Bairoch A. Unpublished observations (1997).

- 15 690. Uncharacterized protein family UPF0005 signature

The following proteins seem to be evolutionary related [1]: - Mammalian protein TEGT (Testis Enhanced Gene Transcript). - *Escherichia coli* hypothetical protein yccA and HI0044, the corresponding *Haemophilus influenzae* protein. - A probable *Pseudomonas aeruginosa* ortholog of yccA. These are proteins of about 25 Kd which seem to contain seven

20 transmembrane domains. A signature pattern that corresponds to a region that starts with the beginning of the third transmembrane domain and ends in the middle of the fourth one has been developed.

- Consensus pattern: G-[LIVM SEQ ID NO:4)](2)-[SA]-x(5,8)-G-x(2)-[LIVM SEQ ID NO:4)]-G-P-x-L-x(4)-[SAG]- x(4,6)-[LIVM SEQ ID NO:4)](2)-x(2)-A-x(3)-T-A-[LIVM
- 25 SEQ ID NO:4)](2)-F

[1] Walter L., Marynen P., Szpirer J., Levan G., Guenther E. *Genomics* 28:301-304(1995).

691. Uncharacterized protein family UPF0006 signatures

- 30 The following uncharacterized proteins have been shown [1] to share regions of similarities: - Yeast chromosome II hypothetical protein YBL055c. - *Escherichia coli* hypothetical protein ycfH and HI0454, the corresponding *Haemophilus influenzae* protein. - *Escherichia coli* hypothetical protein yigW. - *Escherichia coli* hypothetical protein yjjV and HI0081, the

corresponding *Haemophilus influenzae* protein. - *Bacillus subtilis* hypothetical protein yabD. - *Haemophilus influenzae* hypothetical protein HI1664. - *Mycoplasma genitalium* hypothetical protein MG009. These are proteins of from 24 to 47 Kd which contain a number of conserved regions. They can be picked up in the database by the following patterns.

Consensus pattern: [LIVMFY SEQ ID NO:18])(2)-D-[STA]-H-x-H-[LIVMF SEQ ID NO:2)]-[DN

Consensus pattern: P-[LIVM SEQ ID NO:4)]-x-[LIVM SEQ ID NO:4)]-H-x-R-x-[TA]-x-[DE

Consensus pattern: [LVSA SEQ ID NO:631)]-[LIVA SEQ ID NO:219)]-x(2)-[LIVM SEQ ID NO:4)]-[PS]-x(3)-L-[LIVM SEQ ID NO:4)]-[LIVMS SEQ ID NO:429)]-E-T- D-x-P

[1] Bairoch A., Rudd K.E. Unpublished observations (1995).

692. Uncharacterized protein family UPF0007 signature

The following proteins seems to be evolutionary related [1]: - *Escherichia coli* hypothetical protein ygbP and HI0672, the corresponding *Haemophilus influenzae* protein. - *Bacillus subtilis* hypothetical protein yacM. - *Mycobacterium tuberculosis* hypothetical protein MtCY06G11.29c. - *Synechocystis* strain PCC 6803 hypothetical protein slr0951. - A *Rhodobacter capsulatus* hypothetical protein in nifR3 5'region. Except for the *Rhodobacter* protein which contains a C-terminal extension, all these proteins have from 225 to 236 amino acids. They are hydrophilic proteins that can be picked up in the database by the following pattern.

Consensus pattern: V-L-[IV]-H-D-[GA]-A-R

[1] Bairoch A. Unpublished observations (1997).

693. Uncharacterized protein family UPF0015 signature

The following uncharacterized proteins have been shown [1] to share regions of similarities: - Yeast chromosome II hypothetical protein YBR002c. - Yeast chromosome XIII hypothetical protein YMR101c. - *Escherichia coli* hypothetical protein yaeU and HI0920, the corresponding *Haemophilus influenzae* protein. - *Helicobacter pylori* hypothetical protein HP1221. - *Mycobacterium leprae* hypothetical protein B1937_F2_65. - A *Corynebacterium glutamicum* hypothetical protein in aroF 3'region. - A *Streptomyces fradiae* hypothetical

565

protein in transposon Tn4556. - Synechocystis strain PCC 6803 hypothetical protein sll0505. - Methanococcus jannaschii hypothetical protein MJ1372. These are proteins of about 26 to 40 Kd whose central region is well conserved. They can be picked up in the database by the following pattern.

- 5 Consensus pattern: [DE]-[LIVMF SEQ ID NO:2)](3)-R-T-[SG]-G-x(2)-R-x-S-x-[FY]-[LIVM SEQ ID NO:4)](2)-W-Q-
[1] Wolfe K.H., Lohan A.J.E. Yeast 10:S41-S46(1994).

10 694. Uncharacterized protein family UPF0016 signature

The following uncharacterized proteins have been shown [1] to share regions of similarities: - Yeast hypothetical protein YBR187w. - Fission yeast hypothetical protein SpAC17G8.08c. - Mouse protein pFT27. - Synechocystis strain PCC 6803 hypothetical protein sll0615. These are hydrophobic proteins of 200 to 320 amino acids that seem to contain six or seven
15 transmembrane domains. A conserved region which seems, in the eukaryotic proteins of this family, to directly follow the second transmembrane domain has been selected as a signature pattern.

Consensus pattern: E-[LIVM SEQ ID NO:4)]-G-D-K-T-F-[LIVMF SEQ ID NO:2)](2)-A-
[1] Bairoch A. Unpublished observations (1996).

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695. Uncharacterized protein family UPF0021 signature

The following uncharacterized proteins have been shown [1] to share regions of similarities: - Yeast chromosome VII hypothetical protein YGL211w. - Dictyostelium discoideum protein veg136. - Methanococcus jannaschii hypothetical proteins MJ1157 and MJ1478. These are
25 proteins of from 300 to 360 residues. They can be picked up in the database by the following pattern which is located in their N-terminal section.

Consensus pattern: C-K-x(2)-F-x(4)-E-x(22,23)-S-G-G-K-D
[1] Bairoch A. Unpublished observations (1997).

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696. Uncharacterized protein family UPF0023 signature

The following uncharacterized proteins have been shown [1] to share regions of similarities: -
Mouse protein 22A3. - Yeast chromosome XII hypothetical protein YLR022c. -

Caenorhabditis elegans hypothetical protein W06E11.4. - Methanococcus jannaschii
hypothetical protein MJ0592. These are hydrophilic proteins of about 30 Kd. They can be
5 picked up in the database by the following pattern.

Consensus pattern: D-x-D-E-[LIV]-L-x(4)-V-F-x(3)-S-K-G-

[1] Bairoch A. Unpublished observations (1997).

- 10 697. Uncharacterized protein family UPF0024 signature. The following uncharacterized
proteins have been shown [1] to share regions of similarities: - Escherichia coli hypothetical
protein ygbO and HI0701, the corresponding Haemophilus influenzae protein. - Helicobacter
pylori hypothetical protein HP0926. - Yeast chromosome XV hypothetical protein YOR243c.
- Caenorhabditis elegans hypothetical protein B0024.11. - Methanococcus jannaschii
15 hypothetical proteins MJ0588 and MJ1364. These are hydrophilic proteins of from 39 to 77
Kd. They can be picked up in the database by the following pattern.

Consensus pattern: G-x-K-D-[KR]-x-A-[LV]-T-x-Q-x-[LIVF SEQ ID NO:127)]-[SGC]-

- 20 [1] Bairoch A. Unpublished observations (1997).

698. Uncharacterized protein family UPF0025 signature

The following uncharacterized proteins have been shown [1] to share regions of similarities: -

- 25 Escherichia coli hypothetical protein yfcE. - Bacillus subtilis hypothetical protein ysnB. -
Mycoplasma genitalium and pneumoniae hypothetical protein MG207. - Methanococcus
jannaschii hypothetical proteins MJ0623 and MJ0936. These are hydrophilic proteins of
about 20 Kd. They can be picked up in the database by the following pattern.

Consensus pattern: D-V-[LIV]-x(2)-G-H-[ST]-H-x(12)-[LIVMF SEQ ID NO:2)]-N-P-G

- 30 [1] Bairoch A. Unpublished observations (1997).

699. Uncharacterized protein family UPF0029 signature

The following uncharacterized proteins have been shown [1] to share regions of similarities: - Yeast chromosome III hypothetical protein YCR59c. - Yeast chromosome IV hypothetical protein YDL177C. - Escherichia coli hypothetical protein yigZ and HI0722, the corresponding Haemophilus influenzae protein. - Bacillus subtilis hypothetical protein yvyE. - A Thermus aquaticus hypothetical protein in pol 5' region. These proteins can be picked up in the database by the following pattern.

Consensus pattern: G-x(2)-[LIVM SEQ ID NO:4]](2)-x(2)-[LIVM SEQ ID NO:4]]-x(4)-[LIVM SEQ ID NO:4]]-x(5)-[LIVM SEQ ID NO:4]](2)-x- R-[FYW](2)-G-G-x(2)-[LIVM SEQ ID NO:4]]-G

[1] Koonin E.V., Bork P., Sander C. EMBO J. 13:493-503(1994).

700. Uncharacterized protein family UPF0030 signature

The following uncharacterized proteins have been shown [1] to be highly similar: - Yeast chromosome VI hypothetical protein YFL060c. - Yeast chromosome XIII hypothetical protein YMR095c. - Yeast chromosome XIV hypothetical protein YNL334c. - Bacillus subtilis hypothetical protein yaaE. - Haemophilus influenzae hypothetical protein HI1648. - Methanococcus jannaschii hypothetical protein MJ1661. These are hydrophilic proteins of about 19 to 25 Kd. They can be picked up in the database by the following pattern.

Consensus pattern: [GA]-L-I-[LIV]-P-G-G-E-S-T-[STA]

[1] Bairoch A. Unpublished observations (1997).

701. Uncharacterized protein family UPF0032 signature

The following uncharacterized proteins have been shown [1] to share regions of similarities: - Escherichia coli hypothetical protein yigU and HI0188, the corresponding Haemophilus influenzae protein. - Bacillus subtilis hypothetical protein ycbT. - Mycobacterium tuberculosis hypothetical protein MtCY49.33c and U2126A, the corresponding Mycobacterium leprae protein. - Synechocystis strain PCC 6803 hypothetical protein sl10194. - Odontella sinensis and Porphyra purpurea chloroplast hypothetical protein ycf43. These proteins have from 245 to 317 amino acids and seem to contain at least six or seven transmembrane regions. A conserved region located in the central section of these proteins has been developed as a signature pattern.

Consensus pattern: Y-x(2)-F-[LIVMA SEQ ID NO:30]](2)-x-L-x(4)-G-x(2)-F-[EQ]-[LIVMF SEQ ID NO:2)]-P- [LIVM SEQ ID NO:4)] –

[1] Bairoch A., Rudd K.E. Unpublished observations (1996).

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702. Uncharacterized protein family UPF0034 signature

The following uncharacterized proteins have been shown [1] to share regions of similarities: -

Escherichia coli hypothetical protein yhdG and HI0979, the corresponding Haemophilus influenzae protein. - Escherichia coli hypothetical protein yjbN and HI0634, the

10 corresponding Haemophilus influenzae protein. - Escherichia coli hypothetical protein yohI and HI0270, the corresponding Haemophilus influenzae protein. - Bacillus subtilis

hypothetical protein yacF. - Rhodobacter capsulatus protein nifR3 and related proteins in Azospirillum brasilense and Rhizobium leguminosarum. - Synechocystis strain PCC 6803

hypothetical protein slr0644. - Synechocystis strain PCC 6803 hypothetical protein slI0926. -

15 Caenorhabditis elegans hypothetical protein C45G9.2. - Yeast protein SMM1. - Yeast

hypothetical protein YLR401c. - Yeast hypothetical protein YLR405w. - Yeast hypothetical protein YML080w. Although it has been proposed [2] that Rhodobacter capsulatus nifR3 is a

transcriptional regulatory protein, it is believed that these proteins constitute a family of enzymes whose active site could include a conserved cysteine which has been used as the

20 central part of a signature pattern.

Consensus pattern: [LIVM SEQ ID NO:4)]-[DNG]-[LIVM SEQ ID NO:4)]-N-x-G-C-P-x(3)-[LIVMASQ SEQ ID NO:632)]-x(5)-G-[SAC]

[1] Bairoch A., Rudd K.E. Unpublished observations (1995).[2] Foster-Hartnett D., Cullen P.J., Gabbert K.K., Kranz R.G. Mol. Microbiol. 8:903-914(1993).

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703. Uncharacterized protein family UPF0038 signature

The following uncharacterized proteins have been shown [1] to share regions of similarities: -

Escherichia coli hypothetical protein yacE and HI0890, the corresponding Haemophilus

30 influenzae protein. - Mycobacterium tuberculosis hypothetical protein MtCY01B2.23 and O410, the corresponding Mycobacterium leprae protein. - Synechocystis strain PCC 6803

hypothetical protein slr0553. - Other hypothetical proteins from Aeromonas hydrophila,

Bacteroides nodosus, Neisseria gonorrhoeae, Pseudomonas putida, Thermus thermophilus

and *Xanthomonas campestris*. - Human hypothetical protein pOV-2. - Yeast hypothetical protein YDR196C. - *Caenorhabditis elegans* hypothetical protein T05G5.5. These proteins all contain, in their N-terminal extremity, an ATP/GTP-binding motif 'A' (P-loop) (see <PDOC00017>). The size of these proteins range from 200 to 290 residues (with the exception of the Mycobacterial sequences which are 410 residues long). A conserved region some 50 residues away from the ATP-binding P-loop has been developed as a signature pattern.

Consensus pattern: G-x-[LI]-x-R-x(2)-L-x(4)-F-x(8)-[LIV]-x(5)-P-x-[LIV] -

[1] Rudd K.E., Bairoch A. Unpublished observations (1997).

704. Ubiquitin-conjugating enzymes active site

Ubiquitin-conjugating enzymes (UBC or E2 enzymes) [1,2,3] catalyze the covalent attachment of ubiquitin to target proteins. An activated ubiquitin moiety is transferred from an ubiquitin-activating enzyme (E1) to E2 which later ligates ubiquitin directly to substrate proteins with or without the assistance of 'N-end' recognizing proteins (E3). In most species there are many forms of UBC (at least 9 in yeast) which are implicated in diverse cellular functions. A cysteine residue is required for ubiquitin-thiolester formation. There is a single conserved cysteine in UBC's and the region around that residue is conserved in the sequence of known UBC isozymes. That region has been used as a signature pattern.

Consensus pattern: [FYWLSP SEQ ID NO:633]-H-[PC]-[NH]-[LIV]-x(3,4)-G-x-[LIV]-C-[LIV]-x- [LIV] [C is the active site residue]

[1] Jentsch S., Seufert W., Sommer T., Reins H.-A. Trends Biochem. Sci. 15:195-

198(1990).[2] Jentsch S., Seufert W., Hauser H.-P. Biochim. Biophys. Acta 1089:127-

139(1991).[3] Hershko A. Trends Biochem. Sci. 16:265-268(1991).

705. Uroporphyrinogen decarboxylase signatures

Uroporphyrinogen decarboxylase (URO-D), the fifth enzyme of the heme biosynthetic pathway, catalyzes the sequential decarboxylation of the four acetyl side chains of uroporphyrinogen to yield coproporphyrinogen [1]. URO-D deficiency is responsible for the Human genetic diseases familial porphyria cutanea tarda (fPCT) and hepatoerythropoietic porphyria (HEP). The sequence of URO-D has been well conserved throughout evolution.

The best conserved region is located in the N-terminal section; it contains a perfectly conserved hexapeptide. There are two arginine residues in this hexapeptide which could be involved in the binding, via salt bridges, to the carboxyl groups of the propionate side chains of the substrate. This region has been used as a signature pattern. A second signature pattern is based on another well conserved region which is located in the central section of the protein.

Consensus pattern: P-x-W-x-M-R-Q-A-G-R

Consensus pattern: G-F-[STAGCV SEQ ID NO:159]-[STAGC SEQ ID NO:45]-x-P-[FYW]-T-[LV]-x(2)-Y-x(2)-[AE]-[GK]

[1] Garey J.R., Labbe-Bois R., Chelstowska A., Rytka J., Harrison L., Kushner J., Labbe P. Eur. J. Biochem. 205:1011-1016(1992).

706. ubiE/COQ5 methyltransferase family signatures

The following methyltransferases have been shown [1] to share regions of similarities: - *Escherichia coli* ubiE, which is involved in both ubiquinone and menaquinone biosynthesis and which catalyzes the S-adenosylmethionine dependent methylation of 2-polyprenyl-6-methoxy-1,4-benzoquinol into 2-polyprenyl-3-methyl-6-methoxy-1,4-benzoquinol and of demethylmenaquinol into menaquinol. - Yeast COQ5, a ubiquinone biosynthesis methyltransferase. - *Bacillus subtilis* spore germination protein C2 (gene: *gercB* or *gerC2*), a probable menaquinone biosynthesis methyltransferase. - *Lactococcus lactis* *gerC2* homolog. - *Caenorhabditis elegans* hypothetical protein ZK652.9. - *Leishmania donovani* amastigote-specific protein A41. These are hydrophilic proteins of about 30 Kd (except for ZK652.9 which is 65Kd). They can be picked up in the database by the following patterns.

Consensus pattern: Y-D-x-M-N-x(2)-[LIVM SEQ ID NO:4]-S-x(3)-H-x(2)-W

Consensus pattern: R-V-[LIVM SEQ ID NO:4]-K-[PV]-G-G-x-[LIVMF SEQ ID NO:2]-x(2)-[LIVM SEQ ID NO:4]-E-x-S

[1] Lee P.T., Hsu A.Y., Ha H.T., Clarke C.F. J. Bacteriol. 179:1748-1754(1997).

707. Uricase signature

Uricase (urate oxidase) [1] is the peroxisomal enzyme responsible for the degradation of urate into allantoin. Some species, like primates and birds, have lost the gene for uricase and

are therefore unable to degradeurate. Uricase is a protein of 300 to 400 amino acids. A highly conserved region located in the central part of the sequence has been used as a signature pattern.

Consensus pattern: [LV]-x-[LV]-[LIV]-K-[STV]-[ST]-x-[SN]-x-F-x(2)-[FY]-x(4)- [FY]-x(2)-L-x(5)-R

[1] Motojima K., Kanaya S., Goto S. J. Biol. Chem. 263:16677-16681(1988).

708. Universal stress protein family (Usp)

By a wide range of stress conditions members of the Usp family are predicted to be related to the MADS-box proteins transcript_fact and bind to DNA [2]. Number of members: 39

[1] Expression and role of the universal stress protein, UspA, of Escherichia coli during growth arrest. Nystrom T, Neidhardt FC; Mol Microbiol 1994; 11:537-544.

[2] Sequence analysis of eukaryotic developmental proteins: ancient and novel domains. Mushegian AR, Koonin EV; Genetics 1996; 144:817-828.

709. Ubiquitin domain signature and profile

Ubiquitin [1,2,3] is a protein of seventy six amino acid residues, found in all eukaryotic cells and whose sequence is extremely well conserved from protozoan to vertebrates. It plays a key role in a variety of cellular processes, such as ATP-dependent selective degradation of cellular proteins, maintenance of chromatin structure, regulation of gene expression, stress response and ribosome biogenesis. In most species, there are many genes coding for ubiquitin. However they can be classified into two classes. The first class produces polyubiquitin molecules consisting of exact head to tail repeats of ubiquitin. The number of repeats is variable (up to twelve in a Xenopus gene). In the majority of polyubiquitin precursors, there is a final amino-acid after the last repeat. The second class of genes produces precursor proteins consisting of a single copy of ubiquitin fused to a C-terminal extension protein (CEP). There are two types of CEP proteins and both seem to be ribosomal proteins. Ubiquitin is a globular protein, the last four C-terminal residues (Leu-Arg- Gly-Gly) extending from the compact structure to form a 'tail', important for its function. The latter is

mediated by the covalent conjugation of ubiquitin to target proteins, by an isopeptide linkage between the C-terminal glycine and the epsilon amino group of lysine residues in the target proteins. There are a number of proteins which are evolutionary related to ubiquitin: -

Ubiquitin-like proteins from baculoviruses as well as in some strains of bovine viral diarrhea viruses (BVDV). These proteins are highly similar to their eukaryotic counterparts. -

Mammalian protein GDX [4]. GDX is composed of two domains, a N-terminal ubiquitin-like domain of 74 residues and a C-terminal domain of 83 residues with some similarity with the thyroglobulin hormonogenic site. - Mammalian protein FAU [5]. FAU is a fusion protein

which consist of a N-terminal ubiquitin-like protein of 74 residues fused to ribosomal protein S30. - Mouse protein NEDD-8 [6], a ubiquitin-like protein of 81 residues. - Human protein

BAT3, a large fusion protein of 1132 residues that contains a N-terminal ubiquitin-like domain. - *Caenorhabditis elegans* protein ubl-1 [7]. Ubl-1 is a fusion protein which consist of a N-terminal ubiquitin-like protein of 70 residues fused to ribosomal protein S27A. - Yeast

DNA repair protein RAD23 [8]. RAD23 contains a N-terminal domain that seems to be

distantly, yet significantly, related to ubiquitin. - Mammalian RAD23-related proteins

RAD23A and RAD23B. - Mammalian BCL-2 binding athanogene-1 (BAG-1). BAG-1 is a protein of 274 residues that contains a central ubiquitin-like domain. - Human spliceosome

associated protein 114 (SAP 114 or SF3A120). - Yeast protein DSK2, a protein involved in spindle pole body duplication and which contains a N-terminal ubiquitin-like domain. -

Human protein CKAP1/TFCB, *Schizosaccharomyces pombe* protein alp11 and

Caenorhabditis elegans hypothetical protein F53F4.3. These proteins contain a N-terminal

ubiquitin domain and a C-terminal CAP-Gly domain. - *Schizosaccharomyces pombe*

hypothetical protein SpAC26A3.16. This protein contains a N-terminal ubiquitin domain. -

Yeast protein SMT3. - Human ubiquitin-like proteins SMT3A and SMT3B. - Human

ubiquitin-like protein SMT3C (also known as PIC1; Ubl1, Sumo-1; Gmp-1 or Sentrin). This protein is involved in targeting ranGAP1 to the nuclear pore complex protein ranBP2. -

SMT3-like proteins in plants and *Caenorhabditis elegans*. To identify ubiquitin and related

proteins, a pattern has been developed based on conserved positions in the central section of the sequence. A profile was also developed that spans the complete length of the ubiquitin

domain.

Consensus pattern: K-x(2)-[LIVM SEQ ID NO:4)]-x-[DESAK SEQ ID NO:634)]-x(3)-[LIVM SEQ ID NO:4)]-[PA]-x(3)-Q-x-[LIVM SEQ ID NO:4)]- [LIVMC SEQ ID NO:142)]-[LIVMFY SEQ ID NO:18)]-x-G-x(4)-[DE]

[1] Jentsch S., Seufert W., Hauser H.-P. *Biochim. Biophys. Acta* 1089:127-139(1991).[2] Monia B.P., Ecker D.J., Croke S.T. *Bio/Technology* 8:209-215(1990).[3] Finley D., Varshavsky A. *Trends Biochem. Sci.* 10:343-347(1985).[4] Filippi M., Tribioli C., Toniolo D. *Genomics* 7:453-457(1990).[5] Olvera J., Wool I.G. *J. Biol. Chem.* 268:17967-17974(1993).[6] Kumar S., Yoshida Y., Noda M. *Biochem. Biophys. Res. Commun.* 195:393-399(1993).[7] Jones D., Candido E.P. *J. Biol. Chem.* 268:19545-19551(1993).[8] Melnick L., Sherman F. *J. Mol. Biol.* 233:372-388(1993).

10 710. VHS domain

Domain present in VPS-27, Hrs and STAM. Number of members: 27

711. Vinculin family signatures

15 Vinculin [1] is a eukaryotic protein that seems to be involved in the attachment of the actin-based microfilaments to the plasma membrane. Vinculin is located at the cytoplasmic side of focal contacts or adhesion plaques. In addition to actin, vinculin interacts with other structural proteins such as talin and alpha-actinins. Vinculin is a large protein of 116 Kd (about a 1000 residues). Structurally the protein consists of an acidic N-terminal domain of about 90 Kd
20 separated from a basic C-terminal domain of about 25 Kd by a proline-rich region of about 50 residues. The central part of the N-terminal domain consists of a variable number (3 in vertebrates, 2 in *Caenorhabditis elegans*) of repeats of a 110 amino acids domain. Catenins [2] are proteins that associate with the cytoplasmic domain of a variety of cadherins. The association of catenins to cadherins produces a complex which is linked to the actin filament
25 network, and which seems to be of primary importance for cadherins cell-adhesion properties. Three different types of catenins seem to exist: alpha, beta, and gamma. Alpha-catenins are proteins of about 100 Kd which are evolutionary related to vinculin. In terms of their structure the most significant differences are the absence, in alpha-catenin, of the repeated domain and of the proline-rich segment. Two signature patterns for this family of
30 proteins have been developed. The first pattern is located in the N-terminal section of both vinculin and alpha-catenins and is part, in vinculin, of a domain that seems to be involved with the interaction with talin. The second pattern is based on a conserved region in the N-terminal part of the repeated domain of vinculin.

Consensus pattern: [KR]-x-[LIVMF SEQ ID NO:2)]-x(3)-[LIVMA SEQ ID NO:30)]-x(2)-[LIVM SEQ ID NO:4)]-x(6)-R-Q-Q-E-L

Consensus pattern: [LIVM SEQ ID NO:4)]-x-[QA]-A-x(2)-W-[IL]-x-[DN]-P

[1] Otto J.J. Cell Motil. Cytoskeleton 16:1-6(1990).[2] Herrenknecht K., Ozawa M.,

5 Eckerskorn C., Lottspeich F., Lenter M., Kemler R. Proc. Natl. Acad. Sci. U.S.A. 88:9156-9160(1991).

712. (Vitellogenin N) Lipoprotein amino terminal region

10 This family contains regions from: Vitellogenin, Microsomal triglyceride transfer protein and apolipoprotein B-100. These proteins are all involved in lipid transport [1]. This family contains the LV1n chain from lipovitellin, that contains two structural domains.

Number of members: 33

[1] The structural basis of lipid interactions in lipovitellin, a soluble lipoprotein.

15 Anderson TA, Levitt DG, Banaszak LJ Structure 1998;6:895-909.

713. (VMSA) Major surface antigen from hepadnavirus

20

714. ssDNA binding protein (Viral DNA bp)

This protein is found in herpesviruses and is needed for replication.

25

715. (Votage CLC) Voltage gated chloride channels

This family of ion channels contains 10 or 12 transmembrane helices. Each protein forms a single pore. It has been shown that some members of this family form homodimers. These
30 proteins contain two CBS domains.

[1] Schmidt-Rose T, Jentsch TJ; J Biol Chem 1997;272:20515-20521.

[2] Zhang J, George AL Jr, Griggs RC, Fouad GT, Roberts J, Kwiecinski H, Connolly AM, Ptacek LJ; Neurology 1996;47:993-998.

- 5 716. von Willebrand factor type A domain (vwa)
More von Willebrand factor type A domains? Sequence
similarities with malaria thrombospondin-related
anonymous protein, dihydropyridine-sensitive calcium
channel and inter-alpha-trypsin inhibitor.
- 10 Bork P, Rohde K;
Biochem J 1991;279:908-911.
1. RUGGERI, Z.M. and WARE, J.
von Willebrand factor.
15 FASEB J. 7 308-316 (1993).
2. COLOMBATTI, A., BONALDO, P. and DOLIANA, R.
Type A modules: interacting domains found in several non-fibrillar
collagens and in other extracellular matrix proteins.
20 MATRIX 13 297-306 (1993).
3. PERKINS, S.J., SMITH, K.F., WILLIAMS, S.C., HARIS, P.I., CHAPMAN, D.
and SIM, R.B.
The secondary structure of the von Willebrand factor type A domain in
25 factor B of human complement by Fourier transform infrared spectroscopy.
Its occurrence in collagen types VI, VII, XII and XIV, the integrins and
other proteins by averaged structure predictions.
J.MOL.BIOL. 238 104-119 (1994).
- 30 4. BORK, P. and ROHDE, K.
More von Willebrand factor type A domains? Sequence similarities with
malaria thrombospondin-related anonymous protein, dihydropyridine-
sensitive calcium channel and inter-alpha-trypsin inhibitor.

BIOCHEM.J. 279 908-910 (1991).

5. EDWARDS, Y.J.K. and PERKINS, S.J.

The protein fold of the von Willebrand factor type A domain is predicted
5 to be similar to the open twisted beta-sheet flanked by alpha-helices
found in human ras-p21.

FEBS LETT. 358 283-286 (1995).

6. LEE, J.O., RIEU, P., ARNAOUT, M.A. and LIDDINGTON, R.

10 Crystal structure of the A domain from the alpha subunit of integrin CR3
(CD11b/CD18).

CELL 80 631-638 (1995).

7. QU, A. and LEAHY, D.J.

15 Crystal structure of the I-domain from the CD11a/CD18 (LFA-1,
alpha L beta 2) integrin.

PROC.NATL.ACAD.SCI.USA 92 10277-10281 (1995).

20 The von Willebrand factor is a large multimeric glycoprotein found in blood
plasma. Mutant forms are involved in the aetiology of bleeding disorders
[1]. In von Willebrand factor, the type A domain (vWF) is the prototype for
a protein superfamily. The vWF domain is found in various plasma proteins:
complement factors B, C2, CR3 and CR4; the integrins (I-domains); collagen
types VI, VII, XII and XIV; and other extracellular proteins [2-4]. Proteins
25 that incorporate vWF domains participate in numerous biological events
(e.g., cell adhesion, migration, homing, pattern formation, and signal
transduction), involving interaction with a large array of ligands [2].

Secondary structure prediction from 75 aligned vWF sequences has revealed
a largely alternating sequence of alpha-helices and beta-strands [3]. Fold
30 recognition algorithms were used to score sequence compatibility with a
library of known structures: the vWF domain fold was predicted to be a
doubly-wound, open, twisted beta-sheet flanked by alpha-helices [5].

3D structures have been determined for the I-domains of integrins CD11b

(with bound magnesium) [6] and CD11a (with bound manganese) [7]. The domain adopts a classic alpha/beta Rossmann fold and contains an unusual metal ion coordination site at its surface. It has been suggested that this site represents a general metal ion-dependent adhesion site (MIDAS) for binding protein ligands [6]. The residues constituting the MIDAS motif in the CD11b and CD11a I-domains are completely conserved, but the manner in which the metal ion is coordinated differs slightly [7].

VWFADOMAIN is a 3-element fingerprint that provides a signature for the vWF domain superfamily. The fingerprint was derived from an initial alignment of 14 sequences. Motif 1 includes the first beta-strand and 3 conserved residues involved in metal ion coordination in I-domains (Asp and 2 serines in positions 8, 10 and 12, respectively); motif 2 spans strands beta-2 and beta-2'; and motif 3 encodes beta-strand 3 and a conserved Asp (in position 7), which coordinates the metal ion [6,7]. Three iterations on OWL27.0 were required to reach convergence, at which point a true set comprising 56 sequences was identified. Numerous partial matches were also found.

717. (WD40) WD domain, G-beta repeat

The ancient regulatory-protein family of WD-repeat proteins.

Neer EJ, Schmidt CJ, Nambudripad R, Smith TF;

Nature 1994;371:297-300.

Beta-transducin (G-beta) is one of the three subunits (alpha, beta, and gamma) of the guanine nucleotide-binding proteins (G proteins) which act as intermediaries in the transduction of signals generated by transmembrane receptors [1]. The alpha subunit binds to and hydrolyzes GTP; the functions of the beta and gamma subunits are less clear but they seem to be required for the replacement of GDP by GTP as well as for membrane anchoring and receptor recognition.

In higher eukaryotes G-beta exists as a small multigene family of highly conserved proteins of about 340 amino acid residues. Structurally G-beta

consists of eight tandem repeats of about 40 residues, each containing a central Trp-Asp motif (this type of repeat is sometimes called a WD-40 repeat). Such a repetitive segment has been shown [E1,2,3,4,5] to exist in a number of other proteins listed below:

5

- Yeast STE4, a component of the pheromone response pathway. STE4 is a G-beta like protein that associates with GPA1 (G-alpha) and STE18 (G-gamma).
- Yeast MS11, a negative regulator of RAS-mediated cAMP synthesis. MS11 is most probably also a G-beta protein.

10

- Human and chicken protein 12.3. The function of this protein is not known, but on the basis of its similarity to G-beta proteins, it may also function in signal transduction.
- Chlamydomonas reinhardtii gblp. This protein is most probably the homolog of vertebrate protein 12.3.
- Human LIS1, a neuronal protein involved in type-1 lissencephaly [E2].
- Mammalian coatamer beta' subunit (beta'-COP), a component of a cytosolic protein complex that reversibly associates with Golgi membranes to form vesicles that mediate biosynthetic protein transport.

20

- Yeast CDC4, essential for initiation of DNA replication and separation of the spindle pole bodies to form the poles of the mitotic spindle.
- Yeast CDC20, a protein required for two microtubule-dependent processes: nuclear movements prior to anaphase and chromosome separation.
- Yeast MAK11, essential for cell growth and for the replication of M1 double-stranded RNA.
- Yeast PRP4, a component of the U4/U6 small nuclear ribonucleoprotein with a probable role in mRNA splicing.
- Yeast PWP1, a protein of unknown function.
- Yeast SKI8, a protein essential for controlling the propagation of double-stranded RNA.
- Yeast SOF1, a protein required for ribosomal RNA processing which associates with U3 small nucleolar RNA.

30

- Yeast TUP1 (also known as AER2 or SFL2 or CYC9), a protein which has been implicated in dTMP uptake, catabolite repression, mating sterility, and many other phenotypes.
- Yeast YCR57c, an ORF of unknown function from chromosome III.
- 5 - Yeast YCR72c, an ORF of unknown function from chromosome III.
- Slime mold coronin, an actin-binding protein.
- Slime mold AAC3, a developmentally regulated protein of unknown function.
- 10 - Drosophila protein Groucho (formerly known as E(spl); 'enhancer of split'), a protein involved in neurogenesis and that seems to interact with the Notch and Delta proteins.
- Drosophila TAF-II-80, a protein that is tightly associated with TFIID.
- 15 The number of repeats in the above proteins varies between 5 (PRP4, TUP1, and Groucho) and 8 (G-beta, STE4, MSII, AAC3, CDC4, PWP1, etc.). In G-beta and G-beta like proteins, the repeats span the entire length of the sequence, while in other proteins, they make up the N-terminal, the central or the C-terminal section.
- 20 A signature pattern can be developed from the central core of the domain (positions 9 to 23).
- Consensus pattern: [LIVMSTAC SEQ ID NO:151)]-[LIVMFYWSTAGC SEQ ID NO:635)]-[LIMSTAG SEQ ID NO:636)]-[LIVMSTAGC SEQ ID NO:637)]-x(2)-[DN]-x(2)-[LIVMWSTAC SEQ ID NO:638)]-x-[LIVMFSTAG SEQ ID NO:639)]-W-[DEN]-[LIVMFSTAGCN SEQ ID NO:640)]
- 25
- [1] Gilman A.G.
- 30 Annu. Rev. Biochem. 56:615-649(1987).
- [2] Duronio R.J., Gordon J.I., Boguski M.S.
- Proteins 13:41-56(1992).
- [3] van der Voorn L., Ploegh H.L.

FEBS Lett. 307:131-134(1992).

[4] Neer E.J., Schmidt C.J., Nambudripad R., Smith T.F.

Nature 371:297-300(1994).

[5] Smith T.F., Gaiatzes C.G., Saxena K., Neer E.J.

5 Biochemistry In Press(1998).

718. WHEP-TRS domain containing proteins

10 A conserved domain of 46 amino acids has been shown [1] to exist in a number of higher eukaryote aminoacyl-transfer RNA synthetases. This domain is present one to six times in the following enzymes:

- 15 - Mammalian multifunctional aminoacyl-tRNA synthetase. The domain is present three times in a region that separates the N-terminal glutamyl-tRNA synthetase domain from the C-terminal prolyl-tRNA synthetase domain.
- Drosophila multifunctional aminoacyl-tRNA synthetase. The domain is present six times in the intercatalytic region.
- Mammalian tryptophanyl-tRNA synthetase. The domain is found at the N-terminal extremity.
- 20 - Mammalian, insect, nematode and plant glycyl-tRNA synthetase. The domain is found at the N-terminal extremity [2].
- Mammalian histidyl-tRNA synthetase. The domain is found at the N-terminal extremity.

25 This domain, which is called WHEP-TRS, could contain a central alpha-helical region and may play a role in the association of tRNA-synthetases into multienzyme complexes.

30 A signature pattern based on the first 29 positions of the WHEP-Domain has been developed.

-Consensus pattern: [QY]-G-[DNEA SEQ ID NO:641)]-x-[LIV]-[KR]-x(2)-K-x(2)-[KRNG SEQ ID NO:642)]-[AS]-x(4)-

[LIV]-[DENK SEQ ID NO:643)]-x(2)-[IV]-x(2)-L-x(3)-K

[1] Cerini C., Kerjan P., Astier M., Gratecos D., Mirande M., Semeriva M.
EMBO J. 10:4267-4277(1991).

5 [2] Nada S., Chang P.K., Dignam J.D.
J. Biol. Chem. 268:7660-7667(1993).

719. (Worm family 8) Putative membrane protein

10 Analysis of protein domain families in *Caenorhabditis elegans*.

Sonnhammer EL, Durbin R;

Genomics 1997;46:200-216.

This family called family 8 in [1], may be a transmembrane protein

The specific function of this protein is unknown.

15

720. Xylose isomerase

Xylose isomerase (EC 5.3.1.5) [1] is an enzyme found in microorganisms which
catalyzes the interconversion of D-xylose to D-xylulose. It can also isomerize

20 D-ribose to D-ribulose and D-glucose to D-fructose. Xylose isomerase seems to
require magnesium for its activity, while cobalt is necessary to stabilize the
tetrameric structure of the enzyme. A number of residues are conserved in all
known xylose isomerases.

25 Xylose isomerase also exists in plants [2] where it is homodimeric and is
manganese-dependent.

Two signatures patterns for xylose isomerase have been developed. The first one is
derived from a stretch of five conserved amino acids that includes a glutamic
30 acid residue known to be one of the four residues involved in the binding of
the magnesium ion [3]; this pattern also includes a lysine residue which is
involved in the catalytic activity. The second pattern is derived from a
conserved region in the N-terminal section of the enzyme that include an

histidine residue which has been shown [4] to be involved in the catalytic mechanism of the enzyme.

-Consensus pattern: [LI]-E-P-K-P-x(2)-P

5 [E is a magnesium ligand]

[K is an active site residue]

-Consensus pattern: [FL]-H-D-x-D-[LIV]-x-[PD]-x-[GDE]

[H is an active site residue]

10 [1] Dauter Z., Dauter M., Hemker J., Witzel H., Wilson K.S.

FEBS Lett. 247:1-8(1989).

[2] Kristo P.A., Saarelainen R., Fagerstrom R., Aho S., Korhola M.

Eur. J. Biochem. 237:240-246(1996).

[3] Henrick K., Collyer C.A., Blow D.M.

15 J. Mol. Biol. 208:129-157(1989).

[4] Vangrysperre W., Ampe C., Kersters-Hilderson H., Tempst P.

Biochem. J. 263:195-199(1989).

20 721. XPG protein signatures. Xeroderma pigmentosum (XP) [1] is a human autosomal recessive disease, characterized by a high incidence of sunlight-induced skin cancer. People's skin cells with this condition are hypersensitive to ultraviolet light, due to defects in the incision step of DNA excision repair. There are a minimum of seven genetic complementation groups involved in this pathway: XP-A to XP-G. The defect in XP-G can
25 be corrected by a 133 Kd nuclear protein called XPG (or XPGC) [2]. XPG belongs to a family of proteins [2,3,4,5,6] that are composed of two main subsets: - Subset 1, to which belongs XPG, RAD2 from budding yeast and rad13 from fission yeast. RAD2 and XPG are single-stranded DNA endonucleases [7,8]. XPG makes the 3' incision in human DNA nucleotide excision repair [9]. - Subset 2, to which belongs mouse and human FEN-1, rad2 from fission
30 yeast, and RAD27 from budding yeast. FEN-1 is a structure-specific endonuclease. In addition to the proteins listed in the above groups, this family also includes: - Fission yeast exo1, a 5'→3' double-stranded DNA exonuclease that could act in a pathway that corrects mismatched base pairs. - Yeast EXO1 (DHS1), a protein with probably the same function as

exo1. - Yeast DIN7. Sequence alignment of this family of proteins reveals that similarities are largely confined to two regions. The first is located at the N-terminal extremity (N-region) and corresponds to the first 95 to 105 amino acids. The second region is internal (I-region) and found towards the C-terminus; it spans about 140 residues and contains a highly conserved core of 27 amino acids that includes a conserved pentapeptide (E-A-[DE]-A-[QS]). It is possible that the conserved acidic residues are involved in the catalytic mechanism of DNA excision repair in XPG. The amino acids linking the N- and I-regions are not conserved; indeed, they are largely absent from proteins belonging to the second subset. Two signature patterns have been developed for these proteins. The first corresponds to the central part of the N-region, the second to part of the I-region and includes the putative catalytic core pentapeptide

Consensus pattern: [VI]-[KRE]-P-x-[FYIL SEQ ID NO:644)]-V-F-D-G-x(2)-[PIL]-x-[LVC]-K-

Consensus pattern: [GS]-[LIVM SEQ ID NO:4)]-[PER]-[FYS]-[LIVM SEQ ID NO:4)]-x-A-P-x-E-A-[DE]-[PAS]-[QS]-[CLM]-

[1] Tanaka K., Wood R.D. Trends Biochem. Sci. 19:83-86(1994).[2] Scherly D., Nospikel T., Corlet J., Ucla C., Bairoch A., Clarkson S.G. Nature 363:182-185(1993).[3] Carr A.M., Sheldrick K.S., Murray J.M., Al-Harithy R., Watts F.Z., Lehmann A.R. Nucleic Acids Res. 21:1345-1349(1993).[4] Murray J.M., Tavassoli M., Al-Harithy R., Sheldrick K.S., Lehmann A.R., Carr A.M., Watts F.Z. Mol. Cell. Biol. 14:4878-4888(1994).[5] Harrington J.J., Lieber M.R. Genes Dev. 8:1344-1355(1994).[6] Szankasi P., Smith G.R. Science 267:1166-1169(1995).[7] Habraken Y., Sung P., Prakash L., Prakash S. Nature 366:365-368(1993).[8] O'Donovan A., Scherly D., Clarkson S.G., Wood R.D. J. Biol. Chem. 269:15965-15968(1994).[9] O'Donovan A., Davies A.A., Moggs J.G., West S.C., Wood R.D. Nature 371:432-435(1994).

722. Xanthine/uracil permeases family

The following transport proteins which are involved in the uptake of xanthine or uracil are evolutionary related [1]:

- Uric acid-xanthine permease (gene uapA) from *Aspergillus nidulans*.
- Purine permease (gene uapC) from *Aspergillus nidulans*.
- Xanthine permease from *Bacillus subtilis* (gene pbuX).
- Uracil permease from *Escherichia coli* (gene uraA) [2] and *Bacillus* (gene pyrP).
- Hypothetical protein ycdG from *Escherichia coli*.
- Hypothetical protein ygfO from *Escherichia coli*.
- Hypothetical protein ygfU from *Escherichia coli*.
- Hypothetical protein yicE from *Escherichia coli*.
- Hypothetical protein yunJ from *Bacillus subtilis*.
- Hypothetical protein yunK from *Bacillus subtilis*.

They are proteins of from 430 to 595 residues that seem to contain 12 transmembrane domains.

- The best conserved region which corresponds with what seems to be the tenth transmembrane domain has been selected as a signature pattern.

-Consensus pattern: [LIVM SEQ ID NO:4]-P-x-[PASIF SEQ ID NO:645]-V-[LIVM SEQ ID NO:4]-G-G-x(4)-[LIVM SEQ ID NO:4]-[FY]-[GSA]-x-

[LIVM SEQ ID NO:4]-x(3)-G

[1] Diallinas G., Gorfinkiel L., Arst G., Cecchetto G., Scazzocchio C.

J. Biol. Chem. 270:8610-8622(1995).

[2] Andersen P.S., Frees D., Fast R., Mygind B.

J. Bacteriol. 177:2008-2013(1995).

723. Hypothetical yabO/yceC/sfhB family

The following proteins, which seems to belong to a family of pseudouridine synthases (EC 4.2.1.70) [1] have been shown to share regions of similarities:

- *Escherichia coli* and *Haemophilus influenzae* ribosomal large subunit pseudouridine synthase A (gene rluA). It is responsible for synthesis of pseudouridine from uracil-746 IN 23S rRNA.

- *Escherichia coli* and *Haemophilus influenzae* ribosomal large subunit pseudouridine synthase C (gene rluC). It is responsible for synthesis of pseudouridine from uracil at positions 955, 2504 and 2580 in 23S rRNA.
- *Escherichia coli* protein and homologs in other bacteria large subunit pseudouridine synthase D (gene rluD).
- Yeast DRAP deaminase (gene RIB2).
- *Escherichia coli* hypothetical protein yqcB and HI1435, the corresponding *Haemophilus influenzae* protein.
- *Haemophilus influenzae* hypothetical protein HI0042.
- *Aquifex aeolicus* hypothetical protein AQ_1758.
- *Bacillus subtilis* hypothetical protein yhcT.
- *Bacillus subtilis* hypothetical protein yjbO.
- *Bacillus subtilis* hypothetical protein ylyB.
- *Helicobacter pylori* hypothetical protein HP0347.
- *Helicobacter pylori* hypothetical protein HP0745.
- *Helicobacter pylori* hypothetical protein HP0956.
- *Mycoplasma genitalium* hypothetical protein MG209.
- *Mycoplasma genitalium* hypothetical protein MG370.
- *Synechocystis* strain PCC 6803 hypothetical protein slr1592.
- *Synechocystis* strain PCC 6803 hypothetical protein slr1629.
- Yeast hypothetical protein YDL036c.
- Yeast hypothetical protein YGR169c.
- Fission yeast hypothetical protein SpAC18B11.02c.
- *Caenorhabditis elegans* hypothetical protein K07E8.7.

These are proteins of from 21 to 50 Kd which contain a number of conserved regions in their central section. They can be picked up in the database by the following highly conserved pattern.

- Consensus pattern: [LIVCA SEQ ID NO:646)]-[NHYT SEQ ID NO:647)]-R-[LI]-D-x(2)-T-[STA]-G-[LIVAGC SEQ ID NO:648)]-[LIVMF SEQ ID NO:2)](2)-[LIVMFGC SEQ ID NO:649)]-[SGTACV SEQ ID NO:650)]

[1] Conrad J., Sun D., Englund N., Ofengand J.
J. Biol. Chem. 273:18562-18566(1998).

In addition, the following bacterial proteins, which seems to belong to a family of
pseudouridine synthases (EC 4.2.1.70) [1] also have been shown to share regions of
similarities:

- Escherichia coli and Haemophilus influenzae 16S pseudouridylate synthase (EC 4.2.1.70) (gene: rsuA). This enzyme is responsible for the formation of pseudouridine from uracil-516 in 16S ribosomal RNA.
- Escherichia coli hypothetical protein yciL and HI1199, the corresponding Haemophilus influenzae protein.
- Escherichia coli hypothetical protein yjbC.
- Escherichia coli hypothetical protein ymfC and HI0694, the corresponding Haemophilus influenzae protein.
- Aquifex aeolicus hypothetical protein AQ_554.
- Aquifex aeolicus hypothetical protein AQ_1464.
- Bacillus subtilis hypothetical protein ypuL.
- Bacillus subtilis hypothetical protein ytzF.
- Borrelia burgdorferi hypothetical protein BB0129.
- Helicobacter pylori hypothetical protein HP1459.
- Synechocystis strain PCC 6803 hypothetical protein slr0361.
- Synechocystis strain PCC 6803 hypothetical protein slr0612.

These are proteins of from 25 to 40 Kd which contain a number of conserved regions in their central section. They can be picked up in the database by the following highly conserved pattern.

-Consensus pattern: G-R-L-D-x(2)-[STA]-x-G-[LIVFA SEQ ID NO:129)]-[LIVMF SEQ ID NO:2)](3)-[ST]-[DNST SEQ ID NO:265)]

[1] Wrzesinski J., Bakin A., Nurse K., Lane B.G., Ofengand J.
Biochemistry 34:8904-8913(1995).

724. Zinc finger present in dystrophin, CBP/p300

ZZ in dystrophin binds calmodulin

5 Putative zinc finger; binding not yet shown.

725. Zinc carboxypeptidase

10 There are a number of different types of zinc-dependent carboxypeptidases (EC 3.4.17.-) [1,2]. All these enzymes seem to be structurally and functionally related. The enzymes that belong to this family are listed below.

- Carboxypeptidase A1 (EC 3.4.17.1), a pancreatic digestive enzyme that can removes all C-terminal amino acids with the exception of Arg, Lys and Pro.
- 15 - Carboxypeptidase A2 (EC 3.4.17.15), a pancreatic digestive enzyme with a specificity similar to that of carboxypeptidase A1, but with a preference for bulkier C-terminal residues.
- Carboxypeptidase B (EC 3.4.17.2), also a pancreatic digestive enzyme, but that preferentially removes C-terminal Arg and Lys.
- 20 - Carboxypeptidase N (EC 3.4.17.3) (also known as arginine carboxypeptidase), a plasma enzyme which protects the body from potent vasoactive and inflammatory peptides containing C-terminal Arg or Lys (such as kinins or anaphylatoxins) which are released into the circulation.
- Carboxypeptidase H (EC 3.4.17.10) (also known as enkephalin convertase or carboxypeptidase E), an enzyme located in secretory granules of pancreatic islets, adrenal gland, pituitary and brain. This enzyme removes residual C-terminal Arg or Lys remaining after initial endoprotease cleavage during prohormone processing.
- 25 - Carboxypeptidase M (EC 3.4.17.12), a membrane bound Arg and Lys specific enzyme.
- 30

It is ideally situated to act on peptide hormones at local tissue sites where it could control their activity before or after interaction with specific plasma membrane receptors.

- Mast cell carboxypeptidase (EC 3.4.17.1), an enzyme with a specificity to carboxypeptidase A, but found in the secretory granules of mast cells.
- *Streptomyces griseus* carboxypeptidase (Cpase SG) (EC 3.4.17.-) [3], which combines the specificities of mammalian carboxypeptidases A and B.
- 5 - *Thermoactinomyces vulgaris* carboxypeptidase T (EC 3.4.17.18) (CPT) [4], which also combines the specificities of carboxypeptidases A and B.
- AEBP1 [5], a transcriptional repressor active in preadipocytes. AEBP1 seems to regulate transcription by cleavage of other transcriptional proteins.
- Yeast hypothetical protein YHR132c.

10

All of these enzymes bind an atom of zinc. Three conserved residues are implicated in the binding of the zinc atom: two histidines and a glutamic acid. Two signature patterns which contain these three zinc-ligands have been derived.

- 15 -Consensus pattern: [PK]-x-[LIVMFY SEQ ID NO:18)]-x-[LIVMFY SEQ ID NO:18)]-x(4)-H-[STAG SEQ ID NO:20)]-x-E-x-[LIVM SEQ ID NO:4)]-[STAG SEQ ID NO:20)]-x(6)-[LIVMFYTA SEQ ID NO:651)]
[H and E are zinc ligands]
- Consensus pattern: H-[STAG SEQ ID NO:20)]-x(3)-[LIVME SEQ ID NO:652)]-x(2)-
20 [LIVMFYW SEQ ID NO:26)]-P-[FYW]
[H is a zinc ligand]

[1] Tan F., Chan S.J., Steiner D.F., Schilling J.W., Skidgel R.A.

J. Biol. Chem. 264:13165-13170(1989).

- 25 [2] Reynolds D.S., Stevens R.L., Gurley D.S., Lane W.S., Austen K.F.,

Serafin W.E.

J. Biol. Chem. 264:20094-20099(1989).

- [3] Narahashi Y.

J. Biochem. 107:879-886(1990).

- 30 [4] Teplyakov A., Polyakov K., Obmolova G., Strokopytov B., Kuranova I.,

Osterman A.L., Grishin N.V., Smulevitch S.V., Zagnitko O.P.,

Galperina O.V., Matz M.V., Stepanov V.M.

Eur. J. Biochem. 208:281-288(1992).

[5] He G.-P., Muise A., Li A.W., Ro H.-S.

Nature 378:92-96(1995).

[6] Hourdou M.-L., Guinand M., Vacheron M.J., Michel G., Denoroy L.,

Duez C.M., Englebert S., Joris B., Weber G., Ghuysen J.-M.

5 Biochem. J. 292:563-570(1993).

[7] Rawlings N.D., Barrett A.J.

Meth. Enzymol. 248:183-228(1995).

10 726. Zinc finger, C2H2 type

The C2H2 zinc finger is the classical zinc finger domain.

The two conserved cysteines and histidines co-ordinate a zinc ion. The following pattern describes the zinc finger.

#-X-C-X(1-5)-C-X3-#-X5-#-X2-H-X(3-6)-[H/C]

15 Where X can be any amino acid, and numbers in brackets indicate the number of residues. The positions marked # are those that are important for the stable fold of the zinc finger. The final position can be either his or cys.

The C2H2 zinc finger is composed of two short beta strands
20 followed by an alpha helix. The amino terminal part of the helix binds the major groove in DNA binding zinc fingers.

'Zinc finger' domains [1-5] are nucleic acid-binding protein structures first identified in the *Xenopus* transcription factor TFIID. These domains have
25 since been found in numerous nucleic acid-binding proteins. A zinc finger domain is composed of 25 to 30 amino-acid residues. There are two cysteine or histidine residues at both extremities of the domain, which are involved in the tetrahedral coordination of a zinc atom. It has been proposed that such a domain interacts with about five nucleotides. A schematic representation of a
30 zinc finger domain is shown below:

x x

x x

```

      x x
      x x
      x x
      x x
5     C  H
      x \ / x
      x  Zn  x
      x / \ x
      C  H
10    x x x x x x x x x x

```

Many classes of zinc fingers are characterized according to the number and positions of the histidine and cysteine residues involved in the zinc atom coordination. In the first class to be characterized, called C2H2, the first pair of zinc coordinating residues are cysteines, while the second pair are histidines. A number of experimental reports have demonstrated the zinc-dependent DNA or RNA binding property of some members of this class.

Some of the proteins known to include C2H2-type zinc fingers are listed below.

The number of zinc finger regions found in each of these proteins are indicated between brackets; a '+' symbol indicates that only partial sequence data is available and that additional finger domains may be present.

- *Saccharomyces cerevisiae*: ACE2 (3), ADR1 (2), AZF1 (4), FZF1 (5), MIG1 (2), MSN2 (2), MSN4 (2), RGM1 (2), RIM1 (3), RME1 (3), SFP1 (2), SSL1 (1), STP1 (3), SWI5 (3), VAC1 (1) and ZMS1 (2).

- *Emmericella nidulans*: brlA (2), creA (2).

- *Drosophila*: AEF-1 (4), Cf2 (7), ci-D (5), Disconnected (2), Escargot (5), Glass (5), Hunchback (6), Kruppel (5), Kruppel-H (4+), Odd-skipped (4), Odd-paired (4), Pep (3), Snail (5), Spalt-major (7), Serependity locus beta (6), delta (7), h-1 (8), Suppressor of hairy wing su(Hw) (12), Suppressor of variegation suvar(3)7 (5), Teashirt (3) and Tramtrack (2).

- *Xenopus*: transcription factor TFIIIA (9), p43 from RNP particle (9), Xfin

(37 !!), Xsna (5), gastrula XlcGF5.1 to XlcGF71.1 (from 4+ to 11+), Oocyte XlcOF2 to XlcOF22 (from 7 to 12).

- Mammalian: basonuclein (6), BCL-6/LAZ-3 (6), erythroid krueppel-like transcription factor (3), transcription factors Sp1 (3), Sp2 (3), Sp3 (3) and Sp4 (3), transcriptional repressor YY1 (4), Wilms' tumor protein (4), EGR1/Krox24 (3), EGR2/Krox20 (3), EGR3/Pilot (3), EGR4/AT133 (4), Evi-1 (10), GLI1 (5), GLI2 (4+), GLI3 (3+), HIV-EP1/ZNF40 (4), HIV-EP2 (2), KR1 (9+), KR2 (9), KR3 (15+), KR4 (14+), KR5 (11+), HF.12 (6+), REX-1 (4), Zfx (13), Zfy (13), Zfp-35 (18), ZNF7 (15), ZNF8 (7), ZNF35 (10), ZNF42/MZF-1 (13), ZNF43 (22), ZNF46/Kup (2), ZNF76 (7), ZNF91 (36), ZNF133 (3).

In addition to the conserved zinc ligand residues it has been shown [6] that a number of other positions are also important for the structural integrity of the C2H2 zinc fingers. The best conserved position is found four residues after the second cysteine; it is generally an aromatic or aliphatic residue.

-Consensus pattern: C-x(2,4)-C-x(3)-[LIVMFYWC SEQ ID NO:86])-x(8)-H-x(3,5)-H
[The two C's and two H's are zinc ligands]

[1] Klug A., Rhodes D.

Trends Biochem. Sci. 12:464-469(1987).

[2] Evans R.M., Hollenberg S.M.

Cell 52:1-3(1988).

[3] Payre F., Vincent A.

FEBS Lett. 234:245-250(1988).

[4] Miller J., McLachlan A.D., Klug A.

EMBO J. 4:1609-1614(1985).

[5] Berg J.M.

Proc. Natl. Acad. Sci. U.S.A. 85:99-102(1988).

[6] Rosenfeld R., Margalit H.

J. Biomol. Struct. Dyn. 11:557-570(1993).

727. Zinc finger, C3HC4 type (RING finger)

A number of eukaryotic and viral proteins contain a conserved cysteine-rich domain of 40 to 60 residues (called C3HC4 zinc-finger or 'RING' finger) [1] that binds two atoms of zinc, and is probably involved in mediating protein-protein interactions. The 3D structure of the zinc ligation system is unique to the RING domain and is referred to as the "cross-brace" motif. The spacing of the cysteines in such a domain is C-x(2)-C-x(9 to 39)-C-x(1 to 3)-H-x(2 to 3)-C-x(2)-C-x(4 to 48)-C-x(2)-C.

10 Proteins currently known to include the C3HC4 domain are listed below (references are only provided for recently determined sequences).

- Mammalian V(D)J recombination activating protein (gene RAG1). RAG1 activates the rearrangement of immunoglobulin and T-cell receptor genes.
- 15 - Mouse rpt-1. Rpt-1 is a trans-acting factor that regulates gene expression directed by the promoter region of the interleukin-2 receptor alpha chain or the LTR promoter region of HIV-1.
- Human rfp. Rfp is a developmentally regulated protein that may function in male germ cell development. Recombination of the N-terminal section of rfp
- 20 with a protein tyrosine kinase produces the ret transforming protein.
- Human 52 Kd Ro/SS-A protein. A protein of unknown function from the Ro/SS-A ribonucleoprotein complex. Sera from patients with systemic lupus erythematosus or primary Sjogren's syndrome often contain antibodies that react with the Ro proteins.
- 25 - Human histocompatibility locus protein RING1.
- Human PML, a probable transcription factor. Chromosomal translocation of PML with retinoic receptor alpha creates a fusion protein which is the cause of acute promyelocytic leukemia (APL).
- Mammalian breast cancer type 1 susceptibility protein (BRCA1) [E1].
- 30 - Mammalian cbl proto-oncogene.
- Mammalian bmi-1 proto-oncogene.
- Vertebrate CDK-activating kinase (CAK) assembly factor MAT1, a protein that stabilizes the complex between the CDK7 kinase and cyclin H (MAT1 stands

for 'Menage A Trois').

- Mammalian mel-18 protein. Mel-18 which is expressed in a variety of tumor cells is a transcriptional repressor that recognizes and bind a specific DNA sequence.
- 5 - Mammalian peroxisome assembly factor-1 (PAF-1) (PMP35), which is somewhat involved in the biogenesis of peroxisomes. In humans, defects in PAF-1 are responsible for a form of Zellweger syndrome, an autosomal recessive disorder associated with peroxisomal deficiencies.
- Human MAT1 protein, which interacts with the CDK7-cyclin H complex.
- 10 - Human RING1 protein.
- Xenopus XNF7 protein, a probable transcription factor.
- Trypanosoma protein ESAG-8 (T-LR), which may be involved in the postranscriptional regulation of genes in VSG expression sites or may interact with adenylate cyclase to regulate its activity.
- 15 - Drosophila proteins Posterior Sex Combs (Psc) and Suppressor two of zeste (Su(z)2). The two proteins belong to the Polycomb group of genes needed to maintain the segment-specific repression of homeotic selector genes.
- Drosophila protein male-specific msl-2, a DNA-binding protein which is involved in X chromosome dosage compensation (the elevation of
- 20 transcription of the male single X chromosome).
- Arabidopsis thaliana protein COP1 which is involved in the regulation of photomorphogenesis.
- Fungal DNA repair proteins RAD5, RAD16, RAD18 and rad8.
- Herpesviruses trans-acting transcriptional protein ICP0/IE110. This protein
- 25 which has been characterized in many different herpesviruses is a trans-activator and/or -repressor of the expression of many viral and cellular promoters.
- Baculoviruses protein CG30.
- Baculoviruses major immediate early protein (PE-38).
- 30 - Baculoviruses immediate-early regulatory protein IE-N/IE-2.
- Caenorhabditis elegans hypothetical proteins F54G8.4, R05D3.4 and T02C1.1.
- Yeast hypothetical proteins YER116c and YKR017c.

The central region of the domain was selected as a signature pattern for the C3HC4 finger.

-Consensus pattern: C-x-H-x-[LIVMFY SEQ ID NO:18)]-C-x(2)-C-[LIVMYA SEQ ID NO:609)]

[1] Borden K.L.B., Freemont P.S.
Curr. Opin. Struct. Biol. 6:395-401(1996).

728. Zinc finger C-x8-C-x5-C-x3-H type (and similar).

729. Zinc finger, CCHC class

A family of CCHC zinc fingers, mostly from retroviral gag proteins (nucleocapsid). Prototype structure is from HIV. Also contains members involved in eukaryotic gene regulation, such as *C. elegans* GLH-1. Structure is an 18-residue zinc finger; no examples of indels in the alignment.

730. Zn-finger in Ran binding protein and others.

731. AN1-like Zinc finger

Zinc finger at the C-terminus of An1 [Swiss:Q91889](#), a ubiquitin-like protein in *Xenopus laevis*. The following pattern describes the zinc finger. C-X2-C-X(9-12)-C-X(1-2)-C-X4-C-X2-H-X5-H-X-C Where X can be any amino acid, and numbers in brackets indicate the number of residues.

[1] Linnen JM, Bailey CP, Weeks DL; Gene 1993;128:181-188.

732. 14-3-3 proteins

Structure of a 14-3-3 protein and implications for coordination of multiple signalling pathways.

Xiao B, Smerdon SJ, Jones DH, Dodson GG, Soneji Y, Aitken A, Gamblin SJ;
Nature 1995;376:188-191.

Crystal structure of the zeta isoform of the 14-3-3 protein.

Liu D, Bienkowska J, Petosa C, Collier RJ, Fu H, Liddington R;
Nature 1995;376:191-194.

Interaction of 14-3-3 with signaling proteins is mediated by the recognition of phosphoserine.

Muslin AJ, Tanner JW, Allen PM, Shaw AS;
Cell 1996;84:889-897.

The 14-3-3 protein binds its target proteins with a common site located towards the C-terminus.

Ichimura T, Ito M, Itagaki C, Takahashi M, Horigome T, Omata S, Ohno S, Isobe T
FEBS Lett 1997;413:273-276.

Molecular evolution of the 14-3-3 protein family.

Wang W, Shakes DC

J Mol Evol 1996;43:384-398.

Function of 14-3-3 proteins.

Jin DY, Lyu MS, Kozak CA, Jeang KT
Nature 1996;382:308-308.

The 14-3-3 proteins [1,2,3] are a family of closely related acidic homodimeric proteins of about 30 Kd which were first identified as being very abundant in mammalian brain tissues and located preferentially in neurons. The 14-3-3 proteins seem to have multiple biological activities and play a key role in

signal transduction pathways and the cell cycle. They interact with kinases such as PKC or Raf-1; they seem to also function as protein-kinase dependent activators of tyrosine and tryptophan hydroxylases and in plants they are associated with a complex that binds to the G-box promoter elements.

5

The 14-3-3 family of proteins are ubiquitously found in all eukaryotic species studied and have been sequenced in fungi (yeast BMH1 and BMH2, fission yeast rad24 and rad25), plants, Drosophila, and vertebrates. The sequences of the 14-3-3 proteins are extremely well conserved. Two highly conserved regions have been selected as signature patterns: the first is a peptide of 11 residues located in the N-terminal section; the second, a 20 amino acid region located in the C-terminal section.

10

-Consensus pattern: R-N-L-[LIV]-S-[VG]-[GA]-Y-[KN]-N-[IVA]

15

-Consensus pattern: Y-K-[DE]-S-T-L-I-[IM]-Q-L-[LF]-[RHC]-D-N-[LF]-T-[LS]-W-[TAN]-[SAD]

[1] Aitken A.

Trends Biochem. Sci. 20:95-97(1995).

20

[2] Morrison D.

Science 266:56-57(1994).

[3] Xiao B., Smerdon S.J., Jones D.H., Dodson G.G., Soneji Y., Aitken A., Gamblin S.J.

Nature 376:188-191(1995).

25

733. D-isomer specific 2-hydroxyacid dehydrogenases (2 Hacid DH)

This Pfam covers the Formate dehydrogenase, D-glycerate dehydrogenase and D-lactate dehydrogenase families in SCOP. A number of NAD-dependent 2-hydroxyacid dehydrogenases which seem to be specific for the D-isomer of their substrate have been shown [1,2,3,4] to be functionally and structurally related. These enzymes are listed below.

30

- D-lactate dehydrogenase (EC 1.1.1.28), a bacterial enzyme which catalyzes the reduction of D-lactate to pyruvate.

- D-glycerate dehydrogenase (EC 1.1.1.29) (NADH-dependent hydroxypyruvate reductase), a plant leaf peroxisomal enzyme that catalyzes the reduction of hydroxypyruvate to glycerate. This reaction is part of the glycolate pathway of photorespiration.
- 5 - D-glycerate dehydrogenase from the bacteria *Hyphomicrobium methylovorum* and *Methylobacterium extorquens*.
- 3-phosphoglycerate dehydrogenase (EC 1.1.1.95), a bacterial enzyme that catalyzes the oxidation of D-3-phosphoglycerate to 3-phosphohydroxypyruvate. This reaction is the first committed step in the 'phosphorylated' pathway of serine biosynthesis.
- 10 - Erythronate-4-phosphate dehydrogenase (EC 1.1.1.-) (gene *pdxB*), a bacterial enzyme involved in the biosynthesis of pyridoxine (vitamin B6).
- D-2-hydroxyisocaproate dehydrogenase (EC 1.1.1.-) (*D*-hicDH), a bacterial enzyme that catalyzes the reversible and stereospecific interconversion between 2-ketocarboxylic acids and D-2-hydroxy-carboxylic acids.
- 15 - Formate dehydrogenase (EC 1.2.1.2) (FDH) from the bacteria *Pseudomonas* sp. 101 and various fungi [5].
- Vancomycin resistance protein *vanH* from *Enterococcus faecium*; this protein is a D-specific alpha-keto acid dehydrogenase involved in the formation of a peptidoglycan which does not terminate by D-alanine thus preventing vancomycin binding.
- 20 - *Escherichia coli* hypothetical protein *ycdW*.
- *Escherichia coli* hypothetical protein *yiaE*.
- *Haemophilus influenzae* hypothetical protein HI1556.
- 25 - Yeast hypothetical protein YER081w.
- Yeast hypothetical protein YIL074w.

All these enzymes have similar enzymatic activities and are structurally related. Three of the most conserved regions of these proteins have been selected to develop patterns. The first pattern is based on a glycine-rich region located in the central section of these enzymes; this region probably corresponds to the NAD-binding domain. The two other patterns contain a number of conserved charged residues, some of which may play a role in the catalytic mechanism.

598

-Consensus pattern: [LIVMA SEQ ID NO:30)]-[AG]-[IVT]-[LIVMFY SEQ ID NO:18)]-[AG]-x-G-[NHKRQGSAC SEQ ID NO:653)]-[LIV]-G-x(13,14)-[LIVfMT SEQ ID NO:654)]-x(2)-[FYwCTH SEQ ID NO:655)]-[DNSTK SEQ ID NO:656)]

-Consensus pattern: [LIVMFYWA SEQ ID NO:41)]-[LIVFYWC SEQ ID NO:657)]-x(2)-[SAC]-[DNQHR SEQ ID NO:658)]-[IVFA SEQ ID NO:659)]-[LIVF SEQ ID NO:127)]-x-[LIVF SEQ ID NO:127)]-[HNI]-x-P-x(4)-[STN]-x(2)-[LIVMF SEQ ID NO:2)]-x-[GSDN SEQ ID NO:660)]

-Consensus pattern: [LMFATC SEQ ID NO:661)]-[KPQ]-x-[GSTDN SEQ ID NO:662)]-x-[LIVMFYWR SEQ ID NO:85)]-[LIVMFYW SEQ ID NO:26)](2)-N-x-[STAGC SEQ ID NO:45)]-R-[GP]-x-[LIVH SEQ ID NO:663)]-[LIVMC SEQ ID NO:142)]-[DNV]

[1] Grant G.A. Biochem. Biophys. Res. Commun. 165:1371-1374(1989).

[2] Kochhar S., Hunziker P., Leong-Morgenthaler P.M., Hottinger H. Biochem. Biophys. Res. Commun. 184:60-66(1992).

[3] Ohta T., Taguchi H. J. Biol. Chem. 266:12588-12594(1991).

[4] Goldberg J.D., Yoshida T., Brick P. J. Mol. Biol. 236:1123-1140(1994).

[5] Popov V.O., Lamzin V.S. Biochem. J. 301:625-643(1994).

734. 2-oxo acid dehydrogenases acyltransferase (catalytic domain)

Refined crystal structure of the catalytic domain of dihydrolipoyl transacetylase (E2P) from azotobacter vineelandii at 2.6 angstroms resolution.

Mattevi A, Obmolova G, Kalk KH, Westphal AH, De Kok A, Hol WG;

J Mol Biol 1993;230:1183-1199.

These proteins contain one to three copies of a lipoyl binding domain followed by the catalytic domain.

735. 3-beta hydroxysteriod dehydrogenase/isomerase family

Structure and tissue-specific expression of 3

beta-hydroxysteroid dehydrogenase/5-ene-4-ene isomerase

genes in human and rat classical and peripheral

steroidogenic tissues.

Labrie F, Simard J, Luu-The V, Pelletier G, Belanger A,
Lachance Y, Zhao HF, Labrie C, Breton N, de Launoit Y, et al
J Steroid Biochem Mol Biol 1992;41:421-435.

- 5 The enzyme 3 beta-hydroxysteroid dehydrogenase/5-ene-4-ene
isomerase (3 beta-HSD) catalyzes the oxidation and isomerization
of 5-ene-3 beta-hydroxypregnene and 5-ene-hydroxyandrostene
steroid precursors into the corresponding 4-ene-ketosteroids necessary
for the formation of all classes of steroid hormones.

10

736. 3-hydroxyacyl-CoA dehydrogenase

This family also includes lambda crystallin.

Structure of L-3-hydroxyacyl-coenzyme A dehydrogenase:

- 15 preliminary chain tracing at 2.8-A resolution.

Birktoft JJ, Holden HM, Hamlin R, Xuong NH, Banaszak LJ;
Proc Natl Acad Sci U S A 1987;84:8262-8266.

- 20 3-hydroxyacyl-CoA dehydrogenase (EC 1.1.1.35) (HCDH) [1] is an enzyme involved
in fatty acid metabolism, it catalyzes the reduction of 3-hydroxyacyl-CoA to
3-oxoacyl-CoA. Most eukaryotic cells have 2 fatty-acid beta-oxidation systems,
one located in mitochondria and the other in peroxisomes. In peroxisomes
3-hydroxyacyl-CoA dehydrogenase forms, with enoyl-CoA hydratase (ECH) and
3,2-trans-enoyl-CoA isomerase (ECI) a multifunctional enzyme where the N-
25 terminal domain bears the hydratase/isomerase activities and the C-terminal
domain the dehydrogenase activity. There are two mitochondrial enzymes: one
which is monofunctional and the other which is, like its peroxisomal
counterpart, multifunctional.

- 30 In *Escherichia coli* (gene *fadB*) and *Pseudomonas fragi* (gene *faoA*) HCDH is part
of a multifunctional enzyme which also contains an ECH/ECI domain as well as a
3-hydroxybutyryl-CoA epimerase domain [2].

The other proteins structurally related to HCDH are:

- Bacterial 3-hydroxybutyryl-CoA dehydrogenase (EC 1.1.1.157) which reduces 3-hydroxybutanoyl-CoA to acetoacetyl-CoA [3].
- 5 - Eye lens protein lambda-crystallin [4], which is specific to lagomorphes (such as rabbit).

There are two major region of similarities in the sequences of proteins of the HCDH family, the first one located in the N-terminal, corresponds to the NAD-binding site, the second one is located in the center of the sequence. A signature pattern has been derived from this central region.

-Consensus pattern: [DNE]-x(2)-[GA]-F-[LIVMFY SEQ ID NO:18)]-x-[NT]-R-x(3)-[PA]-[LIVMFY SEQ ID NO:18)](2)-
 15 x(5)-[LIVMFYCT SEQ ID NO:447)]-[LIVMFY SEQ ID NO:18)]-x(2)-[GV]

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 Proc. Natl. Acad. Sci. U.S.A. 84:8262-8266(1987).

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 20 Nucleic Acids Res. 18:4937-4937(1990).

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 Tabaqchali S.
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 25 de Jong W.W.
 J. Biol. Chem. 263:15462-15466(1988).

737. 60s Acidic ribosomal protein

30 Proteins P1, P2, and P0, components of the eukaryotic ribosome stalk. New structural and functional aspects.

Remacha M, Jimenez-Diaz A, Santos C, Briones E, Zambrano R,
 Rodriguez Gabriel MA, Guarinos E, Ballesta JP;

Biochem Cell Biol 1995;73:959-968.

This family includes archaeobacterial L12, eukaryotic P0, P1 and P2.

- 5 738. 6-phosphogluconate dehydrogenases
6-phosphogluconate dehydrogenase (EC 1.1.1.44) (6PGD) catalyzes the third step
in the hexose monophosphate shunt, the decarboxylating reduction of
6-phosphogluconate in to ribulose 5-phosphate.
- 10 Prokaryotic and eukaryotic 6PGD are proteins of about 470 amino acids whose
sequence are highly conserved [1]. A region which has been shown [2], from studies
of the sheep 6PGD tertiary structure, to be involved in the binding of 6-phosphogluconate
has been selected as a signature pattern.
- 15 -Consensus pattern: [LIVM SEQ ID NO:4)]-x-D-x(2)-[GA]-[NQS]-K-G-T-G-x-W
- [1] Reizer A., Deutscher J., Saier M.H. Jr., Reizer J.
Mol. Microbiol. 5:1081-1089(1991).
- [2] Adams M.J., Archibald I.G., Bugg C.E., Carne A., Gover S.,
20 Helliwell J.R., Pickersgill R.W., White S.W.
EMBO J. 2:1009-1014(1983).
- 25 739. (7tm 1) G-protein coupled receptors [1 to 4,E1,E2] (also called R7G) are an extensive
group of hormones, neurotransmitters, odorants and light receptors which
transduce extracellular signals by interaction with guanine nucleotide-
binding (G) proteins. The receptors that are currently known to belong to this
family are listed below.
- 30 - 5-hydroxytryptamine (serotonin) 1A to 1F, 2A to 2C, 4, 5A, 5B, 6 and 7 [5].
- Acetylcholine, muscarinic-type, M1 to M5.
- Adenosine A1, A2A, A2B and A3 [6].
- Adrenergic alpha-1A to -1C; alpha-2A to -2D; beta-1 to -3 [7].

- Angiotensin II types I and II.
- Bombesin subtypes 3 and 4.
- Bradykinin B1 and B2.
- c3a and C5a anaphylatoxin.
- 5 - Cannabinoid CB1 and CB2.
- Chemokines C-C CC-CKR-1 to CC-CKR-8.
- Chemokines C-X-C CXC-CKR-1 to CXC-CKR-4.
- Cholecystokinin-A and cholecystokinin-B/gastrin.
- Dopamine D1 to D5 [8].
- 10 - Endothelin ET-a and ET-b [9].
- fMet-Leu-Phe (fMLP) (N-formyl peptide).
- Follicle stimulating hormone (FSH-R) [10].
- Galanin.
- Gastrin-releasing peptide (GRP-R).
- 15 - Gonadotropin-releasing hormone (GNRH-R).
- Histamine H1 and H2 (gastric receptor I).
- Lutropin-choriogonadotropic hormone (LSH-R) [10].
- Melanocortin MC1R to MC5R.
- Melatonin.
- 20 - Neuromedin B (NMB-R).
- Neuromedin K (NK-3R).
- Neuropeptide Y types 1 to 6.
- Neurotensin (NT-R).
- Octopamine (tyramine), from insects.
- 25 - Odorants [11].
- Opioids delta-, kappa- and mu-types [12].
- Oxytocin (OT-R).
- Platelet activating factor (PAF-R).
- Prostacyclin.
- 30 - Prostaglandin D2.
- Prostaglandin E2, EP1 to EP4 subtypes.
- Prostaglandin F2.
- Purinoreceptors (ATP) [13].

- Somatostatin types 1 to 5.
- Substance-K (NK-2R).
- Substance-P (NK-1R).
- Thrombin.
- 5 - Thromboxane A2.
- Thyrotropin (TSH-R) [10].
- Thyrotropin releasing factor (TRH-R).
- Vasopressin V1a, V1b and V2.
- Visual pigments (opsins and rhodopsin) [14].
- 10 - Proto-oncogene mas.
- A number of orphan receptors (whose ligand is not known) from mammals and birds.
- *Caenorhabditis elegans* putative receptors C06G4.5, C38C10.1, C43C3.2, T27D1.3 and ZC84.4.
- 15 - Three putative receptors encoded in the genome of cytomegalovirus: US27, US28, and UL33.
- ECRF3, a putative receptor encoded in the genome of herpesvirus saimiri.

The structure of all these receptors is thought to be identical. They have
20 seven hydrophobic regions, each of which most probably spans the membrane.
The N-terminus is located on the extracellular side of the membrane and is
often glycosylated, while the C-terminus is cytoplasmic and generally
phosphorylated. Three extracellular loops alternate with three intracellular
loops to link the seven transmembrane regions. Most, but not all of these
25 receptors, lack a signal peptide. The most conserved parts of these proteins
are the transmembrane regions and the first two cytoplasmic loops. A conserved
acidic-Arg-aromatic triplet is present in the N-terminal extremity of the
second cytoplasmic loop [15] and could be implicated in the interaction with G
proteins.

30

To detect this widespread family of proteins, a pattern that contains the conserved
triplet and that also spans the major part of the third transmembrane helix has
been developed.

-Consensus pattern: [GSTALIVMFYWC SEQ ID NO:664)]-[GSTANCPDE SEQ ID NO:665)]-{EDPKRH SEQ ID NO:666}}-x(2)-[LIVMNQGA SEQ ID NO:667)]-x(2)-[LIVMFT SEQ ID NO:282)]-[GSTANC SEQ ID NO:668)]-[LIVMFYWSTAC SEQ ID NO:669)]-[DENH SEQ ID NO:670)]-R-[FYWCSH SEQ ID NO:671)]-x(2)-[LIVM SEQ ID NO:4)]

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Eur. J. Biochem. 196:1-10(1991).

[2] Kerlavage A.R.

Curr. Opin. Struct. Biol. 1:394-401(1991).

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Curr. Biol. 1:20-22(1991).

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Curr. Biol. 3:668-674(1993).

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[13] Barnard E.A., Burnstock G., Webb T.E.

Trends Pharmacol. Sci. 15:67-70(1994).

[14] Applebury M.L., Hargrave P.A.

Vision Res. 26:1881-1895(1986).

[15] Attwood T.K., Eliopoulos E.E., Findlay J.B.C.

Gene 98:153-159(1991).

5

(7tm 1) Visual pigments (opsins) retinal binding site

Visual pigments [1,2] are the light-absorbing molecules that mediate vision.

They consist of an apoprotein, opsin, covalently linked to the chromophore

cis-retinal. Vision is effected through the absorption of a photon by cis-

10 retinal which is isomerized to trans-retinal. This isomerization leads to a
change of conformation of the protein. Opsins are integral membrane proteins
with seven transmembrane regions that belong to family 1 of G-protein coupled
receptors.

15 In vertebrates four different pigments are generally found. Rod cells, which
mediate vision in dim light, contain the pigment rhodopsin. Cone cells, which
function in bright light, are responsible for color vision and contain three
or more color pigments (for example, in mammals: red, blue and green).

20 In Drosophila, the eye is composed of 800 facets or ommatidia. Each
ommatidium contains eight photoreceptor cells (R1-R8): the R1 to R6 cells are
outer cells, R7 and R8 inner cells. Each of the three types of cells (R1-R6,
R7 and R8) expresses a specific opsin.

25 Proteins evolutionary related to opsins include squid retinochrome, also known
as retinal photoisomerase, which converts various isomers of retinal into 11-
cis retinal and mammalian retinal pigment epithelium (RPE) RGR [3], a protein
that may also act in retinal isomerization.

30 The attachment site for retinal in the above proteins is a conserved lysine
residue in the middle of the seventh transmembrane helix. The pattern
that had been developed includes this residue.

606

-Consensus pattern: [LIVMWAC SEQ ID NO:672)]-[PGC]-x(3)-[SAC]-K-[STALIMR SEQ ID NO:673)]-[GSACPNV SEQ ID NO:674)]-[STACP SEQ ID NO:384)]-x(2)-[DENF SEQ ID NO:675)]-[AP]-x(2)-[IY]
[K is the retinal binding site]

5

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Vision Res. 26:1881-1895(1986).

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Biochemistry 33:13117-13125(1994).

The following descriptions of protein family functions are not provided by the Pfam or Prosite databases.

15

740. BAH

BAH domain. Number of members: 65

20 [1] Medline: 97074677. Molecular cloning of polybromo, a nuclear protein containing multiple domains including five bromodomains, a truncated HMG-box, and two repeats of a novel domain. Nicolas RH, Goodwin GH; Gene 1996;175:233-240.

[2] Medline: 99198739. The BAH (bromo-adjacent homology) domain: a link between DNA methylation, replication and transcriptional regulation. Callebaut I, Courvalin J-C,
25 Mornon JP; FEBS letts 1999;446:189-193.

741. ELM2.

ELM2 domain. The ELM2 (Egl-27 and MTA1 homology 2) domain is a small domain of
30 unknown function. Number of members: 10

742. Euk proin. EUKARYOTIC_PORIN The major protein of the outer mitochondrial membrane of eukaryotes is a porin that forms a voltage-dependent anion-selective channel (VDAC) that behaves as a general diffusion pore for small hydrophilic molecules [1 to 4]. The channel adopts an open conformation at low or zero membrane potential and a

This protein contains about 280 amino acids and its sequence is composed of between 12 to 16 beta-strands that span the mitochondrial outer membrane. Yeast contains two members of this family (genes POR1 and POR2); vertebrates have at least three members (genes VDAC1, VDAC2 and VDAC3) [5].

A conserved region located at the C-terminal part of these proteins was selected as a signature pattern.

Consensus pattern[YH]-x(2)-D-[SPCAD SEQ ID NO:676)]-x-[STA]-x(3)-[TAG]-[KR]-[LIVMF SEQ ID NO:2)]-[DNSTA SEQ ID NO:677)]-[DNS]-x(4)-[GSTAN SEQ ID NO:296)]-[LIVMA SEQ ID NO:30)]-x-[LIVMY SEQ ID NO:141)]

[1] Benz R. Biochim. Biophys. Acta 1197:167-196(1994).

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743. Glyco hydor 19

Chitinases family 19 signatures

cross-reference(s) CHITINASE_19_1, CHITINASE_19_2

Chitinases (EC 3.2.1.14) [1] are enzymes that catalyze the hydrolysis of the beta-1,4-N-acetyl-D-glucosamine linkages in chitin polymers. From the view point of sequence similarity chitinases belong to either family 18 or 19 in the classification of glycosyl

hydrolases [2,E1]. Chitinases of family 19 (also known as classes IA or I and IB or II) are enzymes from plants that function in the defense against fungal and insect pathogens by destroying their chitin-containing cell wall. Class IA/I and IB/II enzymes differ in the presence (IA/I) or absence (IB/II) of a N-terminal chitin-binding domain (see the relevant

entry <PDOC00025>). The catalytic domain of these enzymes consist of about 220 to 230 amino acid residues.

Two highly conserved regions were selected as signature patterns, the first one is located in the N-terminal section and contains one of the six cysteines which are conserved in most, if not all, of these chitinases and which is probably involved in a disulfide bond.

Consensus pattern C-x(4,5)-F-Y-[ST]-x(3)-[FY]-[LIVMF SEQ ID NO:2)]-x-A-x(3)-[YF]-x(2)-F-[GSA]

Consensus pattern [LIVM SEQ ID NO:4)]-[GSA]-F-x-[STAG SEQ ID NO:20)](2)-[LIVMFY SEQ ID NO:18)]-W-[FY]-W-[LIVM SEQ ID NO:4)]

[1]Flach J., Pilet P.-E., Jolles P. *Experientia* 48:701-716(1992).

[2] Henrissat B. *Biochem. J.* 280:309-316(1991).

744. MBD

Methyl-CpG binding domain

The Methyl-CpG binding domain (MBD) binds to DNA that contains one or more symmetrically methylated CpGs [1]. DNA methylation in animals is associated with alterations in chromatin structure and silencing of gene expression. MBD has negligible non-specific affinity for DNA. In vitro foot-printing with MeCP2 showed the MBD can protect a 12 nucleotide region surrounding a methyl CpG pair [1]. MBDs are found in several Methyl-CpG binding proteins and also DNA demethylase [2]. Number of members: 11

[1]Medline: 94232813. Dissection of the methyl-CpG binding domain from the chromosomal protein MeCP2. Nan X, Meehan RR, Bird A; *Nucleic Acids Res* 1993;21:4886-4892.

[2]Medline: 99158138. A mammalian protein with specific demethylase activity for mCpG DNA. Bhattacharya SK, Ramchandani S, Cervoni N, Szyf M; *Nature* 1999;397:579-583.

745. Peptidase C1

Eukaryotic thiol (cysteine) proteases active sites

cross-reference(s) THIOLEPROTEASE_CYS; THIOLEPROTEASE_HIS;
THIOLEPROTEASE_ASN

Eukaryotic thiol proteases (EC 3.4.22.-) [1] are a family of proteolytic enzymes which contain an active site cysteine. Catalysis proceeds through a thioester intermediate and is facilitated by a nearby histidine side chain; an asparagine completes the essential catalytic triad. The proteases which are currently known to belong to this family are listed below (references are only provided for recently determined sequences).

- Vertebrate lysosomal cathepsins B (EC 3.4.22.1), H (EC 3.4.22.16), L (EC 3.4.22.15), and S (EC 3.4.22.27) [2].

- Vertebrate lysosomal dipeptidyl peptidase I (EC 3.4.14.1) (also known as cathepsin C) [2].

- Vertebrate calpains (EC 3.4.22.17). Calpains are intracellular calcium-activated thiol protease that contain both a N-terminal catalytic domain and a C-terminal calcium-binding domain.

- Mammalian cathepsin K, which seems involved in osteoclastic bone resorption [3].

- Human cathepsin O [4].

- Bleomycin hydrolase. An enzyme that catalyzes the inactivation of the antitumor drug BLM (a glycopeptide).

- Plant enzymes: barley aleurain (EC 3.4.22.16), EP-B1/B4; kidney bean EP-C1, rice bean SH-EP; kiwi fruit actinidin (EC 3.4.22.14); papaya latex papain (EC 3.4.22.2), chymopapain (EC 3.4.22.6), caricain (EC 3.4.22.30), and proteinase IV (EC 3.4.22.25); pea turgor-responsive protein 15A; pineapple stem bromelain (EC 3.4.22.32); rape COT44; rice oryzain alpha, beta, and gamma; tomato low-temperature induced, Arabidopsis thaliana A494, RD19A and RD21A.

- House-dust mites allergens DerP1 and EurM1.

- Cathepsin B-like proteinases from the worms *Caenorhabditis elegans* (genes gcp-1, cpr-3, cpr-4, cpr-5 and cpr-6), *Schistosoma mansoni* (antigen SM31) and *Japanica* (antigen SJ31), *Haemonchus contortus* (genes AC-1 and AC-2), and *Ostertagia ostertagi* (CP-1 and CP-3).

- Slime mold cysteine proteinases CP1 and CP2.

- Cruzipain from *Trypanosoma cruzi* and *brucei*.

- Trophozoite cysteine proteinase (TCP) from various *Plasmodium* species.

- Proteases from *Leishmania mexicana*, *Theileria annulata* and *Theileria parva*.

- Baculoviruses cathepsin-like enzyme (v-cath).
- Drosophila small optic lobes protein (gene sol), a neuronal protein that contains a calpain-like domain.
- Yeast thiol protease BLH1/YCP1/LAP3.
- 5 - Caenorhabditis elegans hypothetical protein C06G4.2, a calpain-like protein.

Two bacterial peptidases are also part of this family:

- Aminopeptidase C from Lactococcus lactis (gene pepC) [5].
- 10 - Thiol protease tpr from Porphyromonas gingivalis.

Three other proteins are structurally related to this family, but may have lost their proteolytic activity.

- 15 - Soybean oil body protein P34. This protein has its active site cysteine replaced by a glycine.
 - Rat testin, a sertoli cell secretory protein highly similar to cathepsin L but with the active site cysteine is replaced by a serine. Rat testin should not be confused with mouse testin which is a LIM-domain protein (see <PDOC00382>).
 - 20 - Plasmodium falciparum serine-repeat protein (SERA), the major blood stage antigen. This protein of 111 Kd possesses a C-terminal thiol-protease-like domain [6], but the active site cysteine is replaced by a serine.
- The sequences around the three active site residues are well conserved and can be used as signature patterns.

25

Consensus pattern Q-x(3)-[GE]-x-C-[YW]-x(2)-[STAGC SEQ ID NO:45)]-[STAGCV SEQ ID NO:159)] [C is the active site residue]

- Note the residue in position 4 of the pattern is almost always cysteine; the only exceptions are
- 30 calpains (Leu), bleomycin hydrolase (Ser) and yeast YCP1 (Ser). Note the residue in position 5 of the pattern is always Gly except in papaya protease IV where it is Glu.

Consensus pattern[LIVMGSTAN SEQ ID NO:160)]-x-H-[GSACE SEQ ID NO:161)]-
[LIVM SEQ ID NO:4)]-x-[LIVMAT SEQ ID NO:162)](2)-G-x-[GSADNH SEQ ID
NO:163)] [H is the active site residue]

Consensus pattern[FYCH SEQ ID NO:164)]-[WI]-[LIVT SEQ ID NO:165)]-x-[KRQAG
5 SEQ ID NO:166)]-N-[ST]-W-x(3)-[FYW]-G-x(2)-G-[LFYW SEQ ID NO:167)]-[LIVMFY
SEQ ID NO:168)]-x-[LIVMF SEQ ID NO:2)] [N is the active site residue]

Note these proteins belong to family C1 (papain-type) and C2 (calpains) in the classification
of peptidases [7,E1].

- 10 [1]Dufour E. Biochimie 70:1335-1342(1988).
[2]Kirschke H., Barrett A.J., Rawlings N.D. Protein Prof. 2:1587-1643(1995).
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Microbiol. 59:330-333(1993).
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20

746. Peptidase M22

Glycoprotease family signature cross-reference(s) GLYCOPROTEASE

Glycoprotease (GCP) (EC 3.4.24.57) [1], or o-sialoglycoprotein endopeptidase,

- 25 is a metalloprotease secreted by *Pasteurella haemolytica* which specifically
cleaves O-sialoglycoproteins such as glycophorin A. The sequence of GCP is
highly similar to the following uncharacterized proteins:

- *Escherichia coli* hypothetical protein ygjD (ORF-X).
- 30 - *Bacillus subtilis* hypothetical protein ydiE.
- *Mycobacterium leprae* hypothetical protein U229E.
- *Mycobacterium tuberculosis* hypothetical protein MtCY78.10.
- *Synechocystis* strain PCC 6803 hypothetical protein slr0807.

- *Methanococcus jannaschii* hypothetical protein MJ1130.
- *Haloarcula marismortui* hypothetical protein in HSH 3'region.
- Yeast hypothetical protein YKR038c.
- Yeast hypothetical protein QRI7.

5

One of the conserved regions contains two conserved histidines. It is possible that this region is involved in coordinating a metal ion such as zinc.

Consensus pattern[KR]-[GSAT SEQ ID NO:100)]-x(4)-[FYWLH SEQ ID NO:273)]-
 10 [DQNGK SEQ ID NO:274)]-x-P-x-[LIVMFY SEQ ID NO:18)]-x(3)-H-
 x(2)-[AG]-H-[LIVM SEQ ID NO:4)]

Note these proteins belong to family M22 in the classification of peptidases [2,E1].

- 15 [1]Abdullah K.M., Lo R.Y.C., Mellors A. J. Bacteriol. 173:5597-5603(1991).
 [2]Rawlings N.D., Barrett A.J. Meth. Enzymol. 248:183-228(1995).

747. SAM. SAM domain (Sterile alpha motif)

- 20 It has been suggested that SAM is an evolutionarily conserved protein binding domain that is involved in the regulation of numerous developmental processes in diverse eukaryotes. The SAM domain can potentially function as a protein interaction module through its ability to homo- and heterooligomerise with other SAM domains. Number of members: 81

- 25 [1]Medline: 96100659 SAM: A novel motif in yeast sterile alpha and *Drosophila* polyhomeotic proteins Ponting CP; Prot Sci 1995;4:1928-1930.
 [2]Medline: 97160498 SAM as a protein interaction domain involved in developmental regulation. Shultz J, Ponting CP, Hofmann K, Bork P; Prot Sci 1997;6:249-253.
 [3]Medline: 99101382 The crystal structure of an Eph receptor SAM domain reveals a
 30 mechanism for modular dimerization. Reference Author: Stapleton D, Balan I, Pawson T, Sicheri F; Nat Struct Biol 1999;6:44-49.

748. Tyrosinase signatures cross-reference(s) TYROSINASE_1; TYROSINASE_2

Tyrosinase (EC 1.14.18.1) [1] is a copper monooxygenases that catalyzes the hydroxylation of monophenols and the oxidation of o-diphenols to o-quinols.

This enzyme, found in prokaryotes as well as in eukaryotes, is involved in the

5 formation of pigments such as melanins and other polyphenolic compounds.

Tyrosinase binds two copper ions (CuA and CuB). Each of the two copper ion has

been shown [2] to be bound by three conserved histidines residues. The regions

around these copper-binding ligands are well conserved and also shared by some

10 hemocyanins, which are copper-containing oxygen carriers from the hemolymph of many molluscs and arthropods [3,4].

At least two proteins related to tyrosinase are known to exist in mammals:

15 - TRP-1 (TYRP1) [5], which is responsible for the conversion of 5,6-dihydro-xyindole-2-carboxylic acid (DHICA) to indole-5,6-quinone-2-carboxylic acid.

- TRP-2 (TYRP2) [6], which is the melanogenic enzyme DOPAchrome tautomerase (EC 5.3.3.12) that catalyzes the conversion of DOPAchrome to DHICA. TRP-2 differs from tyrosinases and TRP-1 in that it binds two zinc ions instead

20 of copper [7].

Other proteins that belong to this family are:

25 - Plants polyphenol oxidases (PPO) (EC 1.10.3.1) which catalyze the oxidation of mono- and o-diphenols to o-diquinones [8].

- *Caenorhabditis elegans* hypothetical protein C02C2.1.

Two signature patterns for tyrosinase and related proteins have been derived

The first one contains two of the histidines that bind CuA, and is located in

30 the N-terminal section of tyrosinase. The second pattern contains a histidine that binds CuB, that pattern is located in the central section of the enzyme.

Consensus pattern H-x(4,5)-F-[LIVMFTP SEQ ID NO:678)]-x-[FW]-H-R-x(2)-[LM]-x(3)-E

[The two H's are copper ligands]

Consensus pattern D-P-x-F-[LIVMFYW SEQ ID NO:26]-x(2)-H-x(3)-D [H is a copper ligand]

- 5 [1] Lerch K. Prog. Clin. Biol. Res. 256:85-98(1988).
 [2] Jackman M.P., Hajnal A., Lerch K. Biochem. J. 274:707-713(1991).
 [3] Linzen B. Naturwissenschaften 76:206-211(1989).
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 [5] Kobayashi T., Urabe K., Winder A., Jimenez-Cervantes C., Imokawa G., Brewington T.,
 10 Solano F., Garcia-Borrón J.C., Hearing V.J. EMBO J. 13:5818-5825(1994).
 [6] Jackson I.J., Chambers D.M., Tsukamoto K., Copeland N.G., Gilbert D.J., Jenkins N.A.,
 Hearing V. EMBO J. 11:527-535(1992).
 [7] Solano F., Martínez-Liarte J.H., Jimenez-Cervantes C., Garcia-Borrón J.C., Lozano J.A.
 Biochem. Biophys. Res. Commun. 204:1243-1250(1994).
 15 [8] Cary J.W., Lax A.R., Flurkey W.H. Plant Mol. Biol. 20:245-253(1992).

749. (Mur Ligase) Folylpolyglutamate synthase signatures

Folylpolyglutamate synthase (EC 6.3.2.17) (FPGS) [1] is the enzyme of folate metabolism
 20 that catalyzes ATP-dependent addition of glutamate moieties to tetrahydrofolate.

Its sequence is moderately conserved between prokaryotes (gene folC) and eukaryotes.
 We developed two signature patterns based on the conserved regions which are rich in
 glycine residues and could play a role in the catalytical
 25 activity and/or in substrate binding.

Description of pattern(s) and/or profile(s)

Consensus pattern [LIVMFY SEQ ID NO:18]-x-[LIVM SEQ ID NO:4]-[STAG SEQ ID
 NO:20)]-G-T-[NK]-G-K-x-[ST]-x(7)-[LIVM SEQ ID NO:4]](2)-x(3)-[GSK]
 30 Consensus pattern [LIVMFY SEQ ID NO:18]](2)-E-x-G-[LIVM SEQ ID NO:4]-[GA]-G-
 x(2)-D-x-[GST]-x-[LIVM SEQ ID NO:4]](2)

[1]Shane B., Garrow T., Brenner A., Chen L., Choi Y.J., Hsu J.C., Stover P. Adv. Exp. Med. Biol. 338:629-634(1993).

- 5 750. (Peptidase M3) Neutral zinc metallopeptidases, zinc-binding region signature
The majority of zinc-dependent metallopeptidases (with the notable exception of the
carboxypeptidases) share a common pattern of primary structure [1,2,3] in the part of their
sequence involved in the binding of zinc, and can be grouped together as a
superfamily, known as the metzincins, on the basis of this sequence similarity. They can be
10 classified into a number of distinct families [4,E1] which are listed below along with the
proteases which are currently known to belong to these families.

Family M1

- Bacterial aminopeptidase N (EC 3.4.11.2) (gene pepN).
- 15 - Mammalian aminopeptidase N (EC 3.4.11.2).
- Mammalian glutamyl aminopeptidase (EC 3.4.11.7) (aminopeptidase A). It may play a
role in regulating growth and differentiation of early B-lineage cells.
- Yeast aminopeptidase yscII (gene APE2).
- Yeast alanine/arginine aminopeptidase (gene AAP1).
- 20 - Yeast hypothetical protein YIL137c.
- Leukotriene A-4 hydrolase (EC 3.3.2.6). This enzyme is responsible for the hydrolysis of
an epoxide moiety of LTA-4 to form LTB-4; it has been shown that it binds zinc and is
capable of peptidase activity.

25 Family M2

- Angiotensin-converting enzyme (EC 3.4.15.1) (dipeptidyl carboxypeptidase I) (ACE) the
enzyme responsible for hydrolyzing angiotensin I to angiotensin II. There are two forms
of ACE: a testis-specific isozyme and a somatic isozyme which has two active centers.

30 Family M3

- Thimet oligopeptidase (EC 3.4.24.15), a mammalian enzyme involved in the cytoplasmic
degradation of small peptides.

- Neurolysin (EC 3.4.24.16) (also known as mitochondrial oligopeptidase M or microsomal endopeptidase).

- Mitochondrial intermediate peptidase precursor (EC 3.4.24.59) (MIP). It is involved the second stage of processing of some proteins imported in the mitochondrion.

5 - Yeast saccharolysin (EC 3.4.24.37) (proteinase yscD).

- Escherichia coli and related bacteria dipeptidyl carboxypeptidase (EC 3.4.15.5) (gene dcp).

- Escherichia coli and related bacteria oligopeptidase A (EC 3.4.24.70) (gene opdA or prlC).

- Yeast hypothetical protein YKL134c.

10

Family M4

- Thermostable thermolysins (EC 3.4.24.27), and related thermolabile neutral proteases (bacillolysins) (EC 3.4.24.28) from various species of Bacillus.

- Pseudolysin (EC 3.4.24.26) from Pseudomonas aeruginosa (gene lasB).

15 - Extracellular elastase from Staphylococcus epidermidis.

- Extracellular protease prtI from Erwinia carotovora.

- Extracellular minor protease smp from Serratia marcescens.

- Vibriolysin (EC 3.4.24.25) from various species of Vibrio.

- Protease prtA from Listeria monocytogenes.

20 - Extracellular proteinase proA from Legionella pneumophila.

Family M5

- Mycolysin (EC 3.4.24.31) from Streptomyces cacaoi.

25 Family M6

- Immune inhibitor A from Bacillus thuringiensis (gene ina). Ina degrades two classes of insect antibacterial proteins, attacins and cecropins.

Family M7

30 - Streptomyces extracellular small neutral proteases

Family M8

- Leishmanolysin (EC 3.4.24.36) (surface glycoprotein gp63), a cell surface protease from various species of *Leishmania*.

Family M9

- 5 - Microbial collagenase (EC 3.4.24.3) from *Clostridium perfringens* and *Vibrio alginolyticus*.

Family M10A

- 10 - Serralysin (EC 3.4.24.40), an extracellular metalloprotease from *Serratia*.
- Alkaline metalloproteinase from *Pseudomonas aeruginosa* (gene *aprA*).
- Secreted proteases A, B, C and G from *Erwinia chrysanthemi*.
- Yeast hypothetical protein YIL108w.

Family M10B

- 15 - Mammalian extracellular matrix metalloproteinases (known as matrixins) [5]: MMP-1 (EC 3.4.24.7) (interstitial collagenase), MMP-2 (EC 3.4.24.24) (72 Kd gelatinase), MMP-9 (EC 3.4.24.35) (92 Kd gelatinase), MMP-7 (EC 3.4.24.23) (matrylisin), MMP-8 (EC 3.4.24.34) (neutrophil collagenase), MMP-3 (EC 3.4.24.17) (stromelysin-1), MMP-10 (EC 3.4.24.22) (stromelysin-2), and MMP-11 (stromelysin-3), MMP-12 (EC 3.4.24.65) (macrophage
20 metalloelastase).
- Sea urchin hatching enzyme (envelysin) (EC 3.4.24.12). A protease that allows the embryo to digest the protective envelope derived from the egg extracellular matrix.
- Soybean metalloendoproteinase 1.

25 Family M11

- *Chlamydomonas reinhardtii* gamete lytic enzyme (GLE).

Family M12A

- 30 - Astacin (EC 3.4.24.21), a crayfish endoprotease.
- Meprin A (EC 3.4.24.18), a mammalian kidney and intestinal brush border metalloendopeptidase.

- Bone morphogenic protein 1 (BMP-1), a protein which induces cartilage and bone formation and which expresses metalloendopeptidase activity. The *Drosophila* homolog of BMP-1 is the dorsal-ventral patterning protein tolloid.

- Blastula protease 10 (BP10) from *Paracentrotus lividus* and the related protein SpAN from *Strongylocentrotus purpuratus*.

- *Caenorhabditis elegans* protein toh-2.

- *Caenorhabditis elegans* hypothetical protein F42A10.8.

- Choriolysins L and H (EC 3.4.24.67) (also known as embryonic hatching proteins LCE and HCE) from the fish *Oryzias latipes*. These proteases participate in the breakdown of the egg envelope, which is derived from the egg extracellular matrix, at the time of hatching.

Family M12B

- Snake venom metalloproteinases [6]. This subfamily mostly groups proteases that act in hemorrhage. Examples are: adamalysin II (EC 3.4.24.46), atrolysin C/D (EC 3.4.24.42), atrolysin E (EC 3.4.24.44), fibrolase (EC 3.4.24.72), trimereylisin I (EC 3.4.25.52) and II (EC 3.4.25.53).

- Mouse cell surface antigen MS2.

Family M13

- Mammalian neprilysin (EC 3.4.24.11) (neutral endopeptidase) (NEP).

- Endothelin-converting enzyme 1 (EC 3.4.24.71) (ECE-1), which process the precursor of endothelin to release the active peptide.

- Kell blood group glycoprotein, a major antigenic protein of erythrocytes. The Kell protein is very probably a zinc endopeptidase.

- Peptidase O from *Lactococcus lactis* (gene pepO).

Family M27

- Clostridial neurotoxins, including tetanus toxin (TeTx) and the various botulinum toxins (BoNT). These toxins are zinc proteases that block neurotransmitter release by proteolytic cleavage of synaptic proteins such as synaptobrevins, syntaxin and SNAP-25 [7,8].

Family M30

- *Staphylococcus hyicus* neutral metalloprotease.

Family M32

- 5 - Thermostable carboxypeptidase 1 (EC 3.4.17.19) (carboxypeptidase Taq), an enzyme from *Thermus aquaticus* which is most active at high temperature.

Family M34

- 10 - Lethal factor (LF) from *Bacillus anthracis*, one of the three proteins composing the anthrax toxin.

Family M35

- 15 - Deuterolysin (EC 3.4.24.39) from *Penicillium citrinum* and related proteases from various species of *Aspergillus*.

Family M36

- Extracellular elastinolytic metalloproteinases from *Aspergillus*.

20 From the tertiary structure of thermolysin, the position of the residues acting as zinc ligands and those involved in the catalytic activity are known. Two of the zinc ligands are histidines which are very close together in the sequence; C-terminal to the first histidine is a glutamic acid residue which acts as a nucleophile and promotes the attack of a water molecule on the carbonyl carbon of the substrate. A signature pattern which includes the two histidine and the glutamic acid residues is sufficient to detect this superfamily of
25 proteins.

Description of pattern(s) and/or profile(s)

30 Consensus pattern[GSTALIVN SEQ ID NO:679)]-x(2)-H-E-[LIVMFYW SEQ ID NO:26)]-
{DEHRKP SEQ ID NO:680)}-H-x-[LIVMFYWGSPQ SEQ ID NO:681)] [The
two H's are zinc ligands] [E is the active site residue]

Sequences known to belong to this class detected by the patternALL,
except for members of families M5, M7 and M11.

Other sequence(s) detected in SWISS-PROT55; including *Neurospora*

crassa conidiation-specific protein 13 which could be a zinc-protease.

[1]Jongeneel C.V., Bouvier J., Bairoch A.
FEBS Lett. 242:211-214(1989).

5 [2]Murphy G.J.P., Murphy G., Reynolds J.J.
FEBS Lett. 289:4-7(1991).

[3]Bode W., Grams F., Reinemer P., Gomis-Rueth F.-X., Baumann U., McKay D.B., Stoecker W.
Zoology 99:237-246(1996).

10 [4]Rawlings N.D., Barrett A.J.
Meth. Enzymol. 248:183-228(1995).

[5]Woessner J. Jr.
FASEB J. 5:2145-2154(1991).

[6]Hite L.A., Fox J.W., Bjarnason J.B.

15 [7]Montecucco C., Schiavo G.
Trends Biochem. Sci. 18:324-327(1993).

[8]Niemann H., Blasi J., Jahn R.
Trends Cell Biol. 4:179-185(1994).

20

751. PseudoU_synt_1

tRNA pseudouridine synthase is involved in the formation of pseudouridine at the anticodon stem and loop of transfer-RNAs Pseudouridine is an isomer of uridine (5-(beta-D-ribofuranosyl) uracil, and is the most abundant modified nucleoside found in all cellular
25 RNAs. The TruA-like proteins also exhibit a conserved sequence with a strictly conserved aspartic acid, likely involved in catalysis. Number of members: 25

[1]Medline: 98254513. Transfer RNA-pseudouridine synthetase Pus1 of *Saccharomyces cerevisiae* contains one atom of zinc essential for its native conformation and tRNA

30 recognition. Arluison V, Hountondji C, Robert B, Grosjean H; Biochemistry 1998;37:7268-7276.

752. EPSP synthase signatures

EPSP synthase (3-phosphoshikimate 1-carboxyvinyltransferase) (EC 2.5.1.19) catalyzes the sixth step in the biosynthesis from chorismate of the aromatic amino acids (the shikimate pathway) in bacteria (gene *aroA*), plants and fungi (where it is part of a multifunctional enzyme which catalyzes five consecutive steps in this pathway) [1]. EPSP synthase has been extensively studied as it is the target of the potent herbicide glyphosate which inhibits the enzyme.

The sequence of EPSP from various biological sources shows that the structure of the enzyme has been well conserved throughout evolution. Two conserved regions were selected as signature patterns. The first pattern corresponds to a region that is part of the active site and which is also important for the resistance to glyphosate [2]. The second pattern is located in the C-terminal part of the protein and contains a conserved lysine which seems to be important for the activity of the enzyme.

Description of pattern(s) and/or profile(s)

Consensus pattern[LIVM SEQ ID NO:4)]-x(2)-[GN]-N-[SA]-G-T-[STA]-x-R-x-[LIVMY SEQ ID NO:141)]-x-[GSTA SEQ ID NO:19)]

Consensus pattern[KR]-x-[KH]-E-[CST]-[DNE]-R-[LIVM SEQ ID NO:4)]-x-[STA]-[LIVMC SEQ ID NO:142)]-x(2)-[EN]-[LIVMF SEQ ID NO:2)]-x-[KRA]-[LIVMF SEQ ID NO:2)]-G

[1]Stallings W.C., Abdel-Megid S.S., Lim L.W., Shieh H.-S., Dayringer H.E., Leimgruber N.K., Stegeman R.A., Anderson K.S., Sikorski J.A., Padgett S.R., Kishore G.M. Proc. Natl. Acad. Sci. U.S.A. 88:5046-5050(1991).

[2]Padgett S.R., Re D.B., Gaser C.S., Eicholtz D.A., Frazier R.B., Hironaka C.M., Levine E.B., Shah D.M., Fraley R.T., Kishore G.M. J. Biol. Chem. 266:22364-22369(1991).

753. Glyco_hydro_18

Glycosyl hydrolases family 18. Number of members: 173

[1]Medline: 95219379. Crystal structure of a bacterial chitinase at 2.3 Å resolution. Perrakis A, Tews I, Dauter Z, Oppenheim AB, Chet I, Wilson KS, Vorgias CE; Structure 1994;2:1169-1180.

5

754. Esterase

Putative esterase

This family contains Esterase D Swiss:P10768. However it is not clear if all members of the family have the same function. This family is possibly related to the COesterase family.

10 Number of members: 36

755. (HMA) Heavy-metal-associated domain

A conserved domain of about 30 amino acid residues has been found [1] in a number of proteins that transport or detoxify heavy metals. This domain contains two conserved cysteines that could be involved in the binding of these metals. The domain has been termed Heavy-Metal-Associated (HMA). It has been found in:

- A variety of cation transport ATPases (E1-E2 ATPases) (see <PDOC00139>). The human copper ATPases ATP7A and ATP7B which are respectively involved in Menke's and Wilson's diseases. ATP7A and ATP7B both contain 6 tandem copies of the HMA domain. The copper ATPases CCC2 from budding yeast, copA from *Enterococcus faecalis* and synA from *Synechococcus* contain one copy of the HMA domain. The cadmium ATPases cadA from *Bacillus firmus* and from plasmid pI258 from *Staphylococcus aureus* also contain a single HMA domain, while a chromosomal *Staphylococcus aureus* cadA contains two copies. Other, less characterized ATPases that contain the HMA domain are: fixI from *Rhizobium meliloti*, pacS from *Synechococcus* strain PCC 7942), *Mycobacterium leprae* ctpA and ctpB and *Escherichia coli* hypothetical protein yhhO. In all these ATPases the HMA domain(s) are located in the N-terminal section.
- Mercuric reductase (EC 1.16.1.1) (gene merA) which is generally encoded by plasmids carried by mercury-resistant Gram-negative bacteria. Mercuric reductase is a class-1 pyridine nucleotide-disulphide oxidoreductase (see <PDOC00073>). There is

30

generally one HMA domain (with the exception of a chromosomal merA from Bacillus strain RC607 which has two) in the N-terminal part of merA.

- Mercuric transport protein periplasmic component (gene merP), also encoded by plasmids carried by mercury-resistant Gram-negative bacteria. It seems to be a mercury scavenger that specifically binds to one Hg(2+) ion and which passes it to the mercuric reductase via the merT protein. The N-terminal half of merP is a HMA domain.
- Helicobacter pylori copper-binding protein copP.
- Yeast protein ATX1 [2], which could act in the transport and/or partitioning of copper.

The consensus pattern for HMA spans the complete domain.

Description of pattern(s) and/or profile(s)

Consensus pattern[LIVN SEQ ID NO:682)]-x(2)-[LIVMFA SEQ ID NO:81)]-x-C-x-[STAGCDNH SEQ ID NO:683)]-C-x(3)-[LIVFG SEQ ID NO:684)]-x(3)-[LIV]-x(9,11)-[IVA]-x-[LVFY S SEQ ID NO:685)] [The two C's probably bind metals]

[1]Bull P.C., Cox D.W. Trends Genet. 10:246-252(1994).

[2]Lin S.-J., Culotta V.L. Proc. Natl. Acad. Sci. U.S.A. 92:3784-3788(1995).

756. (Peptidase M10) Matrixins cysteine switch

PROSITE cross-reference(s): CYSTEINE_SWITCH

Mammalian extracellular matrix metalloproteinases (EC 3.4.24.-), also known as matrixins [1] (see <PDOC00129>), are zinc-dependent enzymes. They are secreted by cells in an inactive form (zymogen) that differs from the mature enzyme by the presence of an N-terminal propeptide. A highly conserved octapeptide is found two residues downstream of the C-terminal end of the propeptide. This region has been shown to be involved in autoinhibition of matrixins [2,3]; a cysteine within the octapeptide chelates the active site zinc ion, thus inhibiting the enzyme. This region has been called the 'cysteine switch' or 'autoinhibitor region'.

A cysteine switch has been found in the following zinc proteases:

624

- MMP-1 (EC 3.4.24.7) (interstitial collagenase).
- MMP-2 (EC 3.4.24.24) (72 Kd gelatinase).
- MMP-3 (EC 3.4.24.17) (stromelysin-1).
- MMP-7 (EC 3.4.24.23) (matrilysin).
- 5 - MMP-8 (EC 3.4.24.34) (neutrophil collagenase).
- MMP-9 (EC 3.4.24.35) (92 Kd gelatinase).
- MMP-10 (EC 3.4.24.22) (stromelysin-2).
- MMP-11 (EC 3.4.24.-) (stromelysin-3).
- MMP-12 (EC 3.4.24.65) (macrophage metalloelastase).
- 10 - MMP-13 (EC 3.4.24.-) (collagenase 3).
- MMP-14 (EC 3.4.24.-) (membrane-type matrix metalloproteinase 1).
- MMP-15 (EC 3.4.24.-) (membrane-type matrix metalloproteinase 2).
- MMP-16 (EC 3.4.24.-) (membrane-type matrix metalloproteinase 3).
- Sea urchin hatching enzyme (EC 3.4.24.12) (envelysin) [4].
- 15 - Chlamydomonas reinhardtii gamete lytic enzyme (GLE) [5].

Description of pattern(s) and/or profile(s)

Consensus pattern P-R-C-[GN]-x-P-[DR]-[LIVSAPKQ SEQ ID NO:372] [C chelates the zinc ion]

20

[1]Woessner J. Jr. FASEB J. 5:2145-2154(1991).

[2]Sanchez-Lopez R., Nicholson R., Gesnel M.C., Matrisian L.M., Breathnach R. J. Biol. Chem. 263:11892-11899(1988).

[3]Park A.J., Matrisian L.M., Kells A.F., Pearson R., Yuan Z., Navre M. J. Biol. Chem. 266:1584-1590(1991).

[4]Lepage T., Gache C. EMBO J. 9:3003-3012(1990).

[5]Kinoshita T., Fukuzawa H., Shimada T., Saito T., Matsuda Y. Proc. Natl. Acad. Sci. U.S.A. 89:4693-4697(1992).

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757. (Peptidase S8) Serine proteases, subtilase family, active sites

PROSITE cross-reference(s): PS00136; SUBTILASE_ASP, PS00137; SUBTILASE_HIS, PS00138; SUBTILASE_SER

Subtilases [1,2] are an extensive family of serine proteases whose catalytic activity is provided by a charge relay system similar to that of the trypsin family of serine proteases but which evolved by independent convergent evolution. The sequence around the residues involved in the catalytic triad (aspartic acid, serine and histidine) are completely different from that of the analogous residues in the trypsin serine proteases and can be used as signatures specific to that category of proteases.

The subtilase family currently includes the following proteases:

- Subtilisins (EC 3.4.21.62), these alkaline proteases from various *Bacillus* species have been the target of numerous studies in the past thirty years.

- Alkaline elastase YaB from *Bacillus* sp. (gene ale).
- Alkaline serine exoprotease A from *Vibrio alginolyticus* (gene proA).
- Aqualysin I from *Thermus aquaticus* (gene pstI).
- AspA from *Aeromonas salmonicida*.
- Bacillopeptidase F (esterase) from *Bacillus subtilis* (gene bpf).
- C5A peptidase from *Streptococcus pyogenes* (gene scpA).
- Cell envelope-located proteases PI, PII, and PIII from *Lactococcus lactis*.
- Extracellular serine protease from *Serratia marcescens*.
- Extracellular protease from *Xanthomonas campestris*.
- Intracellular serine protease (ISP) from various *Bacillus*.
- Minor extracellular serine protease epr from *Bacillus subtilis* (gene epr).
- Minor extracellular serine protease vpr from *Bacillus subtilis* (gene vpr).
- Nisin leader peptide processing protease nisP from *Lactococcus lactis*.
- Serotype-specific antigene 1 from *Pasteurella haemolytica* (gene ssa1).
- Thermitase (EC 3.4.21.66) from *Thermoactinomyces vulgaris*.
- Calcium-dependent protease from *Anabaena variabilis* (gene prcA).
- Halolysin from halophilic bacteria sp. 172p1 (gene hly).
- Alkaline extracellular protease (AEP) from *Yarrowia lipolytica* (gene xpr2).
- Alkaline proteinase from *Cephalosporium acremonium* (gene alp).
- Cerevisin (EC 3.4.21.48) (vacuolar protease B) from yeast (gene PRB1).
- Cuticle-degrading protease (pr1) from *Metarhizium anisopliae*.
- KEX-1 protease from *Kluyveromyces lactis*.
- Kexin (EC 3.4.21.61) from yeast (gene KEX-2).
- Oryzin (EC 3.4.21.63) (alkaline proteinase) from *Aspergillus* (gene alp).

- Proteinase K (EC 3.4.21.64) from *Tritirachium album* (gene proK).
- Proteinase R from *Tritirachium album* (gene proR).
- Proteinase T from *Tritirachium album* (gene proT).
- Subtilisin-like protease III from yeast (gene YSP3).
- 5 - Thermomycin (EC 3.4.21.65) from *Malbranchea sulfurea*.
- Furin (EC 3.4.21.85), neuroendocrine convertases 1 to 3 (NEC-1 to -3) and PACE4 protease from mammals, other vertebrates, and invertebrates. These proteases are involved in the processing of hormone precursors at sites comprised of pairs of basic amino acid residues [3].
- 10 - Tripeptidyl-peptidase II (EC 3.4.14.10) (tripeptidyl aminopeptidase) from Human.
- Prestalk-specific proteins tagB and tagC from slime mold [4]. Both proteins consist of two domains: a N-terminal subtilase catalytic domain and a C-terminal ABC transporter domain (see <PDOC00185>).
- 15 Description of pattern(s) and/or profile(s)
- Consensus pattern[STAIV SEQ ID NO:130)]-x-[LIVMF SEQ ID NO:2)]-[LIVM SEQ ID NO:4)]-D-[DSTA SEQ ID NO:686)]-G-[LIVMFC SEQ ID NO:90)]-x(2,3)-[DNH] [D is the active site residue]
- Consensus patternH-G-[STM]-x-[VIC]-[STAGC SEQ ID NO:45)]-[GS]-x-[LIVMA SEQ ID NO:30)]-[STAGCLV SEQ ID NO:687)]-[SAGM SEQ ID NO:688)] [H is the active site residue]
- 20 Consensus patternG-T-S-x-[SA]-x-P-x(2)-[STAVC SEQ ID NO:505)]-[AG] [S is the active site residue]
- Note if a protein includes at least two of the three active site signatures, the probability of it
- 25 being a serine protease from the subtilase family is 100%
- Note these proteins belong to family S8 in the classification of peptidases [5,E1].
- [1]Siezen R.J., de Vos W.M., Leunissen J.A.M., Dijkstra B.W. Protein Eng. 4:719-737(1991).
- 30 [2]Siezen R.J. (In) Proceeding subtilisin symposium, Hamburg, (1992).
- [3]Barr P.J. Cell 66:1-3(1991).
- [4]Shaulsky G., Kuspa A., Loomis W.F.; Genes Dev. 9:1111-1122(1995).

[5]Rawlings N.D., Barrett A.J. Meth. Enzymol. 244:19-61(1994).

758. (SSB) Single-strand binding protein family signatures

5 PROSITE cross-reference(s): PS00735; SSB_1,PS00736; SSB_2

The Escherichia coli single-strand binding protein [1] (gene ssb), also known as the helix-destabilizing protein, is a protein of 177 amino acids. It binds tightly, as a homotetramer, to single-stranded DNA (ss-DNA) and plays an important role in DNA replication, recombination and repair.

10

Closely related variants of SSB are encoded in the genome of a variety of large self-transmissible plasmids. SSB has also been characterized in bacteria such as *Proteus mirabilis* or *Serratia marcescens*.

15 Eukaryotic mitochondrial proteins that bind ss-DNA and are probably involved in mitochondrial DNA replication are structurally and evolutionary related to prokaryotic SSB. Proteins currently known to belong to this subfamily are listed below [2].

- Mammalian protein Mt-SSB (P16).

- *Xenopus* Mt-SSBs and Mt-SSBr.

20 - *Drosophila* MtSSB.

- Yeast protein RIM1.

25 Two signature patterns have been developed for these proteins. The first is a conserved region in the N-terminal section of the SSB's. The second is a centrally located region which, in *Escherichia coli* SSB, is known to be involved in the binding of DNA.

Description of pattern(s) and/or profile(s)

30 Consensus pattern[LIVMF SEQ ID NO:2)]-[NST]-[KRT]-[LIVM SEQ ID NO:4)]-x-[LIVMF SEQ ID NO:2)](2)-G-[NHRK SEQ ID NO:689)]-[LIVM SEQ ID NO:4)]- [GST]-x-[DET]

Consensus patternT-x-W-[HY]-[RNS]-[LIVM SEQ ID NO:4)]-x-[LIVMF SEQ ID NO:2)]-[FY]-[NGKR SEQ ID NO:690)]

[1]Meyer R.R., Laine P.S. Microbiol. Rev. 54:342-380(1990).

[2]Stroumbakis N.D., Li Z., Tolias P.P. Gene 143:171-177(1994).

759. KDPG and KHG aldolases active site signatures

5 PROSITE cross-reference(s): PS00159; ALDOLASE_KDPG_KHG_1, PS00160;
ALDOLASE_KDPG_KHG_2

10 4-hydroxy-2-oxoglutarate aldolase (EC 4.1.3.16) (KHG-aldolase) catalyzes the
interconversion of 4-hydroxy-2-oxoglutarate into pyruvate and glyoxylate. Phospho-2-
dehydro-3-deoxygluconate aldolase (EC 4.1.2.14) (KDPG-aldolase) catalyzes the
interconversion of 6-phospho-2-dehydro-3-deoxy-D-gluconate into pyruvate and
glyceraldehyde 3-phosphate.

15 These two enzymes are structurally and functionally related [1]. They are both homotrimeric
proteins of approximately 220 amino-acid residues. They are class I aldolases whose catalytic
mechanism involves the formation of a Schiff-base intermediate between the substrate and
the epsilon-amino group of a lysine residue. In both enzymes, an arginine is required for
catalytic activity.

20 Two signature patterns were developed for these enzymes. The first one contains the active
site arginine and the second, the lysine involved in the Schiff-base formation.

Description of pattern(s) and/or profile(s)

25 Consensus patternG-[LIVM SEQ ID NO:4)]-x(3)-E-[LIV]-T-[LF]-R [R is the active site
residue]

Consensus patternG-x(3)-[LIVMF SEQ ID NO:2)]-K-[LF]-F-P-[SA]-x(3)-G [K is involved
in Schiff-base formation]

[1] Vlahos C J., Dekker E.E. J. Biol. Chem. 263:11683-11691(1988).

30

760. AP endonucleases family 1 signatures. PROSITE cross-reference(s): PS00726;
AP_NUCLEASE_F1_1, PS00727; AP_NUCLEASE_F1_2, PS00728;
AP_NUCLEASE_F1_3

DNA damaging agents such as the antitumor drugs bleomycin and neocarzinostatin or those that generate oxygen radicals produce a variety of lesions in DNA. Amongst these is base-loss which forms apurinic/apyrimidinic (AP) sites or strand breaks with atypical 3'termini.

5 DNA repair at the AP sites is initiated by specific endonuclease cleavage of the phosphodiester backbone. Such endonucleases are also generally capable of removing blocking groups from the 3'terminus of DNA strand breaks.

AP endonucleases can be classified into two families on the basis of sequence similarity.

10 Family 1 groups the enzymes listed below [1].

- Escherichia coli exonuclease III (EC 3.1.11.2) (gene xthA).
- Streptococcus pneumoniae and Bacillus subtilis exonuclease A (gene exoA).
- Mammalian AP endonuclease 1 (AP1) (EC 4.2.99.18).
- 15 - Drosophila recombination repair protein 1 (gene Rrp1).
- Arabidopsis thaliana apurinic endonuclease-redox protein (gene arp).

Except for Rrp1 and arp, these enzymes are proteins of about 300 amino-acid residues.

Rrp1 and arp both contain additional and unrelated sequences in their N-terminal section
20 (about 400 residues for Rrp1 and 270 for arp).

Three signature patterns were developed for this family of enzymes. The patterns are based on the most conserved regions. The first pattern contains a glutamate which has been shown [2], in the Escherichia coli enzyme to bind a divalent metal ion such as magnesium or
25 manganese

Consensus pattern[APF]-D-[LIVMF SEQ ID NO:2)](2)-x-[LIVM SEQ ID NO:4)]-Q-E-x-K
[E binds a divalent metal ion]

Consensus patternD-[ST]-[FY]-R-[KH]-x(7,8)-[FYW]-[ST]-[FYW](2)

30 Consensus patternN-x-G-x-R-[LIVM SEQ ID NO:4)]-D-[LIVMFYH SEQ ID NO:541)]-x-[LV]-x-S

[1] Barzilay G., Hickson I.S. BioEssays 17:713-719(1995).

[2] Mol C.D., Kuo C.-F., Thayer M.M., Cunningham R.P., Tainer J.A. Nature 374:381-386(1995).

761. (ER)Enhancer of rudimentary signature, PROSITE cross-reference(s): PS01290; ER

The Drosophila protein 'enhancer of rudimentary' (gene (e(r)) is a small protein of 104 residues whose function is not yet clear. From an evolutionary point of view, it is highly conserved [1] and has been found to exist in probably all multicellular eukaryotic organisms. It has been proposed that this protein plays a role in the cell cycle.

A conserved region in the central part of the protein was selected as as signaure pattern.

Consensus pattern Y-D-I-[SA]-x-L-[FY]-x-F-[IV]-D-x(3)-D-[LIV]-S

[1] Gelsthorpe M., Pulumati M., McCallum C., Dang-Vu K., Tsubota S.I. Gene 186:189-195(1997).

762. (ETF alpha) Electron transfer flavoprotein alpha-subunit signature, PROSITE cross-reference(s): PS00696; ETF_ALPHA

The electron transfer flavoprotein (ETF) [1,2] serves as a specific electron acceptor for various mitochondrial dehydrogenases. ETF transfers electrons to the main respiratory chain via ETF-ubiquinone oxidoreductase. ETF is an heterodimer that consist of an alpha and a beta subunit and which bind one molecule of FAD per dimer. A similar system also exists in some bacteria.

The alpha subunit of ETF is a protein of about 32 Kd which is structurally related to the bacterial nitrogen fixation protein fixB which could play a role in a redox process and feed electrons to ferredoxin.

Other related proteins are:

- Escherichia coli hypothetical protein ydiR.

- *Escherichia coli* hypothetical protein ygcQ.

A highly conserved region which is located in the C-terminal section was selected as a signature pattern for these proteins.

5

Consensus pattern [LI]-Y-[LIVM SEQ ID NO:4)]-[AT]-x-G-[IV]-[SD]-G-x-[IV]-Q-H-x(2)-G-x(6)-[IV]-x-A-[IV]-N

[1] Finocchiaro G., Ikeda Y., Ito M., Tanaka K. Prog. Clin. Biol. Res. 321:637-652(1990).

10 [2] Tsai M.H., Saier M.H. Jr. Res. Microbiol. 146:397-404(1995).

763. (lectin c) C-type lectin domain signature and profile

PROSITE cross-reference(s): PS00615; C_TYPE_LECTIN_1, PS50041;

C_TYPE_LECTIN_2

15

A number of different families of proteins share a conserved domain which was first characterized in some animal lectins and which seem to function as a calcium-dependent carbohydrate-recognition domain [1,2,3]. This domain, which is known as the C-type lectin domain (CTL) or as the carbohydrate-recognition domain (CRD), consists of about 110 to

20 130 residues. There are four cysteines which are perfectly conserved and involved in two disulfide bonds. A schematic representation of the CTL domain is shown below.

```

      +-----+
      |   |
25  xxxxxxxCxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxCxxxWxCxxxCx
      |   | *****|*
      +---+ +-----+

```

'C': conserved cysteine involved in a disulfide bond.

30 'c': optional cysteine involved in a disulfide bond.

'*': position of the pattern.

The categories of proteins, in which the CTL domain has been found, are listed below.

Type-II membrane proteins where the CTL domain is located at the C-terminal extremity of the proteins:

- 5 - Asialoglycoprotein receptors (ASGPR) (also known as hepatic lectins) [4]. The ASGPR's mediate the endocytosis of plasma glycoproteins to which the terminal sialic acid residue in their carbohydrate moieties has been removed.
- Low affinity immunoglobulin epsilon Fc receptor (lymphocyte IgE receptor), which plays an essential role in the regulation of IgE production and in the differentiation of B cells.
- 10 - Kupffer cell receptor. A receptor with an affinity for galactose and fucose, that could be involved in endocytosis.
- A number of proteins expressed on the surface of natural killer T-cells: NKG2, NKR-P1, YE1/88 (Ly-49), CD69 and on B-cells: CD72, LyB-2. The CTL- domain in these proteins is
- 15 distantly related to other CTL-domains; it is unclear whether they are likely to bind carbohydrates.

Proteins that consist of an N-terminal collagenous domain followed by a CTL- domain [5], these proteins are sometimes called 'collectins':

- 20 - Pulmonary surfactant-associated protein A (SP-A). SP-A is a calcium-dependent protein that binds to surfactant phospholipids and contributes to lower the surface tension at the air-liquid interface in the alveoli of the mammalian lung.
- Pulmonary surfactant-associated protein D (SP-D).
- 25 - Conglutinin, a calcium-dependent lectin-like protein which binds to a yeast cell wall extract and to immune complexes through the complement component (iC3b).
- Mannan-binding proteins (MBP) (also known as mannose-binding proteins). MBP's bind mannose and N-acetyl-D-glucosamine in a calcium-dependent
- 30 manner.
- Bovine collectin-43 (CL-43).

Selectins (or LEC-CAM) [6,7]. Selectins are cell adhesion molecules implicated in the interaction of leukocytes with platelets or vascular endothelium. Structurally, selectins consist of a long extracellular domain, followed by a transmembrane region and a short cytoplasmic domain. The extracellular domain is itself composed of a CTL-domain, followed by an EGF-like domain and a variable number of SCR/Sushi repeats. Known selectins are:

- Lymph node homing receptor (also known as L-selectin, leukocyte adhesion molecule-1, (LAM-1), leu-8, gp90-mel, or LECAM-1)
- Endothelial leukocyte adhesion molecule 1 (ELAM-1, E-selectin or LECAM-2). The ligand recognized by ELAM-1 is sialyl-Lewis x.
- Granule membrane protein 140 (GMP-140, P-selectin, PADGEM, CD62, or LECAM-3). The ligand recognized by GMP-140 is Lewis x.

Large proteoglycans that contain a CTL-domain followed by one copy of a SCR/ Sushi repeat, in their C-terminal section:

- Aggrecan (cartilage-specific proteoglycan core protein). This proteoglycan is a major component of the extracellular matrix of cartilagenous tissues where it has a role in the resistance to compression.
- Brevican.
- Neurocan.
- Versican (large fibroblast proteoglycan), a large chondroitin sulfate proteoglycan that may play a role in intercellular signalling.

In addition to the CTL and Sushi domains, these proteins also contain, in their N-terminal domain, an Ig-like V-type region, two or four link domains (see <PDOC00955>) and up to two EGF-like repeats.

Two type-I membrane proteins:

- Mannose receptor from macrophages. This protein mediates the endocytosis of glycoproteins by macrophages in several recognition and uptake processes.

Its extracellular section consists of a fibronectin type II domain followed by eight tandem repeats of the CTL domain.

- 180 Kd secretory phospholipase A2 receptor (PLA2-R). A protein whose structure is highly similar to that of the mannose receptor.
- 5 - DEC-205 receptor. This protein is used by dendritic cells and thymic epithelial cells to capture and endocytose diverse carbohydrate-binding antigens and direct them to antigen-processing cellular compartments. DEC-205 extracellular section consists of a fibronectin type II domain followed by ten tandem repeats of the CTL domain.
- 10 - Silk moth hemocytin, an humoral lectin which is involved in a self-defence mechanism. It is composed of 2 FA58C domains (see <PDOC00988>), a CTL domain, 2 VWFC domains (see <PDOC00928>), and a CTCK (see <PDOC00912>).

Various other proteins that uniquely consist of a CTL domain:

- 15 - Invertebrate soluble galactose-binding lectins. A category to which belong a humoral lectin from a flesh fly; echinoidin, a lectin from the coelomic fluid of a sea urchin; BRA-2 and BRA-3, two lectins from the coelomic fluid of a barnacle, a lectin from the tunicate *Polyandrocarpa misakiensis* and a newt oviduct lectin. The physiological importance of these lectins is not yet known but they may play an important role in defense mechanisms.
- 20 - Pancreatic stone protein (PSP) (also known as pancreatic thread protein (PTP), or reg), a protein that might act as an inhibitor of spontaneous calcium carbonate precipitation.
- 25 - Pancreatitis associated protein (PAP), a protein that might be involved in the control of bacterial proliferation.
- Tetranectin, a plasma protein that binds to plasminogen and to isolated kringle 4.
- Eosinophil granule major basic protein (MBP), a cytotoxic protein.
- 30 - A galactose specific lectin from a rattlesnake.
- Two subunits of a coagulation factor IX/factor X-binding protein (IX/X-bp), a snake venom anticoagulant protein which binds with factors IX and X in the presence of calcium.

- Two subunits of a phospholipase A2 inhibitor from the plasma of a snake (PLI-A and PLI-B).
- A lipopolysaccharide-binding protein (LPS-BP) from the hemolymph of a cockroach [8].
- 5 - Sea raven antifreeze protein (AFP) [9].

As a signature pattern for this domain, the C-terminal region with its three conserved cysteines was selected.

- 10 Consensus pattern C-[LIVMFYATG SEQ ID NO:691]-x(5,12)-[WL]-x-[DNSR SEQ ID NO:692]-x(2)-C-x(5,6)-[FYWLIVSTA SEQ ID NO:693]-[LIVMSTA SEQ ID NO:433]-C [The three C's are involved in disulfide bonds]
- 15 Note all CTL domains have five Trp residues before the second Cys, with the exception of tunicate lectin and cockroach LPS-BP which have Leu.

Note this documentation entry is linked to both a signature pattern
20 and a profile. As the profile is much more sensitive than the pattern, you should use it if you have access to the necessary software tools to do so.

- [1] Drickamer K. J. Biol. Chem. 263:9557-9560(1988).
- 25 [2] Drickamer K. Prog. Nucleic Acid Res. Mol. Biol. 45:207-232(1993).
- [3] Drickamer K. Curr. Opin. Struct. Biol. 3:393-400(1993).
- [4] Spiess M. Biochemistry 29:10009-10018(1990).
- [5] Weis W.I., Kahn R., Fourme R., Drickamer K., Hendrickson W.A. Science 254:1608-1615(1991).
- 30 [6] Siegelman M. Curr. Biol. 1:125-128(1991).
- [7] Lasky L.A. Science 238:964-969(1992).
- [8] Jomori T., Natori S. J. Biol. Chem. 266:13318-13323(1991).
- [9] Ng N.F.L., Hew C.-L. J. Biol. Chem. 267:16069-16075(1992).

764. (SRCR) Speract receptor repeated domain signature

PROSITE cross-reference(s): PS00420; SPERACT_RECEPTOR,

5 The receptor for the sea urchin egg peptide speract is a transmembrane glycoprotein of 500 amino acid residues [1]. Structurally it consists of a large extracellular domain of 450 residues, followed by a transmembrane region and a small cytoplasmic domain of 12 amino acids. The extracellular domain contains four repeats of a 115 amino acids domain. There are 17 positions that are perfectly conserved in the four repeats, among them are six cysteines, 10 six glycines, and three glutamates.

Such a domain is also found, once, in the C-terminal section of mammalian macrophage scavenger receptor type I [2], a membrane glycoproteins implicated in the pathologic deposition of cholesterol in arterial walls during atherogenesis.

15 The signature pattern that was derived spans part of the N-terminal section of the domain and contains 8 of the 17 conserved residues.

Consensus pattern G-x(5)-G-x(2)-E-x(6)-W-G-x(2)-C-x(3)-[FYW]-x(8)-C-x(3)-G

20 [1] Dangott J.J., Jordan J.E., Bellet R.A., Garbers D.L. Proc. Natl. Acad. Sci. U.S.A. 86:2128-2132(1989).

[2] Freeman M., Ashkenas J., Rees D.J., Kingsley D.M., Copeland N.G., Jenkins N.A., Krieger M. Proc. Natl. Acad. Sci. U.S.A. 87:8810-8814(1990).

765. Bac_surface_Ag

Bacterial surface antigen

This entry includes the following surface antigens; D15 antigen from H.influenzae, OMA87 from P.multocida, OMP85 from N.meningitidis and N.gonorrhoeae. Number of members:

30 14

[1] Medline: 95255676. The sequencing of the 80-kDa D15 protective surface antigen of *Haemophilus influenzae*. Flack FS, Loosmore S, Chong P, Thomas WR; Gene 1995;156:97-99.

[2] Medline: 96333354. Cloning, sequencing, expression, and protective capacity of the oma87 gene encoding the *Pasteurella multocida* 87-kilodalton outer membrane antigen. Ruffolo CG, Adler B; Infect Immun 1996;64:3161-3167.

766. BRCA1 C Terminus (BRCT) domain

The BRCT domain is found predominantly in proteins involved in cell cycle checkpoint functions responsive to DNA damage. It has been suggested that the Retinoblastoma protein contains a divergent BRCT domain, this has not been included in this family. The BRCT domain of XRCC1 forms a homodimer in the crystal structure Medline:99016060. This suggests that pairs of BRCT domains

associate as homo- or heterodimers. Number of members: 131

[1] Medline: 96259550. BRCA1 protein products ...Functional motifs... Koonin EV, Altschul SF, Bork P; Nature Genet 1996;13:266-268.

[2] Medline: 97153217. From BRCA1 to RAP1: A widespread BRCT module closely associated with DNA repair Callebaut I, Mornon JP; Febs lett 1997;400:25-30.

[3] Medline: 97186552. A superfamily of conserved domains in DNA damage responsive cell cycle checkpoint proteins Bork P, Hofmann K, Bucher P, Neuwald AF, Altschul SF, Koonin EV; Faseb J 1997;11:68-76.

[4] Medline: 97402527. Gapped BLAST and PSI-BLAST: a new generation of protein database search programs. Altschul SF, Madden TL, Schaffer AA, Zhang J, Zhang Z, Miller W, Lipman DJ; Nucleic Acids Res 1997;25:3389-3402.

[5] Medline: 99016060. Structure of an XRCC1 BRCT domain: a new protein-protein interaction module. Zhang X, Morera S, Bates PA, Whitehead PC, Coffey AI, Hainbucher K, Nash RA, Sternberg MJ, Lindahl T, Freemont PS;

767. Kappa casein

Kappa-casein is a mammalian milk protein involved in a number of important physiological processes. In the gut, the ingested protein is split into an insoluble peptide (para kappa-casein) and a soluble hydrophilic glycopeptide (caseinomacropeptide). Caseinomacropeptide

is responsible for increased efficiency of digestion, prevention of neonate hypersensitivity to ingested proteins, and inhibition of gastric pathogens. Number of members: 56

[1] Medline: 98072500. Nucleotide sequence evolution at the kappa-casein locus: evidence for positive selection within the family Bovidae. Ward TJ, Honeycutt RL, Derr JN; Genetics 1997;147:1863-1872.

768. Chitinases family 18 active site

PROSITE cross-reference(s) CHITINASE_18

Chitinases (EC 3.2.1.14) [1] are enzymes that catalyze the hydrolysis of the beta-1,4-N-acetyl-D-glucosamine linkages in chitin polymers. From the view point of sequence similarity chitinases belong to either family 18 or 19 in the classification of glycosyl hydrolases [2,E1]. Chitinases of family 18 (also known as classes III or V) groups a variety of proteins:

a) Chitinases from:

- Prokaryotes such as *Alteromonas*, *Bacillus*, *Serratia*, *Streptomyces*, etc.
- Plants such as *Arabidopsis*, cucumber, bean, tobacco, etc.
- Fungi such as *Aphanocladium*, *Rhizopus*, *Saccharomyces*, etc.
- Nematode (*Brugia malayi*).
- Insects (*Manduca sexta*).
- Baculoviruses (*Autographa Californica Nuclear Polyhedrosis virus*).

b) Other proteins:

- Hevamine, a rubber tree protein with chitinase and lysozyme activities.
- *Kluyveromyces lactis* killer toxin alpha subunit, which acts as a chitinase.
- *Flavobacterium* and *Streptomyces* endo-beta-N-acetylglucosaminidases (EC 3.2.1.96).
- Mammalian di-N-acetylchitobiase which is involved in the degradation of asparagine-linked glycoproteins.
- Human cartilage glycoprotein Gp-39.
- Jack bean concanavalin B (conB), a protein that has lost its catalytic activity.

Site directed mutagenesis experiments [3] and crystallographic data [4,5] have shown that a conserved glutamate is involved in the catalytic mechanism and probably acts as a proton donor. This glutamate is at the extremity of the best conserved region in these proteins.

- 5 Consensus pattern[LIVMFY SEQ ID NO:18)]-[DN]-G-[LIVMF SEQ ID NO:2)]-[DN]-[LIVMF SEQ ID NO:2)]-[DN]-x-E [E is the active site residue]

[1] Flach J., Pilet P.-E., Jolles P. *Experientia* 48:701-716(1992).

[2] Henrissat B. *Biochem. J.* 280:309-316(1991).

- 10 [3] Watanabe T., Kohori K., Miyashita K., Fujii T., Sakai H., Uchida M., Tanaka H. *J. Biol. Chem.* 268:18567-18572(1993).

[4] Perrakis A., Tews I., Dauter Z., Oppenheim A.B., Chet I., Wilson K.S., Vorgias C.E. *Structure* 2:1169-1180(1994).

- [5] van Scheltinga A.C.T., Kalk K.H., Beintema J.J., Dijkstra B.W. *Structure* 2:1181-1189(1994).
- 15

769. gag_p17. gag gene protein p17 (matrix protein).

The matrix protein forms an icosahedral shell associated with the inner membrane of the mature immunodeficiency virus. Number of members: 1598

20

[1] Medline: 95055757. Three-dimensional structure of the human immunodeficiency virus type 1 matrix protein. Massiah MA, Starich MR, Paschall C, Summers MF, Christensen AM, Sundquist WI; *J Mol Biol* 1994;244:198-223.

- 25 770. GDA1/CD39 family of nucleoside phosphatases signature

PROSITE cross-reference(s); GDA1_CD39_NTPASE

A number of nucleoside diphosphate and triphosphate hydrolases as well as some yet uncharacterized proteins have been found to belong to the same family [1, 2]. This family currently consist of:

- 30 - Yeast guanosine-diphosphatase (EC 3.6.1.42) (GDPase) (gene GDA1). GDA1 is a golgi integral membrane enzyme that catalyzes the hydrolysis of GDP to GMP.

- Potato apyrase (EC 3.6.1.5) (adenosine diphosphatase) (ADPase). Apyrase acts on both ATP and ADP to produce AMP.

- Mammalian vascular ATP-diphosphohydrolase (EC 3.6.1.5) (also known as lymphoid cell activation antigen CD39).

- *Toxoplasma gondii* nucleoside-triphosphatases (EC 3.6.1.15) (NTPase). NTPase hydrolyses various nucleoside triphosphates to produce the corresponding nucleoside mono- and diphosphates. This enzyme is secreted into the invaded host cell into the parasitophorous vacuole, a specialized compartment where the parasite intracellularly resides.

- Pea nucleoside-triphosphatases (EC 3.6.1.15) (NTPase).

- *Caenorhabditis elegans* hypothetical protein C33H5.14.

- *Caenorhabditis elegans* hypothetical protein R07E4.4.

- Yeast chromosome V hypothetical protein YER005w.

The above uncharacterized proteins all seem to be membrane-bound.

All these proteins share a number of conserved domains. The best conserved of these domains have been selected. It is located in the central section of the proteins.

Consensus pattern[LIVM SEQ ID NO:4)]-x-G-x(2)-E-G-x-[FY]-x-[FW]-[LIVA SEQ ID NO:219)]-[TAG]-x-N-[HY]

[1] Handa M., Guidotti G. Biochem. Biophys. Res. Commun. 218:916-923(1996).

[2] Vasconcelos E.G., Ferreira S.T., de Carvalho T.M.U., de Souza W., Kettlun A.M.,

Mancilla M., Valenzuela M.A., Verjovski-Almeida S. J. Biol. Chem. 271:22139-22145(1996).

771. GTP cyclohydrolase I signatures

PROSITE cross-reference(s); GTP_CYCLOHYDROL_1_1, GTP_CYCLOHYDROL_1_2

GTP cyclohydrolase I (EC 3.5.4.16) catalyzes the biosynthesis of formic acid and dihydroneopterin triphosphate from GTP. This reaction is the first step in the biosynthesis of tetrahydrofolate in prokaryotes, of tetrahydrobiopterin in vertebrates, and of pteridine-containing pigments in insects.

GTP cyclohydrolase I is a protein of from 190 to 250 amino acid residues. The comparison of the sequence of the enzyme from bacterial and eukaryotic sources shows that the structure of this enzyme has been extremely well conserved throughout evolution [1].

5

Two conserved regions were selected as signature patterns. The first contains a perfectly conserved tetrapeptide which is part of the GTP-binding pocket [2], the second region also contains conserved residues involved in GTP-binding.

10 Consensus pattern[DEN]-[LIVM SEQ ID NO:4)](2)-x(2)-[KRNQ SEQ ID NO:694)]-[DEN]-[LIVM SEQ ID NO:4)]-x(3)-[ST]-x-C-E- H-H

Consensus pattern[SA]-x-[RK]-x-Q-[LIVM SEQ ID NO:4)]-Q-E-[RN]-[LI]-[TSN]

[1] Maier J., Witter K., Guetlich M., Ziegler I., Werner T., Ninnemann H. Biochem. Biophys. Res. Commun. 212:705-711(1995).

15

[2] Nar H., Huber R., Meining W., Schmid C., Weinkauff S., Bacher A. Structure 3:459-466(1995).

772. IlvC. Acetohydroxy acid isomeroreductase

20 Acetohydroxy acid isomeroreductase catalyses the conversion of acetohydroxy acids into dihydroxy valerates. This reaction is the second in the synthetic pathway of the essential branched side chain amino acids valine and isoleucine. Number of members: 29

[1] Medline: 97361822. The crystal structure of plant acetohydroxy acid isomeroreductase complexed with NADPH, two magnesium ions and a herbicidal transition state analog determined at 1.65 Å resolution. Biou V, Dumas R, Cohen-Addad C, Douce R, Job D, Pebay-Peyroula E; EMBO J 1997;16:3405-3415.

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773. Prokaryotic membrane lipoprotein lipid attachment site

30 PROSITE cross-reference(s); PROKAR_LIPOPROTEIN

In prokaryotes, membrane lipoproteins are synthesized with a precursor signal peptide, which is cleaved by a specific lipoprotein signal peptidase (signal peptidase II). The peptidase recognizes a conserved sequence and cuts upstream of a cysteine residue to which

a glyceride-fatty acid lipid is attached [1]. Some of the proteins known to undergo such processing currently include (for recent listings see [1,2,3]):

- Major outer membrane lipoprotein (murein-lipoproteins) (gene lpp).
- Escherichia coli lipoprotein-28 (gene nlpA).
- 5 - Escherichia coli lipoprotein-34 (gene nlpB).
- Escherichia coli lipoprotein nlpC.
- Escherichia coli lipoprotein nlpD.
- Escherichia coli osmotically inducible lipoprotein B (gene osmB).
- Escherichia coli osmotically inducible lipoprotein E (gene osmE).
- 10 - Escherichia coli peptidoglycan-associated lipoprotein (gene pal).
- Escherichia coli rare lipoproteins A and B (genes rplA and rplB).
- Escherichia coli copper homeostasis protein cutF (or nlpE).
- Escherichia coli plasmids traT proteins.
- Escherichia coli Col plasmids lysis proteins.
- 15 - A number of Bacillus beta-lactamases.
- Bacillus subtilis periplasmic oligopeptide-binding protein (gene oppA).
- Borrelia burgdorferi outer surface proteins A and B (genes ospA and ospB).
- Borrelia hermsii variable major protein 21 (gene vmp21) and 7 (gene vmp7).
- Chlamydia trachomatis outer membrane protein 3 (gene omp3).
- 20 - Fibrobacter succinogenes endoglucanase cel-3.
- Haemophilus influenzae proteins Pal and Pcp.
- Klebsiella pullulunase (gene pulA).
- Klebsiella pullulunase secretion protein pulS.
- Mycoplasma hyorhina protein p37.
- 25 - Mycoplasma hyorhina variant surface antigens A, B, and C (genes vlpABC).
- Neisseria outer membrane protein H.8.
- Pseudomonas aeruginosa lipopeptide (gene lppL).
- Pseudomonas solanacearum endoglucanase egl.
- Rhodopseudomonas viridis reaction center cytochrome subunit (gene cytC).
- 30 - Rickettsia 17 Kd antigen.
- Shigella flexneri invasion plasmid proteins mxiJ and mxiM.
- Streptococcus pneumoniae oligopeptide transport protein A (gene amiA).
- Treponema pallidum 34 Kd antigen.

- *Treponema pallidum* membrane protein A (gene tmpA).
- *Vibrio harveyi* chitinase (gene chb).
- *Yersinia* virulence plasmid protein yscJ.

- 5 - Halocyanin from *Natrobacterium pharaonis* [4], a membrane associated copper- binding protein. This is the first archaeobacterial protein known to be modified in such a fashion).

From the precursor sequences of all these proteins, we derived a consensus pattern and a set of rules to identify this type of post-translational modification.

10

Consensus pattern{DERK SEQ ID NO:354)}(6)-[LIVMFWSTAG SEQ ID NO:352)](2)-[LIVMFYSTAGCQ SEQ ID NO:353)]-[AGS]-C [C is the lipid attachment site] Additional rules: 1) The cysteine must be between positions 15 and 35 of the sequence in consideration. 2) There must be at least one Lys or one Arg in the first seven positions of the sequence.

15

[1] Hayashi S., Wu H.C. J. Bioenerg. Biomembr. 22:451-471(1990).

[2]Klein P., Somorjai R.L., Lau P.C.K. Protein Eng. 2:15-20(1988).

[3]von Heijne G. Protein Eng. 2:531-534(1989).

[4]Mattar S., Scharf B., Kent S.B.H., Rodewald K., Oesterhelt D., Engelhard M. J. Biol. Chem. 269:14939-14945(1994).

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774. Aminoacyl-transfer RNA synthetases class-II signatures

PROSITE cross-reference(s); AA_TRNA_LIGASE_II_1; AA_TRNA_LIGASE_II_2

Aminoacyl-tRNA synthetases (EC 6.1.1.-) [1] are a group of enzymes which activate amino acids and transfer them to specific tRNA molecules as the first step in protein biosynthesis. In prokaryotic organisms there are at least twenty different types of aminoacyl-tRNA synthetases, one for each different amino acid. In eukaryotes there are

25

generally two aminoacyl-tRNA synthetases for each different amino acid: one cytosolic form and a mitochondrial form. While all these enzymes have a common function, they are widely diverse in terms of subunit size and of quaternary structure.

30

The synthetases specific for alanine, asparagine, aspartic acid, glycine, histidine, lysine, phenylalanine, proline, serine, and threonine are referred to as class-II synthetases [2 to 6]

and probably have a common folding pattern in their catalytic domain for the binding of ATP and amino acid which is different to the Rossmann fold observed for the class I synthetases [7].

- 5 Class-II tRNA synthetases do not share a high degree of similarity, however at least three conserved regions are present [2,5,8]. Signature patterns from two of these regions have been derived.

Consensus pattern[FYH]-R-x-[DE]-x(4,12)-[RH]-x(3)-F-x(3)-[DE]

- 10 Consensus pattern[GSTALVF SEQ ID NO:42)]-{DENQHRKP SEQ ID NO:43)}-[GSTA SEQ ID NO:19)]-[LIVMF SEQ ID NO:2)]-[DE]-R-[LIVMF SEQ ID NO:2)]-x-[LIVMSTAG SEQ ID NO:44)]-[LIVMFY SEQ ID NO:18)]

[1]Schimmel P. Annu. Rev. Biochem. 56:125-158(1987).

- 15 [2]Delarue M., Moras D. BioEssays 15:675-687(1993).

[3]Schimmel P. Trends Biochem. Sci. 16:1-3(1991).

[4]Nagel G.M., Doolittle R.F. Proc. Natl. Acad. Sci. U.S.A. 88:8121-8125(1991).

[5]Cusack S., Haertlein M., Leberman R. Nucleic Acids Res. 19:3489-3498(1991).

[6]Cusack S. Biochimie 75:1077-1081(1993).

- 20 [7]Cusack S., Berthet-Colominas C., Haertlein M., Nassar N., Leberman R. Nature 347:249-255(1990).

[8]Leveque F., Plateau P., Dessen P., Blanquet S. Nucleic Acids Res. 18:305-312(1990).

775. X. Trans-activation protein X

- 25 This protein is found in hepadnaviruses where it is indispensable for replication. Number of members: 91

776. Thymidylate synthase active site

- 30 Thymidylate synthase (EC 2.1.1.45) [1,2] catalyzes the reductive methylation of dUMP to dTMP with concomitant conversion of 5,10-methylenetetrahydrofolate to dihydrofolate. Thymidylate synthase plays an essential role in DNA synthesis and is an important target for certain chemotherapeutic drugs.

Thymidylate synthase is an enzyme of about 30 to 35 Kd in most species except in protozoan and plants where it exists as a bifunctional enzyme that includes a dihydrofolate reductase domain.

A cysteine residue is involved in the catalytic mechanism (it covalently binds the 5,6-dihydro-dUMP intermediate). The sequence around the active site of this enzyme is conserved from phages to vertebrates.

Consensus pattern R-x(2)-[LIVM SEQ ID NO:4)]-x(3)-[FW]-[QN]-x(8,9)-[LV]-x-P-C-[HAVM SEQ ID NO:695)]-x(3)-[QMT]-[FYW]-x-[LV] [C is the active site residue]

[1] Benkovic S.J. Annu. Rev. Biochem. 49:227-251(1980).

[2] Ross P., O'Gara F., Condon S. Appl. Environ. Microbiol. 56:2156-2163(1990).

777. Glycosyl hydrolases family 31 signatures

It has been shown [1,2,3,E1] that the following glycosyl hydrolases can be, on the basis of sequence similarities, classified into a single family:

- Lysosomal alpha-glucosidase (EC 3.2.1.20) (acid maltase) is a vertebrate glycosidase active at low pH, which hydrolyzes alpha(1->4) and alpha(1->6) linkages in glycogen, maltose, and isomaltose.
- Alpha-glucosidase (EC 3.2.1.20) from the yeast *Candida tsukunbaensis*.
- Alpha-glucosidase (EC 3.2.1.20) (gene *malA*) from the archaebacteria *Sulfolobus solfataricus*.
- Intestinal sucrase-isomaltase (EC 3.2.1.48 / EC 3.2.1.10) is a vertebrate membrane-bound, multifunctional enzyme complex which hydrolyzes sucrose, maltose and isomaltose. The sucrase and isomaltase domains of the enzyme are homologous (41% of amino acid identity) and have most probably evolved by duplication.
- Glucoamylase 1 (EC 3.2.1.3) (glucan 1,4-alpha-glucosidase) from various fungal species.
- Yeast hypothetical protein YBR229c.
- Fission yeast hypothetical protein SpAC30D11.01c.

An aspartic acid has been implicated [4] in the catalytic activity of sucrase, isomaltase, and lysosomal alpha-glucosidase. The region around this active residue is highly conserved and can be used as a signature pattern. A second region, which contains two conserved cysteines, has been used as an additional signature pattern.

Consensus pattern [GF]-[LIVMF SEQ ID NO:2)]-W-x-D-M-[NSA]-E [D is the active site residue]

Consensus pattern G-[AV]-D-[LIVMTA SEQ ID NO:311)]-C-G-[FY]-x(3)-[ST]-x(3)-L-C-x-
5 R-W-x(2)-[LV]-[GSA]-[SA]-F-x-P-F-x-R-[DN]

[1] Henrissat B. Biochem. J. 280:309-316(1991).

[2] Kinsella B.T., Hogan S., Larkin A., Cantwell B.A. Eur. J. Biochem. 202:657-664(1991).

[3] Naim H.Y., Niermann T., Kleinhans U., Hollenberg C.P., Strasser A.W.M. FEBS Lett.
10 294:109-112(1991).

[4] Hermans M.M.P., Kroos M.A., van Beeumen J., Oostra B.A., Reuser A.J.J. J. Biol. Chem. 266:13507-13512(1991).

778. Urease signatures

15 Urease (EC 3.5.1.5) is a nickel-binding enzyme that catalyzes the hydrolysis of urea to carbon dioxide and ammonia [1]. Historically, it was the first enzyme to be crystallized (in 1926). It is mainly found in plant seeds, microorganisms and invertebrates. In plants, urease is a hexamer of identical chains. In bacteria [2], it consists of either two or three different subunits (alpha, beta and gamma).

20 Urease binds two nickel ions per subunit; four histidine, an aspartate and a carbamated-lysine serve as ligands to these metals; an additional histidine is involved in the catalytic mechanism [3].

As signatures for this enzyme, a region was selected that contains two histidine that bind one of the nickel ions and the region of the active site histidine.

25 Consensus pattern T-[AY]-[GA]-[GAT]-[LIVM SEQ ID NO:4)]-D-x-H-[LIVM SEQ ID NO:4)]-H-x(3)-P [The two H's bind nickel]

Consensus pattern [LIVM SEQ ID NO:4)](2)-[CT]-H-[HN]-L-x(3)-[LIVM SEQ ID NO:4)]-x(2)-D-[LIVM SEQ ID NO:4)]-x-F-A [H is the active site residue]

[1] Takishima K., Suga T., Mamiya G. Eur. J. Biochem. 175:151-165(1988).

[2] Mobley H.L.T., Husinger R.P. Microbiol. Rev. 53:85-108(1989).

[3] Jabri E., Carr M.B., Hausinger R.P., Karplus P.A. Science 268:998-1004(1995).

779. Tyrosine specific protein phosphatases signature and profiles

Tyrosine specific protein phosphatases (EC 3.1.3.48) (PTPase) [1 to 5] are enzymes that catalyze the removal of a phosphate group attached to a tyrosine residue. These enzymes are very important in the control of cell growth, proliferation, differentiation and transformation. Multiple forms of PTPase have been characterized and can be classified into two categories: soluble PTPases and transmembrane receptor proteins that contain PTPase domain(s). The currently known PTPases are listed below:

10 Soluble PTPases.

- PTPN1 (PTP-1B).
- PTPN2 (T-cell PTPase; TC-PTP).
- PTPN3 (H1) and PTPN4 (MEG), enzymes that contain an N-terminal band 4.1- like domain (see <PDOC00566>) and could act at junctions between the membrane and cytoskeleton.
- PTPN5 (STEP).
- PTPN6 (PTP-1C; HCP; SHP) and PTPN11 (PTP-2C; SH-PTP3; Syp), enzymes which contain two copies of the SH2 domain at its N-terminal extremity. The Drosophila protein corkscrew (gene csw) also belongs to this subgroup.
- PTPN7 (LC-PTP; Hematopoietic protein-tyrosine phosphatase; HePTP).
- PTPN8 (70Z-PEP).
- PTPN9 (MEG2).
- PTPN12 (PTP-G1; PTP-P19).
- Yeast PTP1.
- Yeast PTP2 which may be involved in the ubiquitin-mediated protein degradation pathway.
- Fission yeast pyp1 and pyp2 which play a role in inhibiting the onset of mitosis.
- Fission yeast pyp3 which contributes to the dephosphorylation of cdc2.
- Yeast CDC14 which may be involved in chromosome segregation.
- Yersinia virulence plasmid PTPases (gene yopH).
- Autographa californica nuclear polyhedrosis virus 19 Kd PTPase.

Dual specificity PTPases.

- DUSP1 (PTPN10; MAP kinase phosphatase-1; MKP-1); which dephosphorylates MAP kinase on both Thr-183 and Tyr-185.

- DUSP2 (PAC-1), a nuclear enzyme that dephosphorylates MAP kinases ERK1 and ERK2 on both Thr and Tyr residues.

5 - DUSP3 (VHR).

- DUSP4 (HVH2).

- DUSP5 (HVH3).

- DUSP6 (Pyst1; MKP-3).

- DUSP7 (Pyst2; MKP-X).

10 - Yeast MSG5, a PTPase that dephosphorylates MAP kinase FUS3.

- Yeast YVH1.

- Vaccinia virus H1 PTPase; a dual specificity phosphatase.

Receptor PTPases.

15 Structurally, all known receptor PTPases, are made up of a variable length extracellular domain, followed by a transmembrane region and a C-terminal catalytic cytoplasmic domain. Some of the receptor PTPases contain fibronectin type III (FN-III) repeats, immunoglobulin-like domains, MAM domains or carbonic anhydrase-like domains in their extracellular region. The cytoplasmic region generally contains two copies of the

20 PTPase domain. The first seems to have enzymatic activity, while the second is inactive but seems to affect substrate specificity of the first. In these domains, the catalytic cysteine is generally conserved but some other, presumably important, residues are not.

In the following table, the domain structure of known receptor PTPases is shown:

25

Extracellular	Intracellular
-----	-----
Ig FN-3	CAH MAM PTPase

30 Leukocyte common antigen (LCA) (CD45)	0	2	0	0	2
Leukocyte antigen related (LAR)	3	8	0	0	2
Drosophila DLAR	3	9	0	0	2
Drosophila DPTP	2	2	0	0	2

					649	
	PTP-alpha (LRP)	0	0	0	0	2
	PTP-beta	0	16	0	0	1
	PTP-gamma	0	1	1	0	2
	PTP-delta	0	>7	0	0	2
5	PTP-epsilon	0	0	0	0	2
	PTP-kappa	1	4	0	1	2
	PTP-mu	1	4	0	1	2
	PTP-zeta	0	1	1	0	2

10 PTPase domains consist of about 300 amino acids. There are two conserved cysteines, the second one has been shown to be absolutely required for activity. Furthermore, a number of conserved residues in its immediate vicinity have also been shown to be important.

A signature pattern was derived for PTPase domains centered on the active site cysteine.

15 There are three profiles for PTPases, the first one spans the complete domain and is not specific to any subtype. The second profile is specific to dual-specificity PTPases and the third one to the PTP subfamily.

Consensus pattern [LIVMF SEQ ID NO:2)]-H-C-x(2)-G-x(3)-[STC]-[STAGP SEQ ID NO:213)]-x-[LIVMFY SEQ ID NO:18)] [C is the active site residue]

20 Notethe M-phase inducer phosphatases (cdc25-type phosphatase) are tyrosine- protein phosphatases that are not structurally related to the above PTPases.

Notethis documentation entry is linked to both a signature pattern and to profiles. As profiles are much more sensitive than the pattern, you should use them if you have access to the necessary software tools to do so.

25

[1] Fischer E.H., Charbonneau H., Tonks N.K. Science 253:401-406(1991).

[2] Charbonneau H., Tonks N.K. Annu. Rev. Cell Biol. 8:463-493(1992).

[3] Trowbridge I.S. J. Biol. Chem. 266:23517-23520(1991).

[4] Tonks N.K., Charbonneau H. Trends Biochem. Sci. 14:497-500(1989).

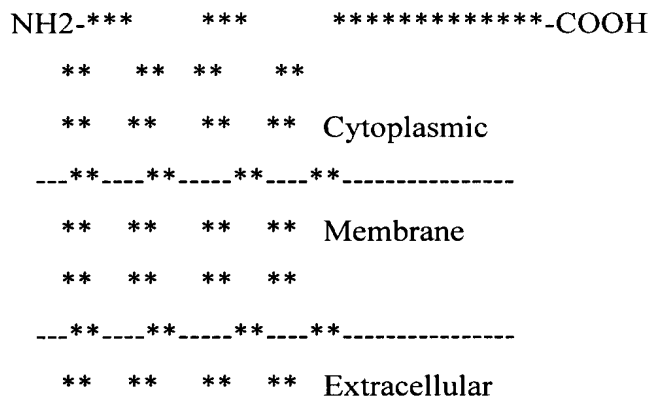
30 [5] Hunter T. Cell 58:1013-1016(1989).

780. Connexins signatures

Gap junctions [1] are specialized regions of the plasma membrane which consist of closely packed pairs of transmembrane channels, the connexons, through which small molecules diffuse from a cell to a neighboring cell. Each connexon is composed of an hexamer of an integral membrane protein which is often referred to as connexin. In a given species there are a number of different, yet structurally related, tissue specific, forms of connexins. The types of connexins which are currently known are listed below.

- Connexin 56 (Cx56).
- Connexin 50 (Cx50) (lens fiber protein MP70).
- Connexin 46 (Cx46) (alpha-3).
- Connexin 45 (Cx45) (alpha-6).
- Connexin 43 (Cx43) (alpha-1).
- Connexin 40 (Cx40) (alpha-5).
- Connexin 38 (Cx38) (alpha-2).
- Connexin 37 (Cx37) (alpha-4).
- Connexin 33 (Cx33) (alpha-7).
- Connexin 32 (Cx32) (beta-1).
- Connexin 31.1 (Cx31.1) (beta-4).
- Connexin 31 (Cx31) (beta-3).
- Connexin 30.3 (Cx30.3) (beta-5).
- Connexin 26 (Cx26) (beta-2).

Structurally the connexins consist of a short cytoplasmic N-terminal domain, followed by four transmembrane segments that delimit two extracellular and one cytoplasmic loops; the C-terminal domain is cytoplasmic and its length is variable (from 20 residues in Cx26 to 260 residues in Cx56). The schematic representation of this structure is shown below.



** ** ** **

** **

The sequences of the two extracellular loops are well conserved. In both loops there are three conserved cysteines which are involved in disulfide bonds. A signature patterns from each of these two loop regions has been built.

Consensus pattern C-[DN]-T-x-Q-P-G-C-x(2)-V-C-[FY]-D [The three C's are involved in disulfide bonds] Consensus pattern C-x(3,4)-P-C-x(3)-[LIVM SEQ ID NO:4)]-[DEN]-C-[FY]-[LIVM SEQ ID NO:4)]-[SA]-[KR]-P [The three C's are involved in disulfide bonds]

[1] Goodenough D.A., Goliger J.A., Paul D.L. Annu. Rev. Biochem. 65:475-502(1996).

781. Gram-positive cocci surface proteins 'anchoring' hexapeptide

Surface proteins from Gram-positive cocci contains a conserved hexapeptide located a few residues downstream of a hydrophobic C-terminal membrane anchor region which is followed by a cluster of basic amino acids [1]. This structure is represented in the following schematic representation:

```

+-----+-----+-----+-----+-----+-----+
| Variable length extracellular domain  |H| Anchor |B|
+-----+-----+-----+-----+-----+-----+

```

'H': conserved hexapeptide.

'B': cluster of basic residues.

It has been proposed that this hexapeptide sequence is responsible for a post-translational modification necessary for the proper anchoring of the proteins which bear it, to the cell wall. Proteins known to contain such hexapeptide are listed below:

- Aggregation substance from streptococcus faecalis (asa1).
- C5a peptidase from Streptococcus pyogenes (scpA).
- C protein alpha-antigen from Streptococcus agalactiae (bca).
- Cell surface antigen I/II (PAC) from Streptococcus mutans.
- Dextranase from Streptococcus downei (dex).
- Fibronectin-binding protein from Staphylococcus aureus (fnbA).

- Fimbrial subunits from *Actinomyces naeslundii* and *viscosus*.
- IgA binding protein from *Streptococcus pyogenes* (arp4).
- IgA binding protein (B antigen) from *Streptococcus agalactiae* (bag).
- IgG binding proteins from *Streptococci* and *Staphylococcus aureus*.
- 5 - Internalin A from *Listeria monocytogenes* (inlA).
- M proteins from streptococci.
- Muramidase-released protein from *Streptococcus suis* (mrp).
- Nisin leader peptide processing protease from *Lactococcus lactis* (nisP).
- Protein A from *Staphylococcus aureus*.
- 10 - Trypsin-resistant surface T protein from streptococci.
- Wall-associated protein from *Streptococcus mutans* (wapA).
- Wall-associated serine proteinases from *Lactococcus lactis*.

Consensus pattern L-P-x-T-G-[STGAVDE SEQ ID NO:696]

15

[1] Schneewind O., Jones K.F., Fischetti V.A. J. Bacteriol. 172:3310-3317(1990).

782. Gamma-glutamyltranspeptidase signature

20 Gamma-glutamyltranspeptidase (EC 2.3.2.2) (GGT) [1] catalyzes the transfer of the gamma-glutamyl moiety of glutathione to an acceptor that may be an amino acid, a peptide or water (forming glutamate). GGT plays a key role in the gamma-glutamyl cycle, a pathway for the synthesis and degradation of glutathione. In prokaryotes and eukaryotes, it is an enzyme that consists of two polypeptide chains, a heavy and a light subunit, processed from a single chain precursor. The active site of GGT is known to be located in the light subunit.

25 The sequences of mammalian and bacterial GGT show a number of regions of high similarity [2]. *Pseudomonas cephalosporin acylases* (EC 3.5.1.-) that convert 7-beta-(4-carboxybutanamido)-cephalosporanic acid (GL-7ACA) into 7-aminocephalosporanic acid (7ACA) and glutaric acid are evolutionary related to GGT and also show some GGT activity [3]. Like GGT, these GL-7ACA acylases, are also composed of two subunits.

30 One of the conserved regions correspond to the N-terminal extremity of the mature light chains of these enzymes. This region has been used as a signature pattern.

Consensus pattern T-[STA]-H-x-[ST]-[LIVMA SEQ ID NO:30)]-x(4)-G-[SN]-x-V-[STA]-x-T-x-T-[LIVM SEQ ID NO:4)]-[NE]-x(1,2)-[FY]-G

[1] Tate S.S., Meister A. Meth. Enzymol. 113:400-419(1985).

5 [2] Suzuki H., Kumagai H., Echigo T., Tochikura T. J. Bacteriol. 171:5169-5172(1989).

[3] Ishiye M., Niwa M. Biochim. Biophys. Acta 1132:233-239(1992).

783. Ferrochelatase signature

10 Ferrochelatase (EC 4.99.1.1) (protoheme ferro-lyase) [1,2] catalyzes the last step in heme biosynthesis: the chelation of a ferrous ion to proto-porphyrin IX, to form protoheme.

In eukaryotes, ferrochelatase is a mitochondrial protein bound to the inner membrane, whose active site faces the mitochondrial matrix. The mature form of eukaryotic ferrochelatase is composed of about 360 amino acids. In bacteria, ferrochelatase (gene hemH) [3] is a protein of from 310 to 380 amino acids.

15 The human autosomal dominant disease protoporphyria is due to the reduced activity of ferrochelatase.

The signature pattern for this enzyme is based on a conserved region which contains a histidine residue which could be involved in binding iron.

20 Consensus pattern [LIVMF SEQ ID NO:2)](2)-x-[ST]-x-H-[GS]-[LIVM SEQ ID NO:4)]-P-x(4,5)-[DENQKR SEQ ID NO:697)]-x-G-[DP]-x(1,2)-Y

[1] Labbe-Bois R. J. Biol. Chem. 265:7278-7283(1990).

[2] Brenner D.A., Frasier F. Proc. Natl. Acad. Sci. U.S.A. 88:849-853(1991).

25 [3] Miyamoto K., Nakahigashi K., Nishimura K., Inokuchi H. J. Mol. Biol. 219:393-398(1991).

784. Cellulose-binding domain, bacterial type

30 The microbial degradation of cellulose and xylans requires several types of enzyme such as endoglucanases (EC 3.2.1.4), cellobiohydrolases (EC 3.2.1.91) (exoglucanases), or xylanases (EC 3.2.1.8) [1].

Structurally, cellulases and xylanases generally consist of a catalytic domain joined to a cellulose-binding domain (CBD) by a short linker sequence rich in proline and/or hydroxy-amino acids.

The CBD of a number of bacterial cellulases has been shown to consist of about 105 amino acid residues [2]. Enzymes known to contain such a domain are:

- Endoglucanase (gene end1) from *Butyrivibrio fibrisolvens*.
- Endoglucanases A (gene cenA) and B (cenB) from *Cellulomonas fimi*.
- Exoglucanases A (gene cbhA) and B (cbhB) from *Cellulomonas fimi*.
- Endoglucanase E-2 (gene celB) from *Thermomonospora fusca*.
- Endoglucanase A (gene celA) from *Microbispora bispora*.
- Endoglucanases A (gene celA), B (celB) and C (celC) from *Pseudomonas fluorescens*.
- Endoglucanase A (gene celA) from *Streptomyces lividans*.
- Exocellobiohydrolase (gene cex) from *Cellulomonas fimi*.
- Xylanases A (gene xynA) and B (xynB) from *Pseudomonas fluorescens*.
- Arabinofuranosidase C (EC 3.2.1.55) (xylanase C) (gene xynC) from *Pseudomonas fluorescens*.
- Chitinase 63 (EC 3.2.1.14) from *Streptomyces plicatus*.
- Chitinase C from *Streptomyces lividans*.

The CBD domain is found either at the N-terminal or at the C-terminal extremity of these enzymes. As it is shown in the following schematic representation, there are two conserved cysteines in this CBD domain - one at each extremity of the domain - which have been shown [3] to be involved in a disulfide bond. There are also four conserved tryptophan residues which could be involved in the interaction of the CBD with polysaccharides.

```

+-----+
|               |
xCxxxxWxxxxxNxxxWxxxxxxxxWxxxxxxxxWNxxxxxGxxxxxxxxxxCx
*****

```

'C': conserved cysteine involved in a disulfide bond. '*': position of the pattern.

Consensus pattern W-N-[STAGR SEQ ID NO:698]-[STDN SEQ ID NO:699]-[LIVM SEQ ID NO:4]-x(2)-[GST]-x-[GST]-x(2)-[LIVMFT SEQ ID NO:282]-[GA]

[1] Gilkes N.R., Henrissat B., Kilburn D.G., Miller R.C. Jr., Warren R.A.J. Microbiol. Rev. 55:303-315(1991).

[2] Meinke A., Gilkes N.R., Kilburn D.G., Miller R.C. Jr., Warren R.A.J. Protein Seq. Data Anal. 4:349-353(1991).

[3] Gilkes N.R., Claeysens M., Aebersold R., Henrissat B., Meinke A., Morrison H.D., Kilburn D.G., Warren R.A.J., Miller R.C. Jr. Eur. J. Biochem. 202:367-377(1991).

785. Amidases signature

It has been shown [1,2,3] that several enzymes from various prokaryotic and eukaryotic organisms which are involved in the hydrolysis of amides (amidases) are evolutionary related. These enzymes are listed below.

- Indoleacetamide hydrolase (EC 3.5.1.-), a bacterial plasmid-encoded enzyme that catalyzes the hydrolysis of indole-3-acetamide (IAM) into indole-3-acetate (IAA), the second step in the biosynthesis of auxins from tryptophan.

- Acetamidase from *Emericella nidulans* (gene *amdS*), an enzyme which allows acetamide to be used as a sole carbon or nitrogen source.

- Amidase (EC 3.5.1.4) from *Rhodococcus* sp. N-774 and *Brevibacterium* sp. R312 (gene *amdA*). This enzyme hydrolyzes propionamides efficiently, and also at a lower efficiency, acetamide, acrylamide and indoleacetamide.

- Amidase (EC 3.5.1.4) from *Pseudomonas chlororaphis*.

- 6-aminohexanoate-cyclic-dimer hydrolase (EC 3.5.2.12) (nylon oligomers degrading enzyme E1) (gene *nylA*), a bacterial plasmid encoded enzyme which catalyzes the first step in the degradation of 6-aminohexanoic acid cyclic dimer, a by-product of nylon manufacture [4].

- Glutamyl-tRNA(Gln) amidotransferase subunit A [5].

- Mammalian fatty acid amide hydrolase (gene *FAAH*) [6].

- A putative amidase from yeast (gene *AMD2*).

- *Mycobacterium tuberculosis* putative amidases *amiA2*, *amiB2*, *amiC* and *amiD*.

All these enzymes contain in their central section a highly conserved region rich in glycine, serine, and alanine residues. This region has been used as a signature pattern.

Consensus pattern: G-[GA]-S-[GS]-[GS]-G-x-[GSA]-[GSAVY SEQ ID NO:700])-x-[LIVM SEQ ID NO:4)]-[GSA]-x(6)-[GSAT SEQ ID NO:100)]-x-[GA]-x-[DE]-x-[GA]-x-S-[LIVM SEQ ID NO:4)]-R-x-P-[GSAC SEQ ID NO:93)]

- 5 [1] Mayaux J.-F., Cerbelaud E., Soubrier F., Faucher D., Petre D. J. Bacteriol. 172:6764-6773(1990).
- [2] Hashimoto Y., Nishiyama M., Ikehata O., Horinouchi S., Beppu T. Biochim. Biophys. Acta 1088:225-233(1991).
- [3] Chang T.-H., Abelson J. Nucleic Acids Res. 18:7180-7180(1990).
- 10 [4] Tsuchiya K., Fukuyama S., Kanzaki N., Kanagawa K., Negoro S., Okada H. J. Bacteriol. 171:3187-3191(1989).
- [5] Curnow A.W., Hong K.W., Yuan R., Kim S.I., Martins O., Winkler W., Henkin T.M., Soll D. Proc. Natl. Acad. Sci. U.S.A. 94:11819-11826(1997).
- [6] Cravatt B.F., Giang D.K., Mayfield S.P., Boger D.L., Lerner R.A., Gilula N.B. Nature
15 384:83-87(1996).

786. Glycosyl hydrolases family 10 active site

The microbial degradation of cellulose and xylans requires several types of enzymes such as endoglucanases (EC 3.2.1.4), cellobiohydrolases (EC 3.2.1.91) (exoglucanases), or
20 xylanases (EC 3.2.1.8) [1,2]. Fungi and bacteria produces a spectrum of cellulolytic enzymes (cellulases) and xylanases which, on the basis of sequence similarities, can be classified into families. One of these families is known as the cellulase family F [3] or as the glycosyl hydrolases family 10 [4,E1]. The enzymes which are currently known to belong to this family are listed below.

- 25 - *Aspergillus awamori* xylanase A (xynA).
- *Bacillus* sp. strain 125 xylanase (xynA).
- *Bacillus stearothermophilus* xylanase.
- *Butyrivibrio fibrisolvens* xylanases A (xynA) and B (xynB).
- *Caldocellum saccharolyticum* bifunctional endoglucanase/exoglucanase (celB). This
30 protein consists of two domains; it is the N-terminal domain, which has exoglucanase activity, which belongs to this family.
- *Caldocellum saccharolyticum* xylanase A (xynA).

- *Caldocellum saccharolyticum* ORF4. This hypothetical protein is encoded in the xynABC operon and is probably a xylanase.
- *Cellulomonas fimi* exoglucanase/xylanase (cex).
- *Clostridium stercorarium* thermostable celloxylanase.
- 5 - *Clostridium thermocellum* xylanases Y (xynY) and Z (xynZ).
- *Cryptococcus albidus* xylanase.
- *Penicillium chrysogenum* xylanase (gene xylP).
- *Pseudomonas fluorescens* xylanases A (xynA) and B (xynB).
- *Ruminococcus flavefaciens* bifunctional xylanase XYLA (xynA). This protein consists of
10 three domains: a N-terminal xylanase catalytic domain that belongs to family 11 of glycosyl hydrolases; a central domain composed of short repeats of Gln, Asn and Trp, and a C-terminal xylanase catalytic domain that belongs to family 10 of glycosyl hydrolases.
- *Streptomyces lividans* xylanase A (xlnA).
- *Thermoanaerobacter saccharolyticum* endoxylanase A (xynA).
- 15 - *Thermoascus aurantiacus* xylanase.
- Thermophilic bacterium Rt8.B4 xylanase (xynA).

One of the conserved regions in these enzymes is centered on a conserved glutamic acid residue which has been shown [5], in the exoglucanase from *Cellulomonas fimi*, to be
20 directly involved in glycosidic bond cleavage by acting as a nucleophile. This region has been used as a signature pattern.

Consensus pattern[GTA]-x(2)-[LIVN SEQ ID NO:682)]-x-[IVMF SEQ ID NO:701)]-[ST]-
E-[LIY]-[DN]-[LIVMF SEQ ID NO:2)] [E is the active site residue]

25

- [1] Beguin P. Annu. Rev. Microbiol. 44:219-248(1990).
- [2] Gilkes N.R., Henrissat B., Kilburn D.G., Miller R.C. Jr., Warren R.A.J. Microbiol. Rev. 55:303-315(1991).
- [3] Henrissat B., Claeyssens M., Tomme P., Lemesle L., Mornon J.-P. Gene 81:83-95(1989).
- 30 [4] Henrissat B. Biochem. J. 280:309-316(1991).
- [5] Tull D., Withers S.G., Gilkes N.R., Kilburn D.G., Warren R.A.J., Aebersold R. J. Biol. Chem. 266:15621-15625(1991).

787. Fructose-bisphosphate aldolase class-II signatures

Fructose-bisphosphate aldolase (EC 4.1.2.13) [1,2] is a glycolytic enzyme that catalyzes the reversible aldol cleavage or condensation of fructose-1,6- bisphosphate into dihydroxyacetone-phosphate and glyceraldehyde 3-phosphate. There are two classes of fructose-bisphosphate aldolases with different catalytic mechanisms. Class-II aldolases [2], mainly found in prokaryotes and fungi, are homodimeric enzymes which require a divalent metal ion – generally zinc - for their activity.

This family also includes the following proteins:

- Escherichia coli galactitol operon protein gatY which catalyzes the transformation of tagatose 1,6-bisphosphate into glycerone phosphate and D- glyceraldehyde 3-phosphate.
- Escherichia coli N-acetyl galactosamine operon protein agaY which catalyzes the same reaction as that of gatY.

As signature patterns for this class of enzyme, two conserved regions were selected. The first pattern is located in the first half of the sequence and contains two histidine residues that have been shown [4] to be involved in binding a zinc ion. The second is located in the C-terminal section and contains clustered acidic residues and glycines.

Consensus pattern[FYVMT SEQ ID NO:702)]-x(1,3)-[LIVMH SEQ ID NO:703)]-[APN]-[LIVM SEQ ID NO:4)]-x(1,2)-[LIVM SEQ ID NO:4)]-H-x-D-H- [GACH SEQ ID NO:704)]
[The two H's are zinc ligands]
Consensus pattern[LIVM SEQ ID NO:4)]-E-x-E-[LIVM SEQ ID NO:4)]-G-x(2)-[GM]-[GSTA SEQ ID NO:19)]-x-E

[1] Perham R.N. Biochem. Soc. Trans. 18:185-187(1990).

[2] Marsh J.J., Lebherz H.G. Trends Biochem. Sci. 17:110-113(1992).

[3] von der Osten C.H., Barbas C.F. III, Wong C.-H., Sinskey A.J. Mol. Microbiol. 3:1625-1637(1989).

[4] Berry A., Marshall K.E. FEBS Lett. 318:11-16(1993).

788. Prolyl oligopeptidase family serine active site

The prolyl oligopeptidase family [1,2,3] consist of a number of evolutionary related peptidases whose catalytic activity seems to be provided by a charge relay system similar to that of the trypsin family of serine proteases, but which evolved by independent convergent evolution. The known members of this family are listed below.

- 5 - Prolyl endopeptidase (EC 3.4.21.26) (PE) (also called post-proline cleaving enzyme). PE is an enzyme that cleaves peptide bonds on the C-terminal side of prolyl residues. The sequence of PE has been obtained from a mammalian species (pig) and from bacteria (*Flavobacterium meningosepticum* and *Aeromonas hydrophila*); there is a high degree of sequence conservation between these sequences.
- 10 - *Escherichia coli* protease II (EC 3.4.21.83) (oligopeptidase B) (gene prtB) which cleaves peptide bonds on the C-terminal side of lysyl and arginyl residues.
- Dipeptidyl peptidase IV (EC 3.4.14.5) (DPP IV). DPP IV is an enzyme that removes N-terminal dipeptides sequentially from polypeptides having unsubstituted N-termini provided that the penultimate residue is proline.
- 15 - Yeast vacuolar dipeptidyl aminopeptidase A (DPAP A) (gene: STE13) which is responsible for the proteolytic maturation of the alpha-factor precursor.
- Yeast vacuolar dipeptidyl aminopeptidase B (DPAP B) (gene: DAP2).
- Acylamino-acid-releasing enzyme (EC 3.4.19.1) (acyl-peptide hydrolase). This enzyme catalyzes the hydrolysis of the amino-terminal peptide bond of an N-acetylated protein to
- 20 generate a N-acetylated amino acid and a protein with a free amino-terminus.

A conserved serine residue has experimentally been shown (in *E.coli* protease II as well as in pig and bacterial PE) to be necessary for the catalytic mechanism. This serine, which is part of the catalytic triad (Ser, His, Asp), is generally located about 150 residues away from the C-terminal extremity of these enzymes (which are all proteins that contains about 700 to 800 amino acids).

Consensus pattern D-x(3)-A-x(3)-[LIVMFYW SEQ ID NO:26]-x(14)-G-x-S-x-G-G-[LIVMFYW SEQ ID NO:26](2) [S is the active site residue]

30

Note these proteins belong to families S9A/S9B/S9C in the classification of peptidases [4,E1].

- [1] Rawlings N.D., Polgar L., Barrett A.J. *Biochem. J.* 279:907-911(1991).
[2] Barrett A.J., Rawlings N.D. *Biol. Chem. Hoppe-Seyler* 373:353-360(1992).
[3] Polgar L., Szabo E.
Biol. Chem. Hoppe-Seyler 373:361-366(1992).
5 [4] Rawlings N.D., Barrett A.J. *Meth. Enzymol.* 244:19-61(1994).

789. Formate--tetrahydrofolate ligase signatures

Formate--tetrahydrofolate ligase (EC 6.3.4.3) (formyltetrahydrofolate synthetase) (FTHFS) is one of the enzymes participating in the transfer of one-carbon units, an essential
10 element of various biosynthetic pathways. In many of these processes the transfers of one-carbon units are mediated by the coenzyme tetrahydrofolate (THF). Various reactions generate one-carbon derivatives of THF which can be interconverted between different oxidation states by FTHFS, methylenetetrahydrofolate dehydrogenase (EC 1.5.1.5) and methenyltetrahydrofolate cyclohydrolase (EC 3.5.4.9).

15 In eukaryotes the FTHFS activity is expressed by a multifunctional enzyme, C-1-tetrahydrofolate synthase (C1-THF synthase), which also catalyzes the dehydrogenase and cyclohydrolase activities. Two forms of C1-THF synthases are known [1], one is located in the mitochondrial matrix, while the second one is cytoplasmic. In both forms the FTHFS domain consist of about 600 amino acid residues and is located in the C-terminal section of
20 C1-THF synthase. In prokaryotes FTHFS activity is expressed by a monofunctional homotetrameric enzyme of about 560 amino acid residues [2].

The sequence of FTHFS is highly conserved in all forms of the enzyme. As signature patterns, two regions that are almost perfectly conserved were selected. The first one is a glycine-rich segment located in the N-terminal part of FTHFS and which could be part of an
25 ATP-binding domain [2]. The second pattern is located in the central section of FTHFS.

Consensus pattern G-[LIVM SEQ ID NO:4)]-K-G-G-A-A-G-G-G-Y

Consensus pattern V-A-T-[IV]-R-A-L-K-x-[HN]-G-G

- 30 [1] Shannon K.W., Rabinowitz J.C. *J. Biol. Chem.* 263:7717-7725(1988).
[2] Lovell C.R., Przybyla A., Ljungdahl L.G. *Biochemistry* 29:5687-5694(1990).

790. Transthyretin signatures

Transthyretin (prealbumin) [1] is a thyroid hormone-binding protein that seems to transport thyroxine (T4) from the bloodstream to the brain. It is a protein of about 130 amino acids that assembles as a homotetramer and forms an internal channel that binds thyroxine. Transthyretin is mainly synthesized in the brain choroid plexus. In humans, variants of the protein are associated with distinct forms of amyloidosis.

The sequence of transthyretin is highly conserved in vertebrates. A number of uncharacterized proteins also belong to this family:

- Escherichia coli hypothetical protein yedX.
- Bacillus subtilis hypothetical protein yunM.
- Caenorhabditis elegans hypothetical protein R09H10.3.
- Caenorhabditis elegans hypothetical protein ZK697.8.

Two regions were selected as signature patterns. The first located in the N-terminal extremity starts with a lysine known to be involved in binding T4. The second pattern is located in the C-terminal extremity.

Consensus pattern[KH]-[IV]-L-[DN]-x(3)-G-x-P-A-x(2)-[IV]-x-[IV] [The K binds thyroxine]
Consensus patternY-[TH]-[IV]-[AP]-x(2)-L-S-[PQ]-[FYW]-[GS]-[FY]-[QS]

[1] Schreiber G., Richardson S.J. Comp. Biochem. Physiol. 116B:137-160(1997).

791. Dihydropteroate synthase signatures

All organisms require reduced folate cofactors for the synthesis of a variety of metabolites. Most microorganisms must synthesize folate de novo because they lack the active transport system of higher vertebrate cells which allows these organisms to use dietary folates. Enzymes that are involved in the biosynthesis of folates are therefore the target of a variety of antimicrobial agents such as trimethoprim or sulfonamides.

Dihydropteroate synthase (EC 2.5.1.15) (DHPS) catalyzes the condensation of 6-hydroxymethyl-7,8-dihydropteridine pyrophosphate to para-aminobenzoic acid to form 7,8-dihydropteroate. This is the second step in the three steps pathway leading from 6-hydroxymethyl-7,8-dihydropteridine to 7,8-dihydrofolate. DHPS is the target of sulfonamides which are substrates analog that compete with para-aminobenzoic acid.

Bacterial DHPS (gene *sul* or *folP*) [1] is a protein of about 275 to 315 amino acid residues which is either chromosomally encoded or found on various antibiotic resistance plasmids. In the lower eukaryote *Pneumocystis carinii*, DHPS is the C-terminal domain of a multifunctional folate synthesis enzyme (gene *fas*) [2].

Two signature patterns for DHPS were developed, the first signature is located in the N-terminal section of these enzymes, while the second signature is located in the central section.

Consensus pattern[LIVM SEQ ID NO:4)]-x-[AG]-[LIVMF SEQ ID NO:2)](2)-N-x-T-x-D-S-F-x-D-x-[SG]

Consensus pattern[GE]-[SA]-x-[LIVM SEQ ID NO:4)](2)-D-[LIVM SEQ ID NO:4)]-G-[GP]-x(2)-[STA]-x-P

[1] Slock J., Stahly D.P., Han C.-Y., Six E.W., Crawford I.P. J. Bacteriol. 172:7211-7226(1990).

[2] Volpes F., Dyer M., Scaife J.G., Darby G., Stammers D.K., Delves C.J. Gene 112:213-218(1992).

792. Phosphatidylinositol 3- and 4-kinases signatures

Phosphatidylinositol 3-kinase (PI3-kinase) (EC 2.7.1.137) [1] is an enzyme that phosphorylates phosphoinositides on the 3-hydroxyl group of the inositol ring. The exact function of the three products of PI3-kinase - PI-3-P, PI-3,4-P(2) and PI-3,4,5-P(3) - is not yet known, although it is proposed that they function as second messengers in cell signalling. Currently, three forms of PI3-kinase are known:

- The mammalian enzyme which is a heterodimer of a 110 Kd catalytic chain (p110) and an 85 Kd subunit (p85) which allows it to bind to activated tyrosine protein kinases. There are at least two different types of p100 subunits (alpha and beta).

- Yeast TOR1/DRR1 and TOR2/DRR2 [2], PI3-kinases required for cell cycle activation. Both are proteins of about 280 Kd.

- Yeast VPS34 [3], a PI3-kinase involved in vacuolar sorting and segregation. VPS34 is a protein of about 100 Kd.

- Arabidopsis thaliana and soybean VPS34 homologs.

Phosphatidylinositol 4-kinase (PI4-kinase) (EC 2.7.1.67) [4] is an enzyme that acts on phosphatidylinositol (PI) in the first committed step in the production of the second messenger inositol-1,4,5,-trisphosphate. Currently the following forms of PI4-kinases are known:

- 5 - Human PI4-kinase alpha.
- Yeast PIK1, a nuclear protein of 120 Kd.
- Yeast STT4, a protein of 214 Kd.

10 The PI3- and PI4-kinases share a well conserved domain at their C-terminal section; this domain seems to be distantly related to the catalytic domain of protein kinases [2]. Two signature patterns were developed from the best conserved parts of this domain.

Four additional proteins belong to this family:

- 15 - Mammalian FKBP-rapamycin associated protein (FRAP) [5], which acts as the target for the cell-cycle arrest and immunosuppressive effects of the FKBP12-rapamycin complex.
- Yeast protein ESR1 [6] which is required for cell growth, DNA repair and meiotic recombination.
- Yeast protein TEL1 which is involved in controlling telomere length.
- Yeast hypothetical protein YHR099w, a distantly related member of this family.
- 20 - Fission yeast hypothetical protein SpAC22E12.16C.

Consensus pattern[LIVMFAC SEQ ID NO:95)]-K-x(1,3)-[DEA]-[DE]-[LIVMC SEQ ID NO:142)]-R-Q-[DE]-x(4)-Q

25 Consensus pattern[GS]-x-[AV]-x(3)-[LIVM SEQ ID NO:4)]-x(2)-[FYH]-[LIVM SEQ ID NO:4)](2)-x-[LIVMF SEQ ID NO:2)]-x-D-R-H-x(2)-N

[1] Hiles I.D., Otsu M., Volinia S., Fry M.J., Gout I., Dhand R., Panayotou G., Ruiz-Larrea F., Thompson A., Totty N.F., Hsuan J.J., Courtneidge S.A., Parker P.J., Waterfield M.D. Cell 70:419-429(1992).

30 [2] Kunz J., Henriquez R., Schneider U., Deuter-Reinhard M., Movva N., Hall M.N. Cell 73:585-596(1993).

[3] Schu P.V., Takegawa K., Fry M.J., Stack J.H., Waterfield M.D., Emr S.D. Science 260:88-91(1993).

[4] Garcia-Bustos J.F., Marini F., Stevenson I., Frei C., Hall M.N. EMBO J. 13:2352-2361(1994).

[5] Brown E.J., Albers M.W., Shin T.B., Ichikawa K., Keith C.T., Lane W.S., Schreiber S.L. Nature 369:756-758(1994).

5 [6] Kato R., Ogawa H. Nucleic Acids Res. 22:3104-3112(1994).

793. FAD-dependent glycerol-3-phosphate dehydrogenase signatures

FAD-dependent glycerol-3-phosphate dehydrogenase (EC 1.1.99.5) (GPD) catalyzes the conversion of glycerol-3-phosphate into dihydroxyacetone phosphate. In bacteria [1] it is associated with the utilization of glycerol coupled to respiration. In *Escherichia coli*, two isozymes are known: one expressed under anaerobic conditions (gene *glpA*) and one in aerobic conditions (gene *glpD*). In eukaryotes, a mitochondrial form of GPD participates in the glycerol phosphate shuttle in conjunction with an NAD-dependent cytoplasmic GPD (EC 1.1.1.8) [2,3].

15 These enzymes are proteins of about 60 to 70 Kd which contain a probable FAD-binding domain in their N-terminal extremity. The mammalian enzyme differs from the bacterial or yeast proteins by having an EF-hand calcium-binding region (See <PDOC00018>) in its C-terminal extremity.

20 Two signature patterns were developed. One based on the first half of the FAD-binding domain and one which corresponds to a conserved region in the central part of these enzymes.

Consensus pattern[IV]-G-G-G-x(2)-G-[STACV SEQ ID NO:146])-G-x-A-x-D-x(3)-R-G

Consensus patternG-G-K-x(2)-[GSTSE SEQ ID NO:705])-Y-R-x(2)-A

25

[1] Austin D., Larson T.J. J. Bacteriol. 173:101-107(1991).

[2] Roennow B., Kielland-Brandt M.C. Yeast 9:1121-1130(1993).

[3] Brown L.J., McDonald M.J., Lehn D.A., Moran S.M. J. Biol. Chem. 269:14363-14366(1994).

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794. NOL1/NOP2/sun family signature

The following proteins seems to be evolutionary related:

- Mammalian proliferating-cell nucleolar antigen p120 (gene NOL1) which may play a role in the regulation of the cell cycle and the increased nucleolar activity that is associated with the cell proliferation.
- Yeast nucleolar protein NOP2 (or YNA1) which could be involved in nucleolar function during the onset of growth, and in the maintenance of nucleolar structure.
- Yeast hypothetical protein YBL024w.
- Bacterial protein sun (also known as fmu).
- Escherichia coli hypothetical protein yebU.
- Mycobacterium tuberculosis hypothetical protein MtCY21B4.24.
- Methanococcus jannaschii hypothetical protein MJ0026.

NOL1 is a protein of 855 residues, NOP2 consists of 618 residues, YBL024w of 684, sun is a protein of about 430 to 450 residues and MJ026 has 274 residues. They share a conserved central domain which contains some highly conserved regions. One of these regions was selected as a signature pattern.

Consensus pattern[FV]-D-[KRA]-[LIVMA SEQ ID NO:30)]-L-x-D-[AV]-P-C-[ST]-[GA]

795. moaA / nifB / pqqE family signature

A number of proteins involved in the biosynthesis of metallo cofactors have been shown [1,2] to be evolutionary related. These proteins are:

- Bacterial and archebacterial protein moaA, which is involved in the biosynthesis of the molybdenum cofactor (molybdopterin; MPT).
- Arabidopsis thaliana cnx2, a protein involved in molybdopterin biosynthesis and which is highly similar to moaA.
- Bacillus subtilis narA, which seems to be the moaA ortholog in that bacteria.
- Bacterial protein nifB (or fixZ) which is involved in the biosynthesis of the nitrogenase iron-molybdenum cofactor.
- Bacterial protein pqqE which is involved in the biosynthesis of the cofactor pyrrolo-quinoline-quinone (PQQ).
- Pyrococcus furiosus cmo, a protein involved in the synthesis of a molybdopterin-based tungsten cofactor.
- Caenorhabditis elegans hypothetical protein F49E2.1.

All these proteins share, in their N-terminal region, a conserved domain that contains three cysteines. In moaA, these cysteines have been shown [1] to be important for the biological activity. They could be involved in the binding of an iron-sulfur cluster.

5

Consensus pattern[LIV]-x(3)-C-[NP]-[LIVMF SEQ ID NO:2)]-[QRS]-C-x-[FYM]-C [The three C's are putative Fe-S ligands

[1] Menendez C., Igloi G., Henninger H., Brandsch R. Arch. Microbiol. 164:142-151(1995).

10 [2] Hoff T., Schnorr K.M., Meyer C., Caboche M. J. Biol. Chem. 270:6100-6107(1995).

796. Forkhead-associated (FHA) domain profile

The forkhead-associated (FHA) domain [1,E1] is a putative nuclear signalling domain found in a variety of otherwise unrelated proteins. The FHA domain comprise approximately
15 55 to 75 amino acids and contains three highly conserved blocks separated by divergent spacer regions. Currently it has been found in the following proteins:

- Four transcription factors that also contain a forkhead (FH) domain: mouse myocyte nuclear factor 1 (MNF1), yeast transcription factor FHL1, which probably controls pre-mRNA processing, and yeast FKH1 and FKH2. In those protein the FHA domain is located
20 N-terminal of the DNA-binding FH domain.
- Kinase-associated protein phosphatase (KAPP) from Arabidopsis thaliana, a protein which specifically interacts with the receptor-type Ser/Thr-kinase RLK5. In KAPP, the FHA domain maps to a region that interacts with the receptor-type protein kinase RLK5 only if the kinase is phosphorylated on serine residues [2].
- 25 - Two protein kinases from yeast that are involved in mediating the nuclear response to DNA damage: DUN1 and SPK1/SAD1 [3]. The latter is the only known protein containing two copies of the FHA domain.
- Protein kinase cds1 from fission yeast contains a FHA domain and might be the ortholog of SPK1.
- 30 - Protein kinase MEK1 from yeast, which is involved in meiotic recombination.
- Human nuclear antigen Ki67 which is expressed only in proliferating cells.
- Yeast hypothetical protein YHR115c, which contains a RING-finger C-terminal of the FHA domain.

- Yeast hypothetical proteins L8083.1 and 9346.10, which contain an extensive coiled-coil region C-terminal of the FHA domain.

- *Caenorhabditis elegans* hypothetical protein ZK632.2.

- *Caenorhabditis elegans* hypothetical protein C01G6.5.

5 - FraH from the prokaryote *Anabaena*, which contains a zinc-finger motif N-terminal of the FHA domain.

- An ORF from the bacterium *Streptomyces*, which is on the opposite strand of the protein kinase pks1, overlapping the ORF of the kinase.

10 [1] Hofmann K.O., Bucher P. Trends Biochem. Sci. 20:347-349(1995).

[2] Stone J.M., Collinge M.A., Smith R.D., Horn M.A., Walker J.C. Science 266:793-795(1994).

[3] Navas T.A., Zhou Z., Elledge S.J. Cell 80:29-39(1995).

15 797. Ald_Xan_dh_C

Aldehyde oxidase and xanthine dehydrogenase, C terminus

[1] Romao MJ, Archer M, Moura I, Moura JJ, LeGall J, Engh R, Schneider M, Hof P, Huber R; Medline: 96072968 "Crystal structure of the xanthine oxidase-related aldehyde oxidoreductase from *D. gigas*." Science 1995;270:1170-1176.

20

Number of members: 54

798. Glyco_hydro_38

25 Glycosyl hydrolases family 38

Glycosyl hydrolases are key enzymes of carbohydrate metabolism.

Number of members: 20

30 [1] Henrissat B; Medline: 98313424; "Glycosidase families" Biochem Soc Trans 1998;26:153-156.

799. HECT

HECT-domain (ubiquitin-transferase).

The name HECT comes from Homologous to the E6-AP Carboxyl Terminus.

5 Number of members: 43

[1] Huijbrechtse JM, Scheffner M, Beaudenon S, Howley PM; Medline: 95223981; "A family of proteins structurally and functionally related to the E6-AP ubiquitin-protein ligase." Proc Natl Acad Sci U S A 1995;92:2563-2567.

10

800. HRDC

HRDC domain

The HRDC (Helicase and RNase D C-terminal) domain has a putative role in nucleic acid binding. Mutations in the HRDC domain cause human disease.

15

Number of members: 19

[1] Morozov V, Mushegian AR, Koonin EV, Bork P; Medline: 98060076; "A putative nucleic acid-binding domain in Bloom's and Werner's syndrome helicases" Trends Biochem Sci 1997;22:417-418.

20

801. Integrase

Integrase mediates integration of a DNA copy of the viral genome into the host chromosome. Integrase is composed of three domains. The amino-terminal domain is a zinc binding domain. The central domain is the catalytic domain [1]. The carboxyl terminal domain is a DNA binding domain [2].

25

Number of members: 581

30 [1] Dyda F, Hickman AB, Jenkins TM, Engelman A, Craigie R, Davies DR; Medline: 95099322. "Crystal structure of the catalytic domain of HIV-1 integrase: similarity to other polynucleotidyl transferases." Science 1994;266:1981-1986.

[2] Lodi PJ, Ernst JA, Kuszewski J, Hickman AB, Engelman A, Craigie R, Clore GM, Gronenborn AM; Medline: 95359147; "Solution structure of the DNA binding domain of HIV-1 integrase." *Biochemistry* 1995;34:9826-9833

5 802. lig_chan

Ligand-gated ion channel

This family includes the four transmembrane regions of the ionotropic glutamate receptors and NMDA receptors.

10 Number of members: 128

[1] Tong G, Shepherd D, Jahr CE; Medline: 95184014; "Synaptic desensitization of NMDA receptors by calcineurin." *Science* 1995;267:1510-1512.

15 803. RhoGAP

RhoGAP domain

GTPase activator proteins towards Rho/Rac/Cdc42-like small GTPases.

Number of members: 97

20

[1] Musacchio A, Cantley LC, Harrison SC; Medline: 97121392; "Crystal structure of the breakpoint cluster region-homology domain from phosphoinositide 3-kinase p85 alpha subunit." *Proc Natl Acad Sci U S A* 1996;93:14373-14378.

[2] Barrett T, Xiao B, Dodson EJ, Dodson G, Ludbrook SB, Nurmahomed K, Gamblin SJ, 25 Musacchio A, Smerdon SJ, Eccleston JF; Medline: 97162209; "The structure of the GTPase-activating domain from p50rhoGAP." *Nature* 1997;385:458-461.

[3] Rittinger K, Walker PA, Eccleston JF, Nurmahomed K, Owen D, Laue E, Gamblin SJ, Smerdon SJ; Medline: 97404320; "Crystal structure of a small G protein in complex with the GTPase-activating protein rhoGAP." *Nature* 1997;388:693-697.

30 [4] Boguski MS, McCormick F; Medline: 94081948; "Proteins regulating Ras and its relatives." *Nature* 1993;366:643-654.

804. vwd

von Willebrand factor type D domain

[1] Bork P; Medline: 93327926; "The modular architecture of a new family of growth regulators related to connective tissue growth factor." FEBS lett 1993;327:125-130.

5

Number of members: 92

805. zf-C4_Topoiso

Topoisomerase DNA binding C4 zinc finger

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[1] Tse-Dinh YC, Beran-Steed RK; Medline: 89034032; "Escherichia coli DNA topoisomerase I is a zinc metalloprotein with three repetitive zinc-binding domains." J Biol Chem 1988;263:15857-15859.

15

[2] Ahumada A, Tse-Dinh YC; Medline: 99011409; "The Zn(II) binding motifs of E. coli DNA topoisomerase I is part of a high-affinity DNA binding domain." Biochem Biophys Res Commun 1998;251:509-514.

Number of members: 51

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806. AIRC

AIR carboxylase

Members of this family catalyse the decarboxylation of 1-(5-phosphoribosyl)-5-amino-4-imidazole-carboxylate (AIR). This family catalyse the sixth step of de novo purine biosynthesis. Some members of this family contain two copies of this domain. Number of members: 35

25

807. Bromodomain signature and profile

PROSITE cross-reference(s): PS00633; BROMODOMAIN_1, PS50014;

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BROMODOMAIN_2

The bromodomain [1,2,3] is a conserved region of about 70 amino acids found in the following proteins:

- Higher eukaryotes transcription initiation factor TFIID 250 Kd subunit (TBP-associated factor p250) (gene CCG1). P250 associated with the TFIID TATA-box binding protein and seems essential for progression of the G1 phase of the cell cycle.

- Human RING3, a protein of unknown function encoded in the MHC class II locus.

5 - Mammalian CREB-binding protein (CBP), which mediates cAMP-gene regulation by binding specifically to phosphorylated CREB protein.

- Drosophila female sterile homeotic protein (gene fsh), required maternally for proper expression of other homeotic genes involved in pattern formation, such as Ubx.

10 - Drosophila brahma protein (gene brm), a protein required for the activation of multiple homeotic genes.

- Mammalian homologs of brahma. In human, three brahma-like proteins are known: SNF2a(hBRM), SNF2b, and BRG1.

- Human BS69, a protein that binds to adenovirus E1A and inhibits E1A transactivation

- Human peregrin (or Br140).

15 - Yeast BDF1 [3], a transcription factor involved in the expression of a broad class of genes including snRNAs.

- Yeast GCN5, a general transcriptional activator operating in concert with certain other DNA-binding transcriptional activators, such as GCN4, HAP2/3/4 or ADA2.

- Yeast NPS1/STH1, involved in G(2) phase control in mitosis.

20 - Yeast SNF2/SWI2, which is part of a complex with the SNF5, SNF6, SWI3 and ADR6/SWI1 proteins. This SWI-complex is involved in transcriptional activation.

- Yeast SPT7, a transcriptional activator of Ty elements and possibly other genes.

- Caenorhabditis elegans protein cbp-1.

- Yeast hypothetical protein YGR056w.

25 - Yeast hypothetical protein YKR008w.

- Yeast hypothetical protein L9638.1.

Some proteins contain a region which, while similar to some extent to a classical bromodomain, diverges from it by either lacking part of the domain or because of an
30 insertion. These proteins are:

- Mammalian protein HRX (also known as All-1 or MLL), a protein involved in translocations leading to acute leukemias and which possibly acts as a transcriptional regulatory factor. HRX contains a region similar to the C- terminal half of the bromodomain.
- *Caenorhabditis elegans* hypothetical protein ZK783.4. The bromodomain of this protein has a 23 amino-acid insertion.
- Yeast protein YTA7. This protein contains a region with significant similarity to the C-terminal half of the bromodomain. As it is a member of the AAA family (see <PDOC00572>) it is also in a functionally different context.

10 The above proteins generally contain a single bromodomain, but some of them contain two copies, this is the case of BDF1, CCG1, fsh, RING3, YKR008w and L9638.1.

The exact function of this domain is not yet known but it is thought to be involved in protein-protein interactions and it may be important for the assembly or activity of multicomponent complexes involved in transcriptional activation.

The consensus pattern that has been developed spans a major part of the bromodomain; a more sensitive detection is available through the use of a profile which spans the whole domain.

20 Consensus pattern[STANVF SEQ ID NO:706)]-x(2)-F-x(4)-[DNS]-x(5,7)-[DENQTF SEQ ID NO:707)]-Y-[HFY]-x(2)-
 [LIVMFY SEQ ID NO:18)]-x(3)-[LIVM SEQ ID NO:4)]-x(4)-[LIVM SEQ ID NO:4)]-
 x(6,8)-Y-x(12,13)-[LIVM SEQ ID NO:4)]-
 25 x(2)-N-[SACF SEQ ID NO:708)]-x(2)-[FY]

References

[1] Haynes S.R., Doolard C., Winston F., Beck S., Trowsdale J., Dawid I.B. *Nucleic Acids Res.* 20:2693-2603(1992).

30 [2] Tamkun J.W., Deuring R., Scott M.P., Kissinger M., Pattatucci A.M., Kaufman T.C., Kennison J.A. *Cell* 68:561-572(1992).

[3] Tamkun J.W. *Curr. Opin. Genet. Dev.* 5:473-477(1995).

808. (CH) Actinin-type actin-binding domain signatures

PROSITE cross-reference(s): PS00019; ACTININ_1, PS00020; ACTININ_2

Alpha-actinin is a F-actin cross-linking protein which is thought to anchor actin to a variety of intracellular structures [1]. The actin-binding domain of alpha-actinin seems to reside in the first 250 residues of the protein. A similar actin-binding domain has been found in the N-terminal region of many different actin-binding proteins [2,3]:

- In the beta chain of spectrin (or fodrin).

- In dystrophin, the protein defective in Duchenne muscular dystrophy (DMD) and which may play a role in anchoring the cytoskeleton to the plasma membrane.

- In the slime mold gelation factor (or ABP-120).

- In actin-binding protein ABP-280 (or filamin), a protein that link actin filaments to membrane glycoproteins.

- In fimbrin (or plastin), an actin-bundling protein. Fimbrin differs from the above proteins in that it contains two tandem copies of the actin-binding domain and that these copies are located in the C-terminal part of the protein.

Two conserved regions were selected as signature patterns for this type of main. The first of this region is located at the beginning of the domain, while the second one is located in the central section and has been shown to be essential for the binding of actin.

Consensus pattern[EQ]-x(2)-[ATV]-[FY]-x(2)-W-x-N

Consensus pattern[LIVM SEQ ID NO:4]-x-[SGN]-[LIVM SEQ ID NO:4]-[DAGHE SEQ ID NO:709]-[SAG]-x-[DNEAG SEQ ID NO:710]-[LIVM SEQ ID NO:4]-x-[DEAG SEQ ID NO:711]-x(4)-[LIVM SEQ ID NO:4]-x-[LM]-[SAG]-[LIVM SEQ ID NO:4]-[LIVMT SEQ ID NO:1]-W-x-[LIVM SEQ ID NO:4](2)

[1] Schleicher M., Andre E., Harmann A., Noegel A.A. Dev. Genet. 9:521-530(1988).

[2] Matsudaira P. Trends Biochem. Sci. 16:87-92(1991).

[3] Dubreuil R.R. BioEssays 13:219-226(1991).

809. (COX1) Heme-copper oxidase subunit I, copper B binding region signature

PROSITE cross-reference(s): PS00077; COX1

Heme-copper respiratory oxidases [1] are oligomeric integral membrane protein complexes that catalyze the terminal step in the respiratory chain: they transfer electrons from cytochrome c or a quinol to oxygen. Some terminal oxidases generate a transmembrane proton gradient across the plasma membrane (prokaryotes) or the mitochondrial inner membrane (eukaryotes). The enzyme complex consists of 3-4 subunits (prokaryotes) up to 13 polypeptides (mammals) of which only the catalytic subunit (equivalent to mammalian subunit 1 (CO I)) is found in all heme-copper respiratory oxidases. The presence of a bimetallic center (formed by a high-spin heme and copper B) as well as a low-spin heme, both ligated to six conserved histidine residues near the outer side of four transmembrane spans within CO I is common to all family members [2-4].

In contrary to eukaryotes the respiratory chain of prokaryotes is branched to multiple terminal oxidases. The enzyme complexes vary in heme and copper composition, substrate type and substrate affinity. The different respiratory oxidases allow the cells to customize their respiratory systems according a variety of environmental growth conditions [1].

Recently also a component of an anaerobic respiratory chain has been found to contain the copper B binding signature of this family: nitric oxide reductase (NOR) exists in denitrifying species of Archae and Eubacteria.

Enzymes that belong to this family are:

- Mitochondrial-type cytochrome c oxidase (EC 1.9.3.1) which uses cytochrome c as electron donor. The electrons are transferred via copper A (Cu(A)) and heme a to the bimetallic center of CO I that is formed by a penta-coordinated heme a and copper B (Cu(B)). Subunit 1 contains 12 transmembrane regions. Cu(B) is said to be ligated to three of the conserved histidine residues within the transmembrane segments 6 and 7.
- Quinol oxidase from prokaryotes that transfers electrons from a quinol to the binuclear center of polypeptide I. This category of enzymes includes

Escherichia coli cytochrome O terminal oxidase complex which is a component of the aerobic respiratory chain that predominates when cells are grown at high aeration.

- FixN, the catalytic subunit of a cytochrome c oxidase expressed in nitrogen-fixing bacteroids living in root nodules. The high affinity for oxygen allows oxidative phosphorylation under low oxygen concentrations. A similar enzyme has been found in other purple bacteria.

- Nitric oxide reductase (EC 1.7.99.7) from *Pseudomonas stutzeri*. NOR reduces nitrate to dinitrogen. It is a heterodimer of norC and the catalytic subunit norB. The latter contains the 6 invariant histidine residues and 12 transmembrane segments [5].

As a signature pattern the copper-binding region was used.

Consensus pattern[YWG]-[LIVFYWTA SEQ ID NO:712)](2)-[VGS]-H-[LNP]-x-V-x(44,47)-H-H [The three H's are copper B ligands]

Notocytochrome bd complexes do not belong to this family.

[1]

Garcia-Horsman J.A., Barquera B., Rumbley J., Ma J., Gennis R.B.
J. Bacteriol. 176:5587-5600(1994).

[2]

Castresana J., Luebben M., Saraste M., Higgins D.G.
EMBO J. 13:2516-2525(1994).

[3]

Capaldi R.A., Malatesta F., Darley-Usmar V.M.
Biochim. Biophys. Acta 726:135-148(1983).

[4]

Holm L., Saraste M., Wikstrom M.
EMBO J. 6:2819-2823(1987).

[5]

Saraste M., Castresana J.
FEBS Lett. 341:1-4(1994).

810. (dehydrog_molyb) Eukaryotic molybdopterin oxidoreductases signature
5 PROSITE cross-reference(s): PS00559; MOLYBDOPTERIN_EUK

A number of different eukaryotic oxidoreductases that require and bind a
molybdopterin cofactor have been shown [1] to share a few regions of sequence
similarity. These enzymes are:

10 - Xanthine dehydrogenase (EC 1.1.1.204), which catalyzes the oxidation of
xanthine to uric acid with the concomitant reduction of NAD. Structurally,
this enzyme of about 1300 amino acids consists of at least three distinct
domains: an N-terminal 2Fe-2S ferredoxin-like iron-sulfur binding domain
15 (see <PDOC00175>), a central FAD/NAD-binding domain and a C-terminal Mo-
pterin domain.

- Aldehyde oxidase (EC 1.2.3.1), which catalyzes the oxidation aldehydes into
acids. Aldehyde oxidase is highly similar to xanthine dehydrogenase in its
sequence and domain structure.

20 - Nitrate reductase (EC 1.6.6.1), which catalyzes the reduction of nitrate
to nitrite. Structurally, this enzyme of about 900 amino acids consists of
an N-terminal Mo-pterin domain, a central cytochrome b5-type heme-binding
domain (see <PDOC00170>) and a C-terminal FAD/NAD-binding cytochrome
reductase domain.

25 - Sulfite oxidase (EC 1.8.3.1), which catalyzes the oxidation of sulfite to
sulfate. Structurally, this enzyme of about 460 amino acids consists of an
N-terminal cytochrome b5-binding domain followed by a Mo-pterin domain.

30 There are a few conserved regions in the sequence of the molybdopterin-binding
domain of these enzymes. The pattern used to detect these proteins is based
on one of them. It contains a cysteine residue which could be involved in
binding the molybdopterin cofactor.

677

Consensus pattern[GA]-x(3)-[KRNQHT SEQ ID NO:396)]-x(11,14)-[LIVMFYWS SEQ ID NO:301)]-x(8)-[LIVMF SEQ ID NO:2)]-x-C-x(2)-[DEN]-R-x(2)-[DE]

5 [1]

Wootton J.C., Nicolson R.E., Cock J.M., Walters D.E., Burke J.F., Doyle W.A., Bray R.C.

Biochim. Biophys. Acta 1057:157-185(1991).

10 811. (DNA_ligase) ATP-dependent DNA ligase signatures

PROSITE cross-reference(s): PS00697; DNA_LIGASE_A1, PS00333; DNA_LIGASE_A2

15 DNA ligase (polydeoxyribonucleotide synthase) is the enzyme that joins two DNA fragments by catalyzing the formation of an internucleotide ester bond between phosphate and deoxyribose. It is active during DNA replication, DNA repair and DNA recombination. There are two forms of DNA ligase: one requires ATP (EC 6.5.1.1), the other NAD (EC 6.5.1.2).

20 Eukaryotic, archaeobacterial, virus and phage DNA ligases are ATP-dependent. During the first step of the joining reaction, the ligase interacts with ATP to form a covalent enzyme-adenylate intermediate. A conserved lysine residue is the site of adenylation [1,2].

25 Apart from the active site region, the only conserved region common to all ATP-dependent DNA ligases is found [3] in the C-terminal section and contains a conserved glutamate as well as four positions with conserved basic residues.

Signature patterns were developed for both conserved regions.

30 Consensus pattern[EDQH SEQ ID NO:713)]-x-K-x-[DN]-G-x-R-[GACIVM SEQ ID NO:714)] [K is the active site residue]

678

Consensus patternE-G-[LIVMA SEQ ID NO:30)]-[LIVM SEQ ID NO:4)](2)-[KR]-x(5,8)-
[YW]-[QNEK SEQ ID NO:715)]-x(2,6)-

[KRH]-x(3,5)-K-[LIVMFY SEQ ID NO:18)]-K

Sequences known to belong to this class detected by the patternALL, except
5 for archebacterial DNA ligases.

[1]

Tomkinson A.E., Totty N.F., Ginsburg M., Lindahl T.
Proc. Natl. Acad. Sci. U.S.A. 88:400-404(1991).

10 [2]

Lindahl T., Barnes D.E.
Annu. Rev. Biochem. 61:251-281(1992).

[3]

Kletzin A.
15 Nucleic Acids Res. 20:5389-5396(1992).

812. (FAD_Gly3P_dh) FAD-dependent glycerol-3-phosphate dehydrogenase signatures
PROSITE cross-reference(s): PS00977; FAD_G3PDH_1, PS00978; FAD_G3PDH_2

20 FAD-dependent glycerol-3-phosphate dehydrogenase (EC 1.1.99.5) (GPD) catalyzes
the conversion of glycerol-3-phosphate into dihydroxyacetone phosphate. In
bacteria [1] it is associated with the utilization of glycerol coupled to
respiration. In Escherichia coli, two isozymes are known: one expressed under
anaerobic conditions (gene glpA) and one in aerobic conditions (gene glpD). In
25 eukaryotes, a mitochondrial form of GPD participates in the glycerol phosphate
shuttle in conjunction with an NAD-dependent cytoplasmic GPD (EC 1.1.1.8) [2,
3].

These enzymes are proteins of about 60 to 70 Kd which contain a probable
30 FAD-binding domain in their N-terminal extremity. The mammalian enzyme differs
from the bacterial or yeast proteins by having an EF-hand calcium-binding
region (See <PDOC00018>) in its C-terminal extremity.

Two signature patterns were developed. One based on the first half of the FAD-binding domain and one which corresponds to a conserved region in the central part of these enzymes.

5 Consensus pattern[IV]-G-G-G-x(2)-G-[STACV SEQ ID NO:146]-G-x-A-x-D-x(3)-R-G

Consensus patternG-G-K-x(2)-[GSTE SEQ ID NO:705]-Y-R-x(2)-A

[1]

Austin D., Larson T.J.

10 J. Bacteriol. 173:101-107(1991).

[2]

Roennow B., Kielland-Brandt M.C.

Yeast 9:1121-1130(1993).

[3]

15 Brown L.J., McDonald M.J., Lehn D.A., Moran S.M.

J. Biol. Chem. 269:14363-14366(1994).

813. (Fapy_DNA_glyco) Formamidopyrimidine-DNA glycosylase signature

PROSITE cross-reference(s): PS01242; FPG

20

Formamidopyrimidine-DNA glycosylase (EC 3.2.2.23) [1] (Fapy-DNA glycosylase) (gene fpg) is a bacterial enzyme involved in DNA repair and which excise oxidized purine bases to release 2,6-diamino-4-hydroxy-5N-methylformamido-pyrimidine (Fapy) and 7,8-dihydro-8-oxoguanine (8-OxoG) residues. In addition
25 to its glycosylase activity, FPG can also nick DNA at apurinic/apyrimidinic sites (AP sites). FPG is a monomeric protein of about 32 Kd which binds and require zinc for its activity.

30

The binding site for zinc seems to be located in the C-terminal part of the enzyme where four conserved and essential [2] cysteines are located. A signature pattern was developed based on this region.

Consensus pattern C-x(2,4)-C-x-[GTAQ SEQ ID NO:716)]-x-[IV]-x(7)-R-[GSTAN SEQ ID NO:296)]-[STA]-x-[FYI]-C-x(2)-C-Q

[The four C's are putative zinc ligands]

5 [1]

Duwat P., de Oliveira R., Ehrlich S.D., Boiteux S.

Microbiology 141:411-417(1995).

[2]

O'Connor T.E., Graves R.J., Demurcia G., Castaing B., Laval J.

10 J. Biol. Chem. 268:9063-9070(1993).

814. (G_glu_transpept) Gamma-glutamyltranspeptidase signature

PROSITE cross-reference(s): PS00462; G_GLU_TRANSPEPTIDASE

15 Gamma-glutamyltranspeptidase (EC 2.3.2.2) (GGT) [1] catalyzes the transfer of the gamma-glutamyl moiety of glutathione to an acceptor that may be an amino acid, a peptide or water (forming glutamate). GGT plays a key role in the gamma-glutamyl cycle, a pathway for the synthesis and degradation of glutathione. In prokaryotes and eukaryotes, it is an enzyme that consists of
20 two polypeptide chains, a heavy and a light subunit, processed from a single chain precursor. The active site of GGT is known to be located in the light subunit.

The sequences of mammalian and bacterial GGT show a number of regions of
25 high similarity [2]. Pseudomonas cephalosporin acylases (EC 3.5.1.-) that convert 7-beta-(4-carboxybutanamido)-cephalosporanic acid (GL-7ACA) into 7-aminocephalosporanic acid (7ACA) and glutaric acid are evolutionary related to GGT and also show some GGT activity [3]. Like GGT, these GL-7ACA acylases, are also composed of two subunits.

30

One of the conserved regions correspond to the N-terminal extremity of the mature light chains of these enzymes. This region was used as a signature pattern.

Consensus patternT-[STA]-H-x-[ST]-[LIVMA SEQ ID NO:30)]-x(4)-G-[SN]-x-V-[STA]-x-T-x-T-[LIVM SEQ ID NO:4)]-[NE]-x(1,2)-[FY]-G

5

[1]

Tate S.S., Meister A.

Meth. Enzymol. 113:400-419(1985).

[2]

10

Suzuki H., Kumagai H., Echigo T., Tochikura T.

J. Bacteriol. 171:5169-5172(1989).

[3]

Ishiye M., Niwa M.

Biochim. Biophys. Acta 1132:233-239(1992).

15

815. G-protein gamma subunit profile

PROSITE cross-reference(s): PS50058; G_PROTEIN_GAMMA

20

Guanine nucleotide-binding proteins (G proteins) [1] act as intermediaries in the transduction of signals generated by transmembrane receptors. G proteins consist of three subunits (alpha, beta, and gamma). The alpha subunit binds to and hydrolyzes GTP; the functions of the beta and gamma subunits are less clear but they seem to be required for the replacement of GDP by GTP as well as for membrane anchoring and receptor recognition.

25

The gamma subunits are small proteins (from 70 to 110 residues) that are bound to the membrane via a isoprenyl group (either a farnesyl or a geranyl-geranyl) covalently linked to their C-terminus. In mammals there are at least 12 different isoforms of gamma subunits.

30

The *Caenorhabditis elegans* protein egl-10, which is a regulator of G-protein signalling, contains a G-protein gamma-like domain.

A profile was developed that spans the complete length of the gamma subunit.

[1]

- 5 Pennington S.R.
Protein Prof. 2:16-315(1995).

816. GNS1/SUR4 family signature

PROSITE cross-reference(s): PS01188; GNS1_SUR4

10

The following group of eukaryotic integral membrane proteins, whose exact function has not yet clearly been established, are evolutionary related [1]:

- Yeast GNS1 [2], a protein involved in synthesis of 1,3-beta-glucan.
- 15 - Yeast SUR4 (or APA1, SRE1) [3], a protein that could act in a glucose-signaling pathway that controls the expression of several genes that are transcriptionally regulated by glucose.
- Yeast hypothetical protein YJL196c.
- Caenorhabditis elegans hypothetical protein C40H1.4.
- 20 - Caenorhabditis elegans hypothetical protein D2024.3.

The proteins have from 290 to 435 amino acid residues. Structurally, they seem to be formed of three sections: a N-terminal region with two transmembrane domains, a central hydrophilic loop and a C-terminal region that contains from
25 one to three transmembrane domains. A conserved region that contains three histidines was selected as a signature pattern. This region is located in the hydrophilic loop.

Consensus pattern L-x-F-L-H-x-Y-H-H

30

[1]

Bairoch A.
Unpublished observations (1996).

[2]

El-Sherbeini M., Clemas J.A.

J. Bacteriol. 177:3227-3234(1995).

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5 Garcia-Arranz M., Maldonado A.M., Mazon M.J., Portillo F.

J. Biol. Chem. 269:18076-18082(1994).

817. Immunoglobulins and major histocompatibility complex proteins signature
PROSITE cross-reference(s): PS00290; IG_MHC

10

The basic structure of immunoglobulin (Ig) [1] molecules is a tetramer of two light chains and two heavy chains linked by disulfide bonds. There are two types of light chains: kappa and lambda, each composed of a constant domain (CL) and a variable domain (VL). There are five types of heavy chains: alpha, delta, epsilon, gamma and mu, all consisting of a variable domain (VH) and three (in alpha, delta and gamma) or four (in epsilon and mu) constant domains (CH1 to CH4).

15

The major histocompatibility complex (MHC) molecules are made of two chains.

20

In class I [2] the alpha chain is composed of three extracellular domains, a transmembrane region and a cytoplasmic tail. The beta chain (beta-2-microglobulin) is composed of a single extracellular domain. In class II [3], both the alpha and the beta chains are composed of two extracellular domains, a transmembrane region and a cytoplasmic tail.

25

It is known [4,5] that the Ig constant chain domains and a single extracellular domain in each type of MHC chains are related. These homologous domains are approximately one hundred amino acids long and include a conserved intradomain disulfide bond. A small pattern around the C-terminal cysteine is involved in this disulfide bond which can be used to detect these category of Ig related proteins.

30

Consensus pattern[FY]-x-C-x-[VA]-x-H-Sequences known to belong to this

class detected by the pattern: Ig heavy chains type Alpha C region : All, in CH2 and CH3. Ig heavy chains type Delta C region : All, in CH3. Ig heavy chains type Epsilon C region: All, in CH1, CH3 and CH4. Ig heavy chains type Gamma C region : All, in CH3 and also CH1 in some cases Ig heavy chains type Mu C region : All, in CH2, CH3 and CH4. Ig light chains type Kappa C region : In all CL except rabbit and Xenopus. Ig light chains type Lambda C region : In all CL except rabbit. MHC class I alpha chains : All, in alpha-3 domains, including in the cytomegalovirus MHC-1 homologous protein [6]. Beta-2-microglobulin : All. MHC class II alpha chains: All, in alpha-2 domains. MHC class II beta chains: All, in beta-2 domains.

[1]

Gough N.

Trends Biochem. Sci. 6:203-205(1981).

[2]

Klein J., Figueroa F.

Immunol. Today 7:41-44(1986).

[3]

Figueroa F., Klein J.

Immunol. Today 7:78-81(1986).

[4]

Orr H.T., Lancet D., Robb R.J., Lopez de Castro J.A., Strominger J.L.

Nature 282:266-270(1979).

[5]

Cushley W., Owen M.J.

Immunol. Today 4:88-92(1983).

[6]

Beck S., Barrel B.G.

Nature 331:269-272(1988).

818. (IGFBP) Insulin-like growth factor binding proteins signature

PROSITE cross-reference(s): PS00222; IGF_BINDING

The insulin-like growth factors (IGF-I and IGF-II) bind to specific binding proteins in extracellular fluids with high affinity [1,2,3]. These IGF-binding proteins (IGFBP) prolong the half-life of the IGFs and have been shown to either inhibit or stimulate the growth promoting effects of the IGFs on cells culture. They seem to alter the interaction of IGFs with their cell surface receptors. There are at least six different IGFBPs and they are structurally related.

The following growth-factor inducible proteins are structurally related to IGFBPs and could function as growth-factor binding proteins [4,5]:

- Mouse protein cyr61 and its probable chicken homolog, protein CEF-10.
- Human connective tissue growth factor (CTGF) and its mouse homolog, protein FISP-12.
- Vertebrate protein NOV.

As a signature pattern a conserved cysteine-rich region located in the N-terminal section of these proteins is used.

Consensus pattern G-C-[GS]-C-C-x(2)-C-A-x(6)-C

Sequences known to belong to this class detected by the pattern ALL, except for IGFBP-6's.

[1]

Rechler M.M.

Vitam. Horm. 47:1-114(1993).

[2] .

Shimasaki S., Ling N.

Prog. Growth Factor Res. 3:243-266(1991).

[3]

Clemmons D.R.

Trends Endocrinol. Metab. 1:412-417(1990).

[4]

Bradham D.M., Igarashi A., Potter R.L., Grotendorst G.R.

J. Cell Biol. 114:1285-1294(1991).

[5]

Maloisel V., Martinerie C., Dambrine G., Plassiart G., Brisac M., Crochet
J., Perbal B.

Mol. Cell. Biol. 12:10-21(1992).

819. LMWPc : Low molecular weight phosphotyrosine protein phosphatase

Number of members: 34

[1]Medline: 94329182, The crystal structure of a low-molecular-weight phosphotyrosine
protein phosphatase. Su XD, Taddei N, Stefani M, Ramponi G, Nordlund P; Nature
1994;370:575-578.

820. (myosin_head) ATP/GTP-binding site motif A (P-loop)

PROSITE cross-reference(s): PS00017; ATP_GTP_A

From sequence comparisons and crystallographic data analysis it has been shown
[1,2,3,4,5,6] that an appreciable proportion of proteins that bind ATP or GTP
share a number of more or less conserved sequence motifs. The best conserved
of these motifs is a glycine-rich region, which typically forms a flexible
loop between a beta-strand and an alpha-helix. This loop interacts with one of
the phosphate groups of the nucleotide. This sequence motif is generally
referred to as the 'A' consensus sequence [1] or the 'P-loop' [5].

There are numerous ATP- or GTP-binding proteins in which the P-loop is found.
A number of protein families for which the relevance of the
presence of such motif has been noted is listed below:

- ATP synthase alpha and beta subunits (see <PDOC00137>).
- Myosin heavy chains.
- Kinesin heavy chains and kinesin-like proteins (see <PDOC00343>).
- Dynamins and dynamin-like proteins (see <PDOC00362>).

- Guanylate kinase (see <PDOC00670>).
- Thymidine kinase (see <PDOC00524>).
- Thymidylate kinase (see <PDOC01034>).
- Shikimate kinase (see <PDOC00868>).
- 5 - Nitrogenase iron protein family (nifH/frxC) (see <PDOC00580>).
- ATP-binding proteins involved in 'active transport' (ABC transporters) [7] (see <PDOC00185>).
- DNA and RNA helicases [8,9,10].
- GTP-binding elongation factors (EF-Tu, EF-1alpha, EF-G, EF-2, etc.).
- 10 - Ras family of GTP-binding proteins (Ras, Rho, Rab, Ral, Ypt1, SEC4, etc.).
- Nuclear protein ran (see <PDOC00859>).
- ADP-ribosylation factors family (see <PDOC00781>).
- Bacterial dnaA protein (see <PDOC00771>).
- Bacterial recA protein (see <PDOC00131>).
- 15 - Bacterial recF protein (see <PDOC00539>).
- Guanine nucleotide-binding proteins alpha subunits (Gi, Gs, Gt, G0, etc.).
- DNA mismatch repair proteins mutS family (See <PDOC00388>).
- Bacterial type II secretion system protein E (see <PDOC00567>).
- 20 Not all ATP- or GTP-binding proteins are picked-up by this motif. A number of proteins escape detection because the structure of their ATP-binding site is completely different from that of the P-loop. Examples of such proteins are the E1-E2 ATPases or the glycolytic kinases. In other ATP- or GTP-binding proteins the flexible loop exists in a slightly different form; this is the
- 25 case for tubulins or protein kinases. A special mention must be reserved for adenylate kinase, in which there is a single deviation from the P-loop pattern: in the last position Gly is found instead of Ser or Thr.

Consensus pattern[AG]-x(4)-G-K-[ST]

30

[1]

Walker J.E., Saraste M., Runswick M.J., Gay N.J.
EMBO J. 1:945-951(1982).

[2]

Moller W., Amons R.

FEBS Lett. 186:1-7(1985).

[3]

5 Fry D.C., Kuby S.A., Mildvan A.S.

Proc. Natl. Acad. Sci. U.S.A. 83:907-911(1986).

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Dever T.E., Glynias M.J., Merrick W.C.

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10 [5]

Saraste M., Sibbald P.R., Wittinghofer A.

Trends Biochem. Sci. 15:430-434(1990).

[6]

Koonin E.V.

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[7]

Higgins C.F., Hyde S.C., Mimmack M.M., Gileadi U., Gill D.R., Gallagher M.P.

J. Bioenerg. Biomembr. 22:571-592(1990).

20 [8]

Hodgman T.C.

Nature 333:22-23(1988) and Nature 333:578-578(1988) (Errata).

[9]

Linder P., Lasko P., Ashburner M., Leroy P., Nielsen P.J., Nishi K.,

25 Schnier J., Slonimski P.P.

Nature 337:121-122(1989).

[10]

Gorbalenya A.E., Koonin E.V., Donchenko A.P., Blinov V.M.

Nucleic Acids Res. 17:4713-4730(1989).

30

821. PE: PE family

This family named after a PE motif near to the amino terminus of the domain. The PE family of proteins all contain an amino-terminal region of about 110 amino acids. The carboxyl

terminus of this family are variable and fall into several classes. The largest class of PE proteins is the highly repetitive PGRS class which have a high glycine content. The function of these proteins is uncertain but it has been suggested that they may be related to antigenic variation of *Mycobacterium tuberculosis* [1]. Number of members: 88

5

[1] Medline: 98295987. Deciphering the biology of *Mycobacterium tuberculosis* from the complete genome sequence. Cole ST, Brosch R, Parkhill J, Garnier T, Churcher C, Harris D, Gordon SV, Eiglmeier K, Gas S, Barry CE 3rd, Tekaia F, Badcock K, Basham D, Brown D, Chillingworth T, Connor R, Davies R, Devlin K, Feltwell T, Gentles S, Hamlin N, Holroyd S, Hornsby T, Jagels K, Barrell BG, et al; Nature 1998;393:537-544.

10

822. (RNB) Ribonuclease II family signature

PROSITE cross-reference(s): PS01175; RIBONUCLEASE_II

15

On the basis of sequence similarities, the following bacterial and eukaryotic proteins seem to form a family:

- *Escherichia coli* and related bacteria ribonuclease II (EC 3.1.13.1) (RNase II) (gene *rnb*) [1]. RNase II is an exonuclease involved in mRNA decay. It degrades mRNA by hydrolyzing single-stranded polyribonucleotides processively in the 3' to 5' direction.

20

- Bacterial protein *vacB*. In *Shigella flexneri*, *vacB* has been shown to be required for the expression of virulence genes at the posttranscriptional level.

25

- Yeast protein SSD1 (or SRK1) which is implicated in the control of the cell cycle G1 phase.

- Yeast protein DIS3 [2], which binds to ran (GSP1) and enhances the nucleotide-releasing activity of RCC1 on ran.

- Fission yeast protein *dis3*, which is implicated in mitotic control.

30

- *Neurospora crassa* *cyt-4*, a mitochondrial protein required for RNA 5' and 3' end processing and splicing.

- Yeast protein MSU1, which is involved in mitochondrial biogenesis.

- *Synechocystis* strain PCC 6803 protein *zam* [3], which control resistance to

the carbonic anhydrase inhibitor acetazolamide.

- *Caenorhabditis elegans* hypothetical protein F48E8.6.

The size of these proteins range from 644 residues (rnb) to 1250 (SSD1). While their sequence is highly divergent they share a conserved domain in their C-terminal section [4]. It is possible that this domain plays a role in a putative exonuclease function that would be common to all these proteins. A signature pattern was developed based on the core of this conserved domain.

Consensus pattern[HI]-[FYE]-[GSTAM SEQ ID NO:32)]-[LIVM SEQ ID NO:4)]-x(4,5)-Y-[STAL SEQ ID NO:471)]-x-[FWVAC SEQ ID NO:717)]-[TV]-[SA]-P-[LIVMA SEQ ID NO:30)]-[RQ]-[KR]-[FY]-x-D-x(3)-[HQ]

[1]

Zilhao R., Camelo L., Arraiano C.M.

Mol. Microbiol. 8:43-51(1993).

[2]

Noguchi E., Hayashi N., Azuma Y., Seki T., Nakamura M., Nakashima N., Yanagida M., He X., Mueller U., Sazer S., Nishimoto T.

EMBO J. 15:5595-5605(1996).

[3]

Beuf L., Bedu S., Cami B., Joset F.

Plant Mol. Biol. 27:779-788(1995).

[4]

Mian I.S.

Nucleic Acids Res. 25:3187-3195(1997).

823. Src homology 2 (SH2) domain profile

PROSITE cross-reference(s): PS50001; SH2

30

The Src homology 2 (SH2) domain is a protein domain of about 100 amino-acid residues first identified as a conserved sequence region between the oncoproteins Src and Fps [1]. Similar sequences were later found in many other

intracellular signal-transducing proteins [2]. SH2 domains function as regulatory modules of intracellular signalling cascades by interacting with high affinity to phosphotyrosine-containing target peptides in a sequence-specific and strictly phosphorylation-dependent manner [3,4,5,6].

5

The SH2 domain has a conserved 3D structure consisting of two alpha helices and six to seven beta-strands. The core of the domain is formed by a continuous beta-meander composed of two connected beta-sheets [7].

10

So far, SH2 domains have been identified in the following proteins:

- Many vertebrate, invertebrate and retroviral cytoplasmic (non-receptor) protein tyrosine kinases. In particular in the Src, Abl, Bcr, Csk and ZAP70 families of kinases.

15

- Mammalian phosphatidylinositol-specific phospholipase C gamma-1 and -2. Two copies of the SH2 domain are found in those proteins in between the catalytic 'X-' and 'Y-boxes' (see <PDOC50007>).

- Mammalian phosphatidylinositol 3-kinase regulatory p85 subunit.

- Some vertebrate and invertebrate protein-tyrosine phosphatases.

20

- Mammalian Ras GTPase-activating protein (GAP).

- Adaptor proteins mediating binding of guanine nucleotide exchange factors to growth factor receptors: vertebrate GRB2, Caenorhabditis elegans sem-5 and Drosophila DRK.

- Mammalian Vav oncoprotein, a guanine-nucleotide exchange factor of the CDC24 family.

25

- Miscellaneous proteins interacting with vertebrate receptor protein tyrosine kinases: oncoprotein Crk, mammalian cytoplasmic proteins Nck, Shc.

- STAT proteins (signal transducers and activators of transcription).

- Chicken tensin.

30

- Yeast transcriptional control protein SPT6.

The profile developed to detect SH2 domains is based on a structural alignment consisting of 8 gap-free blocks and 7 linker regions totaling 92 match

positions.

[1]

Sadowski I., Stone J.C., Pawson T.

5 Mol. Cell. Biol. 6:4396-4408(1986).

[2]

Russel R.B., Breed J., Barton G.J.

FEBS Lett. 304:15-20(1992).

[3]

10 Marangere L.E.M., Pawson T.

J. Cell Sci. Suppl. 18:97-104(1994).

[4]

Pawson T., Schlessinger J.

Curr. Biol. 3:434-442(1993).

15 [5]

Mayer B.J., Baltimore D.

Trends Cell. Biol. 3:8-13(1993).

[6]

Pawson T.

20 Nature 373:573-580(1995).

[7]

Kuriyan J., Cowburn D.

Curr. Opin. Struct. Biol. 3:828-837(1993).

25 824. Sulfate transporters signature

PROSITE cross-reference(s): PS01130; SULFATE_TRANSP

A number of proteins involved in the transport of sulfate across a membrane
as well as some yet uncharacterized proteins have been shown [1,2] to be

30 evolutionary related. These proteins are:

- Neurospora crassa sulfate permease II (gene cys-14).

- Yeast sulfate permeases (genes SUL1 and SUL2).

- Rat sulfate anion transporter 1 (SAT-1).
- Mammalian DTDST, a probable sulfate transporter which, in Human, is involved in the genetic disease, diastrophic dysplasia (DTD).
- Sulfate transporters 1, 2 and 3 from the legume *Stylosanthes hamata*.

5

- Human pendrin (gene PDS), which is involved in a number of hearing loss genetic diseases.
- Human protein DRA (Down-Regulated in Adenoma).
- Soybean early nodulin 70.
- *Escherichia coli* hypothetical protein ychM.
- *Caenorhabditis elegans* hypothetical protein F41D9.5.

10

As expected by their transport function, these proteins are highly hydrophobic and seem to contain about 12 transmembrane domains. The best conserved region seems to be located in the second transmembrane region and is used as a signature pattern.

15

Consensus pattern[PAV]-x-Y-[GS]-L-Y-[STAG SEQ ID NO:20]](2)-x(4)-[LIVFYA SEQ ID NO:718)]-[LIVST SEQ ID NO:474)]-[YI]-
x(3)-[GA]-[GST]-S-[KR]

20

[1]

Sandal N.N., Marcker K.A.

Trends Biochem. Sci. 19:19-19(1994).

25

[2]

Smith F.W., Hawkesford M.J., Prosser I.M., Clarkson D.T.

Mol. Gen. Genet. 247:709-715(1995).

825. TYA: TYA transposon protein

30

Ty are yeast transposons. A 5.7kb transcript codes for p3 a fusion protein of TYA and TYB. The TYA protein is analogous to the gag protein of retroviruses. TYA a is cleaved to form 46kd protein which can form mature virion like particles [1]. Number of members: 59

[1] Medline: 97404699. Cryo-electron microscopy structure of yeast Ty retrotransposon virus-like particles. Palmer KJ, Tichelaar W, Myers N, Burns NR, Butcher SJ, Kingsman AJ, Fuller SD, Saibil HR; J Virol 1997;71:6863-6868.

5 826. Aldolase_II

Class II Aldolase and Adducin N-terminal domain.

-!- This family includes class II aldolases and adducins which have not been ascribed any enzymatic function. Number of members: 37

10 References:

[1] Medline: 93294819. The spatial structure of the class II L-fucose-1-phosphate aldolase from Escherichia coli. Dreyer MK, Schulz GE; J Mol Biol 1993;231:549-553.

[2] Medline: 96256522. Catalytic mechanism of the metal-dependent fucose aldolase from Escherichia coli as derived from the structure. Dreyer MK, Schulz GE; J Mol Biol

15 1996;259:458-466.

827. CBD_2

-!- Two tryptophan residues are involved in cellulose binding.

-!- Cellulose binding domain found in bacteria. Number of members: 51

20

References:

[1] Medline: 95284032. Solution structure of a cellulose-binding domain from Cellulomonas fimi by nuclear magnetic resonance spectroscopy. Xu GY, Ong E, Gilkes NR, Kilburn DG, Muhandiram DR, Harris-Brandts M, Carver JP, Kay LE, Harvey TS; Biochemistry

25 1995;34:6993-7009.

828. P

A unique feature of the eukaryotic subtilisin-like proprotein convertases is the presence of an additional highly conserved sequence of approximately 150 residues (P domain) located

30 immediately downstream of the catalytic domain.

Number of members: 91

References:

[1] Medline: 94252314. A C-terminal domain conserved in precursor processing proteases is required for intramolecular N-terminal maturation of pro-Kex2 protease. Gluschkof P, Fuller RS; EMBO J 1994;13:2280-2288.

[2] Medline: 98225190. Regulatory roles of the P domain of the subtilisin-like prohormone convertases. Zhou A, Martin S, Lipkind G, LaMendola J, Steiner DF; J Biol Chem 1998;273:11107-11114.

829. Uncharacterized protein family UPF0020 signature

PROSITE cross-reference(s): PS01261; UPF0020

The following uncharacterized proteins have been shown [1] to share regions of similarities:

- Escherichia coli hypothetical protein ycbY and HI0116/15, the corresponding Haemophilus influenzae protein.

- Bacillus subtilis hypothetical protein ypsC.

- Synechocystis strain PCC 6803 hypothetical protein slr0064.

- Methanococcus jannaschii hypothetical proteins MJ0438 and MJ0710.

These are hydrophilic proteins of from 40 Kd to about 80 Kd. They can be picked up in the database by the following pattern.

Consensus patternD-P-[LIVMF SEQ ID NO:2)]-C-G-[ST]-G-x(3)-[LI]-E

References:

[1] Bairoch A. Unpublished observations (1997).

830. Uncharacterized protein family UPF0031 signatures

PROSITE cross-reference(s): PS01049; UPF0031_1; PS01050; UPF0031_2

The following uncharacterized proteins have been shown [1] to share regions of similarities:

- Yeast chromosome XI hypothetical protein YKL151c.

- Caenorhabditis elegans hypothetical protein R107.2.

696

- Escherichia coli hypothetical protein yjeF.
- Bacillus subtilis hypothetical protein yxkO.
- Helicobacter pylori hypothetical protein HP1363.
- Mycobacterium tuberculosis hypothetical protein MtCY77.05c.
- 5 - Mycobacterium leprae hypothetical protein B229_C2_201.
- Synechocystis strain PCC 6803 hypothetical protein sl1433.
- Methanococcus jannaschii hypothetical protein MJ1586.

10 These are proteins of about 30 to 40 Kd whose central region is well conserved. They can be picked up in the database by the following patterns.

Consensus pattern[SAV]-[IVW]-[LVA]-[LIV]-G-[PNS]-G-L-[GP]-x-[DENQT SEQ ID NO:719)]

Consensus pattern[GA]-G-x-G-D-[TV]-[LT]-[STA]-G-x-[LIVM SEQ ID NO:4)]

15

831. (ACOX)

Acyl-CoA oxidase

20 This is a family of Acyl-CoA oxidases EC:1.3.3.6. Acyl-coA oxidase converts acyl-CoA into trans-2-enoyl-CoA [1].

Number of members: 39

25 [1] Hayashi H, De Bellis L, Yamaguchi K, Kato A, Hayashi M, Nishimura M; Medline: 98192624. "Molecular characterization of a glyoxysomal long chain acyl-CoA oxidase that is synthesized as a precursor of higher molecular mass in pumpkin." J Biol Chem 1998;273:8301-8307.

30 832. (AICARFT_IMPCHas)
AICARFT/IMPCHase bienzyme

This is a family of bifunctional enzymes catalysing the last steps in de novo purine biosynthesis. The bifunctional enzyme is found in both prokaryotes and eukaryotes. The second last step is catalysed by 5-aminoimidazole-4-carboxamide ribonucleotide formyltransferase EC:2.1.2.3 (AICARFT), this enzyme catalyses the formylation of AICAR with 10-formyl-tetrahydrofolate to yield FAICAR and tetrahydrofolate [1]. The last step is catalysed by IMP (Inosine monophosphate) cyclohydrolase EC:3.5.4.10 (IMPCHase), cyclizing FAICAR (5-formylaminoimidazole-4-carboxamide ribonucleotide) to IMP [1].

Number of members: 22

[1] Akira T, Komatsu M, Nango R, Tomooka A, Konaka K, Yamauchi M, Kitamura Y, Nomura S, Tsukamoto I; Medline: 97473523 "Molecular cloning and expression of a rat cDNA encoding 5-aminoimidazole-4-carboxamide ribonucleotide formyltransferase/IMP cyclohydrolase" [published erratum appears in Gene 1998 Feb 27;208(2):337] Gene 1997;197:289-293.

[2] Rayl EA, Moroson BA, Beardsley GP; Medline: 96147205 "The human purH gene product, 5-aminoimidazole-4-carboxamide ribonucleotide formyltransferase/IMP cyclohydrolase. Cloning, sequencing, expression, purification, kinetic analysis, and domain mapping." J Biol Chem 1996;271:2225-2233.

833. (AOX)

Alternative oxidase

The alternative oxidase is used as a second terminal oxidase in the mitochondria, electrons are transferred directly from reduced ubiquinol to oxygen forming water [2]. This is not coupled to ATP synthesis and is not inhibited by cyanide, this pathway is a single step process [1]. In rice the transcript levels of the alternative oxidase are increased by low temperature [1].

Number of members: 27

[1] Ito Y, Saisho D, Nakazono M, Tsutsumi N, Hirai A; Medline: 98086211 "Transcript levels of tandem-arranged alternative oxidase genes in rice are increased by low temperature." Gene 1997;203:121-129.

- 5 [2] Li Q, Ritzel RG, McLean LL, McIntosh L, Ko T, Bertrand H, Nargang FE; Medline: 96366413 "Cloning and analysis of the alternative oxidase gene of *Neurospora crassa*." Genetics 1996;142:129-140.

10 834. (APH)

Protein kinases signatures and profile

Cross-reference(s): PS00107; PROTEIN_KINASE_ATP, PS00108;
PROTEIN_KINASE_ST, PS00109; PROTEIN_KINASE_TYR, PS50011;

15 PROTEIN_KINASE_DOM

Eukaryotic protein kinases [1 to 5] are enzymes that belong to a very extensive family of proteins which share a conserved catalytic core common to both serine/threonine and tyrosine protein kinases. There are a number of conserved regions in the catalytic domain of protein
20 kinases. Two of these regions have been selected to build signature patterns. The first region, which is located in the N-terminal extremity of the catalytic domain, is a glycine-rich stretch of residues in the vicinity of a lysine residue, which has been shown to be involved in ATP binding. The second region, which is located in the central part of the catalytic domain,
25 contains a conserved aspartic acid residue which is important for the catalytic activity of the enzyme [6]; two signature patterns were derived for that region: one specific for serine/threonine kinases and the other for tyrosine kinases. A profile was developed which is based on the alignment in [1] and covers the entire catalytic domain.

30 Consensus pattern: [LIV]-G-{P}-G-{P}-[FYWMGSTNH SEQ ID NO:441]-[SGA]-{PW}-[LIVCAT SEQ ID NO:442]-{PD}-x-[GSTACLIVMFY SEQ ID NO:443]-x(5,18)-[LIVMFYWCSTAR SEQ ID NO:444]-[AIVP SEQ ID NO:445]-[LIVMFAGCKR SEQ ID NO:446]-K [K binds ATP]

Sequences known to belong to this class detected by the pattern the majority of known protein kinases but it fails to find a number of them, especially viral kinases which are quite divergent in this region and are completely missed by this pattern.

- 5 Consensus pattern: [LIVMFYC SEQ ID NO:6)]-x-[HY]-x-D-[LIVMFY SEQ ID NO:18)]-K-x(2)-N-[LIVMFYCT SEQ ID NO:447)](3) [D is an active site residue]

10 Sequences known to belong to this class detected by the pattern. Most serine/ threonine specific protein kinases with 10 exceptions (half of them viral kinases) and also Epstein-Barr virus BGLF4 and Drosophila ninaC which have respectively Ser and Arg instead of the conserved Lys and which are therefore detected by the tyrosine kinase specific pattern described below.

- 15 Consensus pattern: [LIVMFYC SEQ ID NO:6)]-x-[HY]-x-D-[LIVMFY SEQ ID NO:18)]-[RSTAC SEQ ID NO:448)]-x(2)-N-[LIVMFYC SEQ ID NO:6)](3) [D is an active site residue] tyrosine specific protein kinases with the exception of human ERBB3 and mouse blk. This pattern will also detect most bacterial aminoglycoside phosphotransferases [8,9] and herpesviruses ganciclovir kinases [10]; which are proteins structurally and evolutionary related to protein kinases. Sequences known to belong to this class detected by the profile
- 20 ALL, except for three viral kinases. This profile also detects receptor guanylate cyclases (see <PDOC00430>) and 2-5A-dependent ribonucleases. Sequence similarities between these two families and the eukaryotic protein kinase family have been noticed before. It also detects Arabidopsis thaliana kinase- like protein TMKL1 which seems to have lost its catalytic activity.

- 25 Note if a protein analyzed includes the two protein kinase signatures, the probability of it being a protein kinase is close to 100%. Note eukaryotic-type protein kinases have also been found in prokaryotes such as Myxococcus xanthus [11] and Yersinia pseudotuberculosis. Note the patterns shown above has been updated since their publication in [7]. Note this
- 30 documentation entry is linked to both signature patterns and a profile. As the profile is much more sensitive than the patterns, you should use it if you have access to the necessary software tools to do so.

References

- [1] Hanks S.K., Hunter T., FASEB J. 9:576-596(1995).
[2] Hunter T., Meth. Enzymol. 200:3-37(1991).
[3] Hanks S.K., Quinn A.M., Meth. Enzymol. 200:38-62(1991).
5 [4] Hanks S.K., Curr. Opin. Struct. Biol. 1:369-383(1991).
[5] Hanks S.K., Quinn A.M., Hunter T., Science 241:42-52(1988).
[6] Knighton D.R., Zheng J., Ten Eyck L.F., Ashford V.A., Xuong N.-H., Taylor, S.S.,
Sowadski J.M., Science 253:407-414(1991).
[7] Bairoch A., Claverie J.-M., Nature 331:22(1988).
10 [8] Benner S., Nature 329:21-21(1987).
[9] Kirby R., J. Mol. Evol. 30:489-492(1992).
[10] Littler E., Stuart A.D., Chee M.S., Nature 358:160-162(1992).
[11] Munoz-Dorado J., Inouye S., Inouye M., Cell 67:995-1006(1991).

15

835. (Asp_Glu_race)

Aspartate and glutamate racemases signatures

Cross-reference(s) PS00923; ASP_GLU_RACEMASE_1 PS00924;

20 ASP_GLU_RACEMASE_2

Aspartate racemase (EC 5.1.1.13) and glutamate racemase (EC 5.1.1.3) are two evolutionary related bacterial enzymes that do not seem to require a cofactor for their activity [1].

25 Glutamate racemase, which interconverts L-glutamate into D-glutamate, is required for the biosynthesis of peptidoglycan and some peptide-based antibiotics such as gramicidin S. In addition to characterized aspartate and glutamate racemases, this family also includes a hypothetical protein from Erwinia carotovora and one from Escherichia coli (ygeA). Two conserved cysteines are present in the sequence of these enzymes. They are expected to play a role in catalytic activity by acting as bases in proton abstraction from the substrate.

30 Signature patterns were developed for both cysteines.

Consensus pattern: [IVA]-[LIVM SEQ ID NO:4)]-x-C-x(0,1)-N-[ST]-[MSA]-[STH]-
[LIVFYSTANK SEQ ID NO:720)]

Consensus pattern: [LIVM SEQ ID NO:4])(2)-x-[AG]-C-T-[DEH]-[LIVMFY SEQ ID NO:18)]-[PNGRS SEQ ID NO:721)]-x-[LIVM SEQ ID NO:4]

- 5 [1] Gallo K.A., Knowles J.R., Biochemistry 32:3981-3990(1993).

836. (ATP-sulfurylase)

ATP-sulfurylase

10

This family consists of ATP-sulfurylase or sulfate adenylyltransferase EC:2.7.7.4 some of which are part of a bifunctional polypeptide chain associated with adenosyl phosphosulphate (APS) kinase APS_kinase. Both enzymes are required for PAPS (phosphoadenosine-phosphosulfate) synthesis from inorganic sulphate [2]. ATP sulfurylase catalyses the
15 synthesis of adenosine-phosphosulfate APS from ATP and inorganic sulphate [1].

Number of members: 37

- [1] Kurima K, Warman ML, Krishnan S, Domowicz M, Krueger RC Jr, Deyrup A, Schwartz
20 NB; Medline: 98337975 "A member of a family of sulfate-activating enzymes causes murine brachymorphism" [published erratum appears in Proc Natl Acad Sci U S A 1998 Sep 29;95(20):12071] Proc Natl Acad Sci U S A 1998;95:8681-8685.

- [2] Rosenthal E, Leustek T; Medline: 96096529 "A multifunctional Urechis caupo protein,
25 PAPS synthetase, has both ATP sulfurylase and APS kinase activities." Gene 1995;165:243-248.

837. (ATP-synt_F)

30 ATP synthase (F/14-kDa) subunit

This family includes 14-kDa subunit from vATPases [1], which is in the peripheral catalytic part of the complex [2]. The family also includes archaeobacterial ATP synthase subunit F [3].

Number of members: 23

[1] Guo Y, Kaiser K, Wieczorek H, Dow JA; Medline: 96269411 "The *Drosophila* melanogaster gene *vha14* encoding a 14-kDa F-subunit of the vacuolar ATPase." *Gene* 1996;172:239-243.

[2] Peng SB, Crider BP, Tsai SJ, Xie XS, Stone DK; Medline: 96216416 "Identification of a 14-kDa subunit associated with the catalytic sector of clathrin-coated vesicle H⁺-ATPase." *J Biol Chem* 1996;271:3324-3327.

[3] Wilms R, Freiberg C, Wegerle E, Meier I, Mayer F, Muller V; Medline: 96324968 "Subunit structure and organization of the genes of the A1A0 ATPase from the Archaeon *Methanosarcina mazei* Go1." *J Biol Chem* 1996;271:18843-18852.

838. (CBD_4)

Starch binding domain

Number of members: 48

839. (CbiX)

The function of CbiX is uncertain, however it is found in cobalamin biosynthesis operons and so may have a related function. Some CbiX proteins contain a striking histidine-rich region at their C-terminus, which suggests that it might be involved in metal chelation [1].

Number of members: 6

[1] Raux E, Lanois A, Warren MJ, Rambach A, Thermes C; Medline: 98416126 "Cobalamin (vitamin B12) biosynthesis: identification and characterization of a *Bacillus megaterium* cobI operon." *Biochem J* 1998;335:159-166.

840. (Complex1_51K)

Respiratory-chain NADH dehydrogenase 51 Kd subunit signatures Cross-reference(s)
PS00644; COMPLEX1_51K_1 PS00645; COMPLEX1_51K_2

5

Respiratory-chain NADH dehydrogenase (EC 1.6.5.3) [1,2] (also known as complex I or NADH-ubiquinone oxidoreductase) is an oligomeric enzymatic complex located in the inner mitochondrial membrane which also seems to exist in the chloroplast and in cyanobacteria (as a NADH-plastoquinone oxidoreductase). Among the 25 to 30 polypeptide subunits of this bioenergetic enzyme complex there is one with a molecular weight of 51 Kd (in mammals), which is the second largest subunit of complex I and is a component of the iron-sulfur (IP) fragment of the enzyme. It seems to bind to NAD, FMN, and a 2Fe-2S cluster.

10

The 51 Kd subunit is highly similar to [3,4]:

15

- Subunit alpha of *Alcaligenes eutrophus* NAD-reducing hydrogenase (gene *hoxF*) which also binds to NAD, FMN, and a 2Fe-2S cluster.
- Subunit NQO1 of *Paracoccus denitrificans* NADH-ubiquinone oxidoreductase.
- Subunit F of *Escherichia coli* NADH-ubiquinone oxidoreductase (gene *nuoF*).

20

The 51 Kd subunit and the bacterial hydrogenase alpha subunit contains three regions of sequence similarities. The first one most probably corresponds to the NAD-binding site, the second to the FMN-binding site, and the third one, which contains three cysteines, to the iron-sulfur binding region. Signature patterns have been developed for the FMN-binding and for the 2Fe-2S binding regions.

25

Consensus pattern: G-[AM]-G-[AR]-Y-[LIVM SEQ ID NO:4]-C-G-[DE](2)-[STA](2)-[LIM](2)-[EN]- S

Consensus pattern: E-S-C-G-x-C-x-P-C-R-x-G [The three C's are putative 2Fe-2S ligands]

30

[1] Ragan C.I., Curr. Top. Bioenerg. 15:1-36(1987).

[2] Weiss H., Friedrich T., Hofhaus G., Preis D., Eur. J. Biochem. 197:563-576(1991).

[3] Fearnley I.M., Walker J.E. Biochim. Biophys. Acta 1140:105-134(1992).

[4] Weidner U., Geier S., Ptock A., Friedrich T., Leif H., Weiss H., J. Mol. Biol. 233:109-122(1993).

5 841. (DAP_epimerase)

Diaminopimelate epimerase signature

Cross-reference(s) PS01326; DAP_EPIMERASE

10 Diaminopimelate epimerase (EC 5.1.1.7) catalyzes the isomeriazation of L,L- to D,L-meso-diaminopimelate in the biosynthetic pathway leading from aspartate to lysine. This enzyme is a protein of about 30 Kd. Two conserved cysteines seem [1] to function as the acid and base in the catalytic mechanism. As a signature pattern, the region surrounding the first of these two active site cysteines were selected.

15 Consensus pattern: N-x-D-G-S-x(4)-C-G-N-[GA]-x-R [C is an active site residue] Sequences known to belong to this class detected by the pattern ALL, except for an Anabaena dapF which has a Ser instead of the active site Cys.

20 [1] Cirilli M., Zheng R., Scapin G., Blanchard J.S., Biochemistry 37:16452-16458(1998).

842. (DNA_gyraseB_C)

DNA topoisomerase II signature

25 Cross-reference(s) PS00177; TOPOISOMERASE_II

30 DNA topoisomerase I (EC 5.99.1.2) [1,2,3,4,E1] is one of the two types of enzyme that catalyze the interconversion of topological DNA isomers. Type II topoisomerases are ATP-dependent and act by passing a DNA segment through a transient double-strand break. Topoisomerase II is found in phages, archaebacteria, prokaryotes, eukaryotes, and in African Swine Fever virus (ASF). In bacteriophage T4 topoisomerase II consists of three subunits (the product of genes 39, 52 and 60). In prokaryotes and in archaebacteria the enzyme, known as DNA gyrase, consists of two subunits (genes gyrA and gyrB [E2]). In some bacteria, a second type II topoisomerase has been identified; it is known as

topoisomerase IV and is required for chromosome segregation, it also consists of two subunits (genes parC and parE). In eukaryotes, type II topoisomerase is a homodimer.

There are many regions of sequence homology between the different subtypes of topoisomerase II. The relation between the different subunits is shown in the following representation:

<-----About-1400-residues----->

```

10  [-----Protein 39-*-----][----Protein 52----]      Phage T4
    [-----gyrB-----*-----][-----gyrA-----]  Prokaryote II
                                Archaeobacteria
    [-----parE-----*-----][-----parD-----]  Prokaryote IV
    [-----*-----] Eukaryote and
15                                ASF

```

'*': Position of the pattern.

As a signature pattern for this family of proteins, a region that contains a highly conserved pentapeptide was selected. The pattern is located in gyrB, in parE, and in protein 39 of phage T4 topoisomerase.

Consensus pattern: [LIVMA SEQ ID NO:30)]-x-E-G-[DN]-S-A-x-[STAG SEQ ID NO:20)]

[1] Sternglanz R., Curr. Opin. Cell Biol. 1:533-535(1990).

[2] Bjornsti M.-A., Curr. Opin. Struct. Biol. 1:99-103(1991).

[3] Sharma A., Mondragon A., Curr. Opin. Struct. Biol. 5:39-47(1995).

[4] Roca J., Trends Biochem. Sci. 20:156-160(1995).

843. (DUF16)

Protein of unknown function

The function of this protein is unknown. It appears to only occur in *Mycoplasma pneumoniae*.

Number of members: 26

5

[1] Himmelreich R, Hilbert H, Plagens H, Pirkl E, Li BC, Herrmann R; Medline: 97105885
"Complete sequence analysis of the genome of the bacterium *Mycoplasma pneumoniae*."
Nucleic Acids Res 1996;24:4420-4449.

10

844. (DUF21)

Domain of unknown function

15

This transmembrane region has no known function. Many of the sequences in this family are annotated as hemolysins, however this is due to a similarity to Swiss:Q54318 that does not contain this domain. This domain is found in the N-terminus of the proteins adjacent to two intracellular CBS domains CBS.

20

Number of members: 42

845. (DUF56)

25

Integral membrane protein

The members of this family are putative integral membrane proteins. The function of the family is unknown, however the family includes Sec59 from yeast. Sec59 is a dolichol kinase EC:2.7.1.108, but it is not clear if the enzymatic activity resides in this region or its N terminal region.

30

Number of members: 13

846. (DUF94)

Domain of unknown function

5

The function of this domain is unknown. It is found in both eukaryotes and archaeobacteria. The alignment contains a completely conserved aspartate residue that may be functionally important. The eukaryotic domains contains three conserved cysteines and a histidine that might be metal binding, however these are absent in the archaeobacterial proteins.

10

Number of members: 9

847. (FF)

15

FF domain

This domain may be involved in protein-protein interaction [1].

20

Number of members: 42

[1] Bedford MT, Leder P; Medline: 99322199 "The FF domain: a novel motif that often accompanies WW domains." Trends Biochem Sci 1999;24:264-265.

25

848. (FLO_LFY)

Floricaula / Leafy protein

30

This family consists of various plant development proteins which are homologues of floricaula (FLO) and Leafy (LFY) proteins which are floral meristem identity proteins. Mutations in the sequences of these proteins affect flower and leaf development.

Number of members: 16

[1] Hofer J, Turner L, Hellens R, Ambrose M, Matthews P, Michael A, Ellis N; Medline: 97411151 "UNIFOLIATA regulates leaf and flower morphogenesis in pea." Curr Biol 1997;7:581-587.

- 5 [2] Weigel D, Alvarez J, Smyth DR, Yanofsky MF, Meyerowitz EM; Medline: 92274452 "LEAFY controls floral meristem identity in Arabidopsis." Cell 1992;69:843-859.

849. (G-patch)

10 G-patch domain

This domain is found in a number of RNA binding proteins, and is also found in proteins that contain RNA binding domains. This suggests that this domain may have an RNA binding function. This domain has seven highly conserved glycines.

15

Number of members: 47

[1] Aravind L, Koonin EV; Medline: 10470032 "G-patch: a new conserved domain in eukaryotic RNA-processing proteins and type D retroviral polyproteins." Trends Biochem Sci 1999;24:342-344.

20

850. (Gram-ve_porins)

General diffusion Gram-negative porins signature

25

Cross-reference(s) PS00576; GRAM_NEG_PORIN

The outer membrane of Gram-negative bacteria acts as a molecular filter for hydrophilic compounds. Proteins, known as porins [1], are responsible for the 'molecular sieve' properties of the outer membrane. Porins form large water- filled channels which allows the diffusion of hydrophilic molecules into the periplasmic space. Some porins form general diffusion channels that allows any solutes up to a certain size (that size is known as the exclusion limit) to cross the membrane, while other porins are specific for a solute and contain a binding site for that solute inside the pores (these are known as selective porins). As porins are the major

30

outer membrane proteins, they also serve as receptor sites for the binding of phages and bacteriocins. General diffusion porins generally assemble as trimer in the membrane and the transmembrane core of these proteins is composed exclusively of beta strands [2]. It has been shown [3] that a number of general porins are evolutionary related, these porins are:

- 5 - Enterobacteria phoE.
- Enterobacteria ompC.
- Enterobacteria ompF.
- Enterobacteria nmpC.
- Bacteriophage PA-2 LC.
- 10 - Neisseria PI.A.
- Neisseria PI.B.

As a signature pattern a conserved region was selected, located in the C-terminal part of these proteins, which spans two putative transmembrane beta strands.

15 Consensus pattern: [LIVMFY SEQ ID NO:18)]-x(2)-G-x(2)-Y-x-F-x-K-x(2)-[SN]-[STAV SEQ ID NO:105)]-[LIVMFYW SEQ ID NO:26)]- V

[1] Benz R., Bauer K., Eur. J. Biochem. 176:1-19(1988).

20 [2] Jap B.K., Walian P.J., Q. Rev. Biophys. 23:367-403(1990).

[3] Jeanteur D., Lakey J.H., Pattus F., Mol. Microbiol. 5:2153-2164(1991).

851. (HlyD)

25 HlyD family secretion proteins signature

Cross-reference(s) PS00543; HLYD_FAMILY

Gram-negative bacteria produce a number of proteins which are secreted into the growth medium by a mechanism that does not require a cleaved N-terminal signal sequence. These proteins, while having different functions, require the help of two or more proteins for their secretion across the cell envelope. Amongst which a protein belonging to the ABC transporters family (see the relevant entry <PDOC00185>) and a protein belonging to a family which is currently composed [1 to 5] of the following members:

30

Gene	Species	Protein which is exported
hlyD	<i>Escherichia coli</i>	Hemolysin
appD	<i>A.pleuropneumoniae</i>	Hemolysin
5 lcnD	<i>Lactococcus lactis</i>	Lactococcin A
lktD	<i>A.actinomycetemcomitans</i>	Leukotoxin
	<i>Pasteurella haemolytica</i>	
rtxD	<i>A.pleuropneumoniae</i>	Toxin-III
cyaD	<i>Bordetella pertussis</i>	Calmodulin-sensitive adenylate cyclase-
10		hemolysin (cyclolysin)
cvaA	<i>Escherichia coli</i>	Colicin V
prtE	<i>Erwinia chrysanthemi</i>	Extracellular proteases B and C
aprE	<i>Pseudomonas aeruginosa</i>	Alkaline protease
emrA	<i>Escherichia coli</i>	Drugs and toxins
15 yjcR	<i>Escherichia coli</i>	Unknown

These proteins are evolutionary related and consist of from 390 to 480 amino acid residues. They seem to be anchored in the inner membrane by a N-terminal transmembrane region. Their exact role in the secretion process is not yet known. The C-terminal section of these proteins is the best conserved region; a signature pattern from that region was derived.

20 Consensus pattern: [LIVM SEQ ID NO:4)]-x(2)-G-[LM]-x(3)-[STGAV SEQ ID NO:722)]-x-[LIVMT SEQ ID NO:1)]-x-[LIVMT SEQ ID NO:1)]-[GE]-x-[KR]-x-[LIVMFYW SEQ ID NO:26)](2)-x-[LIVMFYW SEQ ID NO:26)](3)

Sequences known to belong to this class detected by the pattern ALL, except for emrA and
25 yjcR.

References:

- [1] Gilson L., Mahanty H.K., Kolter R., EMBO J. 9:3875-3884(1990).
- [2] Letoffe S., Delepelaire P., Wandersman C., EMBO J. 9:1375-1382(1990).
- 30 [3] Stoddard G.W., Petzel J.P., van Belkum M.J., Kok J., McKay L.L., Appl. Environ. Microbiol. 58:1952-1961(1992).
- [4] Duong F., Lazdunski A., Cami B., Murgier M., Gene 121:47-54(1992).
- [5] Lewis K., Trends Biochem. Sci. 19:119-123(1994).

852. (IBR)

In Between Ring fingers

5

The IBR (In Between Ring fingers) domain is found to occur between pairs of ring fingers (zf-C3HC4). The function of this domain is unknown. This domain has also been called the C6HC domain and DRIL (for double RING finger linked) domain [2].

Number of members: 25

10

[1] Morett E, Bork P; Medline: 10366851 "A novel transactivation domain in parkin." Trends Biochem Sci 1999;24:229-231.

[2] van der Reijden BA, Erpelinck-Verschueren CA, Lowenberg B, Jansen JH; Medline: 99349709 "TRIADs: a new class of proteins with a novel cysteine-rich signature." Protein Sci 1999;8:1557-1561.

15

853. (IPPT)

IPP transferase

20

[1] Durand JM, Bjork GR, Kuwae A, Yoshikawa M, Sasakawa C; Medline: 97440126 "The modified nucleoside 2-methylthio-N6-isopentenyladenosine in tRNA of *Shigella flexneri* is required for expression of virulence genes." J Bacteriol 1997;179:5777-5782.

[2] Boguta M, Hunter LA, Shen WC, Gillman EC, Martin NC, Hopper AK; Medline: 94187700 "Subcellular locations of MOD5 proteins: mapping of sequences sufficient for targeting to mitochondria and demonstration that mitochondrial and nuclear isoforms commingle in the cytosol." Mol Cell Biol 1994;14:2298-2306.

25

[3] Gillman EC, Slusher LB, Martin NC, Hopper AK; Medline: 91203856 "MOD5 translation initiation sites determine N6-isopentenyladenosine modification of mitochondrial and cytoplasmic tRNA." Mol Cell Biol 1991;11:2382-2390.

30

854. (KE2)

KE2 family protein

The function of members of this family is unknown, although they have been suggested to contain a DNA binding leucine zipper motif [2].

5

Number of members: 9

[1] Ha H, Abe K, Artzt K; Medline: 92084131 "Primary structure of the embryo-expressed gene KE2 from the mouse H-2K region." Gene 1991;107:345-346.

10

[2] Shang HS, Wong SM, Tan HM, Wu M; Medline: 95129859 "YKE2, a yeast nuclear gene encoding a protein showing homology to mouse KE2 and containing a putative leucine-zipper motif." Gene 1994;151:197-201.

15

855. (Lipoprotein_6)

Prokaryotic membrane lipoprotein lipid attachment site

Cross-reference(s) PS00013; PROKAR_LIPOPROTEIN

20

In prokaryotes, membrane lipoproteins are synthesized with a precursor signal peptide, which is cleaved by a specific lipoprotein signal peptidase (signal peptidase II). The peptidase recognizes a conserved sequence and cuts upstream of a cysteine residue to which a glyceride-fatty acid lipid is attached [1]. Some of the proteins known to undergo such processing currently include (for recent listings see [1,2,3]):

25

- Major outer membrane lipoprotein (murein-lipoproteins) (gene lpp).

- Escherichia coli lipoprotein-28 (gene nlpA).

- Escherichia coli lipoprotein-34 (gene nlpB).

- Escherichia coli lipoprotein nlpC.

- Escherichia coli lipoprotein nlpD.

- Escherichia coli osmotically inducible lipoprotein B (gene osmB).

30

- Escherichia coli osmotically inducible lipoprotein E (gene osmE).

- Escherichia coli peptidoglycan-associated lipoprotein (gene pal).

- Escherichia coli rare lipoproteins A and B (genes rplA and rplB).

- Escherichia coli copper homeostasis protein cutF (or nlpE).

- *Escherichia coli* plasmids traT proteins.
- *Escherichia coli* Col plasmids lysis proteins.
- A number of *Bacillus* beta-lactamases.
- *Bacillus subtilis* periplasmic oligopeptide-binding protein (gene oppA).
- 5 - *Borrelia burgdorferi* outer surface proteins A and B (genes ospA and ospB).
- *Borrelia hermsii* variable major protein 21 (gene vmp21) and 7 (gene vmp7).
- *Chlamydia trachomatis* outer membrane protein 3 (gene omp3).
- *Fibrobacter succinogenes* endoglucanase cel-3.
- *Haemophilus influenzae* proteins Pal and Pcp.
- 10 - *Klebsiella pullulunase* (gene pulA).
- *Klebsiella pullulunase* secretion protein pulS.
- *Mycoplasma hyorhinis* protein p37.
- *Mycoplasma hyorhinis* variant surface antigens A, B, and C (genes vlpABC).
- *Neisseria* outer membrane protein H.8.
- 15 - *Pseudomonas aeruginosa* lipopeptide (gene lppL).
- *Pseudomonas solanacearum* endoglucanase egl.
- *Rhodopseudomonas viridis* reaction center cytochrome subunit (gene cytC).
- *Rickettsia* 17 Kd antigen.
- *Shigella flexneri* invasion plasmid proteins mxiJ and mxiM.
- 20 - *Streptococcus pneumoniae* oligopeptide transport protein A (gene amiA).
- *Treponema pallidum* 34 Kd antigen.
- *Treponema pallidum* membrane protein A (gene tmpA).
- *Vibrio harveyi* chitobiase (gene chb).
- *Yersinia* virulence plasmid protein yscJ.
- 25 - Halocyanin from *Natrobacterium pharaonis* [4], a membrane associated copper-binding protein. This is the first archaeobacterial protein known to be modified in such a fashion).

From the precursor sequences of all these proteins, a consensus pattern and a set of rules to identify this type of post-translational modification were derived.

30

Consensus pattern: {DERK SEQ ID NO:354}}(6)-[LIVMFWSTAG SEQ ID NO:352)](2)-[LIVMFYSTAGCQ SEQ ID NO:353)]-[AGS]-C [C is the lipid attachment site] Additional rules: 1)

The cysteine must be between positions 15 and 35 of the sequence in consideration. 2) There must be at least one Lys or one Arg in the first seven positions of the sequence. Sequences known to belong to this class detected by the pattern ALL. Other sequence(s) detected in SWISS-PROT some 100 prokaryotic proteins. Some of them are not membrane lipoproteins, but at least half of them could be.

References

- [1] Hayashi S., Wu H.C., J. Bioenerg. Biomembr. 22:451-471(1990).
- [2] Klein P., Somorjai R.L., Lau P.C.K., Protein Eng. 2:15-20(1988).
- [3] von Heijne G., Protein Eng. 2:531-534(1989).
- [4] Mattar S., Scharf B., Kent S.B.H., Rodewald K., Oesterhelt D., Engelhard M. J. Biol. Chem. 269:14939-14945(1994).

856. (Lipoprotein_7)

Adhesin lipoprotein

This family consists of the p50 and variable adherence-associated antigen (Vaa) adhesins from *Mycoplasma hominis*. *M. hominis* is a mycoplasma associated with human urogenital diseases, pneumonia, and septic arthritis [1]. An adhesin is a cell surface molecule that mediates adhesion to other cells or to the surrounding surface or substrate. The Vaa antigen is a 50-kDa surface lipoprotein that has four tandem repetitive DNA sequences encoding a periodic peptide structure, and is highly immunogenic in the human host [1]. p50 is also a 50-kDa lipoprotein, having three repeats A,B and C, that may be a tetramer of 191-kDa in its native environment [2].

Number of members: 18

- [1] Zhang Q, Wise KS; Medline: 96294788 "Molecular basis of size and antigenic variation of a *Mycoplasma hominis* adhesin encoded by divergent vaa genes. " Infect Immun 1996;64:2737-2744.

[2] Henrich B, Kitzerow A, Feldmann RC, Schaal H, Hadding U; Medline: 97047675
"Repetitive elements of the Mycoplasma hominis adhesin p50 can be differentiated by
monoclonal antibodies." Infect Immun 1996;64:4027-4034.

5

857. (MaoC_like)

MaoC like domain

10

The MaoC protein is found to share similarity with a wide variety of enzymes; estradiol 17
beta-dehydrogenase 4, peroxisomal hydratase-dehydrogenase-epimerase, fatty acid synthase
beta subunit. All these enzymes contain other domains. This domain is also present in the
NodN nodulation protein N. No specific function has been assigned to this region of any of
these proteins. The maoC gene is part of a operon with maoA which is involved in the
synthesis of monoamine oxidase [1].

15

Number of members: 46

20

[1] Sugino H, Sasaki M, Azakami H, Yamashita M, Murooka Y Medline: 96235221 "A
monoamine-regulated Klebsiella aerogenes operon containing the monoamine oxidase
structural gene (maoA) and the maoC gene." J Bacteriol 1992;174:2485-2492.

25

858. (MSP)

Manganese-stabilizing protein / photosystem II polypeptide

This family consists of the 33 KDa photosystem II polypeptide from the oxygen evolving
complex (OEC) of plants and cyanobacteria. The protein is also known as the manganese-
stabilizing protein as it is associated with the manganese complex of the OEC and may
provide the ligands for the complex [1].

30

Number of members: 17

[1] Philbrick JB, Zilinskas BA; Medline: 88334494 "Cloning, nucleotide sequence and mutational analysis of the gene encoding the Photosystem II manganese-stabilizing polypeptide of *Synechocystis* 6803." *Mol Gen Genet* 1988;212:418-425.

5

859. (NAC)

[1] Makarova KS, Aravind L, Galperin MY, Grishin NV, Tatusov RL, Wolf YI, Koonin EV; Medline: 99342100 "Comparative genomics of the Archaea (Euryarchaeota): evolution of conserved protein families, the stable core, and the variable shell." *Genome Res* 1999;9:608-628.

10

Number of members: 27

15

860. (Nop)

Putative snoRNA binding domain

This family consists of various Pre RNA processing ribonucleoproteins. The function of the aligned region is unknown however it may be a common RNA or snoRNA or Nop1p binding domain. Nop5p (Nop58p) Swiss:Q12499 from yeast is the protein component of a ribonucleoprotein protein required for pre-18s rRNA processing and is suggested to function with Nop1p in a snoRNA complex [1]. Nop56p Swiss:O00567 and Nop5p interact with Nop1p and are required for ribosome biogenesis [2]. Prp31p Swiss:p49704 is required for pre-mRNA splicing in *S. cerevisiae* [3].

20

25

Number of members: 23

[1] Wu P, Brockenbrough JS, Metcalfe AC, Chen S, Aris JP; Medline: 98298165 "Nop5p is a small nucleolar ribonucleoprotein component required for pre- 18 S rRNA processing in yeast." *J Biol Chem* 1998;273:16453-16463.

30

[2] Gautier T, Berges T, Tollervey D, Hurt E; Medline: 8038777 "Nucleolar KKE/D repeat proteins Nop56p and Nop58p interact with Nop1p and are required for ribosome biogenesis." Mol Cell Biol 1997;17:7088-7098.

[3] Weidenhammer EM, Singh M, Ruiz-Noriega M, Woolford JL Jr; Medline: 96184869

5 "The PRP31 gene encodes a novel protein required for pre-mRNA splicing in *Saccharomyces cerevisiae*." Nucleic Acids Res 1996;24:1164-1170.

861. (Nramp)

10 Natural resistance-associated macrophage protein

The natural resistance-associated macrophage protein (NRAMP) family consists of Nramp1, Nramp2, and yeast proteins Smf1 and Smf2. The NRAMP family is a novel family of functional related proteins defined by a conserved hydrophobic core of ten transmembrane
15 domains [5]. This family of membrane proteins are divalent cation transporters. Nramp1 is an integral membrane protein expressed exclusively in cells of the immune system and is recruited to the membrane of a phagosome upon phagocytosis [1]. By controlling divalent cation concentrations Nramp1 may regulate the interphagosomal replication of bacteria [1]. Mutations in Nramp1 may genetically predispose an individual to susceptibility to diseases
20 including leprosy and tuberculosis conversely this might however provide protection form rheumatoid arthritis [1]. Nramp2 is a multiple divalent cation transporter for Fe²⁺, Mn²⁺ and Zn²⁺ amongst others it is expressed at high levels in the intestine; and is major transferrin-independent iron uptake system in mammals [1]. The yeast proteins Smf1 and Smf2 may also transport divalent cations [3].

25

Number of members: 36

[1] Govoni G, Gros P; Medline: 98383996 "Macrophage NRAMP1 and its role in resistance to microbial infections." Inflamm Res 1998;47:277-284.

30 [2] Agranoff DD, Krishna S Medline: 98294035 "Metal ion homeostasis and intracellular parasitism." Mol Microbiol 1998;28:403-412.

[3] Pinner E, Gruenheid S, Raymond M, Gros P; Medline: 98030569 "Functional complementation of the yeast divalent cation transporter family SMF by NRAMP2, a

member of the mammalian natural resistance- associated macrophage protein family." J Biol Chem 1997;272:28933-28938.

[4] Cellier M, Belouchi A, Gros P; Medline: 96402487 "Resistance to intracellular infections: comparative genomic analysis of Nramp." Trends Genet 1996;12:201-204.

- 5 [5] Cellier M, Prive G, Belouchi A, Kwan T, Rodrigues V, Chia W, Gros P; Medline: 96036029 "Nramp defines a family of membrane proteins." Proc Natl Acad Sci U S A 1995;92:10089-10093.

10 862. (NTP_transf_2)

Nucleotidyltransferase domain

Members of this family belong to a large family of nucleotidyltransferases [1].

15 Number of members: 83

[1] Holm L, Sander C; Medline: 96005605 "DNA polymerase beta belongs to an ancient nucleotidyltransferase superfamily." Trends Biochem Sci 1995;20:345-347.

20

863. (Paramyxo_P)

Paramyxovirus P phosphoprotein

This family consists of paramyxovirus P phosphoprotein from sendai virus and human and
 25 bovine parainfluenza viruses. The P protein is an essential part of the viral RNA polymerase complex formed from the P and L proteins [1]. The exact role of the P protein in this complex is unknown but it is involved in multiple protein-protein interactions and binding the polymerase complex to the nucleocapsid or ribonucleoprotein template [1]. It also appears to be important for the proper folding of the L protein [1]. The paramyxoviruses have a
 30 negative sense ssRNA genome [1].

Number of members: 15

[1] Bowman MC, Smallwood S, Moyer SA; Medline: 99329169 "Dissection of Individual Functions of the Sendai Virus Phosphoprotein in Transcription." J Virol 1999;73:6474-6483.

[2] Matsuoka Y, Curran J, Pelet T, Kolakofsky D, Ray R, Compans RW; Medline: 91237868 "The P gene of human parainfluenza virus type 1 encodes P and C proteins but not a cysteine-rich V protein." J Virol 1991;65:3406-3410.

864. (Patatin)

10 This family consists of various patatin glycoproteins from plants. The patatin protein accounts for up to 40% of the total soluble protein in potato tubers [2]. Patatin is a storage protein but it also has the enzymatic activity of lipid acyl hydrolase, catalysing the cleavage of fatty acids from membrane lipids [2].

15 Number of members: 21

[1] Banfalvi Z, Kostyal Z, Barta E; Medline: 95107249 "Solanum brevidens possesses a non-sucrose-inducible patatin gene." Mol Gen Genet 1994;245:517-522.

20 [2] Mignery GA, Pikaard CS, Park WD; Medline: 88226014 "Molecular characterization of the patatin multigene family of potato." Gene 1988;62:27-44.

865. (Pentapeptide_2)

Pentapeptide repeats (8 copies)

25

These repeats are found in many mycobacterial proteins. These repeats are most common in the PPE family of proteins, where they are found in the MPTR subfamily of PPE proteins.

The function of these repeats is unknown. The repeat can be approximately described as XNXGX, where X can be any amino acid. These repeats are similar to Pentapeptide [1],

30 however it is not clear if these two families are structurally related.

Number of members: 362

[1] Bateman A, Murzin A, Teichmann SA; Medline: 98318059 "Structure and distribution of pentapeptide repeats in bacteria." Protein Sci 1998;7:1477-1480.

[2] Cole ST, Brosch R, Parkhill J, Garnier T, Churcher C, Harris D, Gordon SV, Eiglmeier K, Gas S, Barry CE 3rd, Tekaia F, Badcock K, Basham D, Brown D, Chillingworth T, Connor R, Davies R, Devlin K, Feltwell T, Gentles S, Hamlin N, Holroyd S, Hornsby T, Jagels K, Barrell BG; Medline: 98295987 "Deciphering the biology of Mycobacterium tuberculosis from the complete genome sequence." Nature 1998;393:537-544.

866. (Peptidase_C13)

Peptidase C13 family

This family of peptidases is known as the hemoglobinase family because it contains a globin degrading enzyme from blood parasites Swiss:P42665. However relatives are found in plants and other organisms that have other functions. Members of this family are asparaginyl peptidases [1].

Number of members: 26

[1] Chen JM, Dando PM, Rawlings ND, Brown MA, Young NE, Stevens RA, Hewitt E, Watts C, Barrett AJ; Medline: 97218252 "Cloning, isolation, and characterization of mammalian legumain, an asparaginyl endopeptidase." J Biol Chem 1997;272:8090-8098.

867. (Pro_dh)

Proline dehydrogenase

Number of members: 25

[1] Ling M, Allen SW, Wood JM; Medline: 95055736 "Sequence analysis identifies the proline dehydrogenase and delta 1- pyrroline-5-carboxylate dehydrogenase domains of the multifunctional Escherichia coli PutA protein." J Mol Biol 1994;243:950-956.

868. (PsbP)

5 This family consists of the 23 kDa subunit of oxygen evolving system of photosystem II or PsbP from various plants (where it is encoded by the nuclear genome) and Cyanobacteria. The 23 KDa PsbP protein is required for PSII to be fully operational in vivo, it increases the affinity of the water oxidation site for Cl⁻ and provides the conditions required for high affinity binding of Ca²⁺ [2].

10 Number of members: 25

[1] Rova EM, Mc Ewen B, Fredriksson PO, Styring S; Medline: 97067138 "Photoactivation and photoinhibition are competing in a mutant of *Chlamydomonas reinhardtii* lacking the 23-kDa extrinsic subunit of photosystem II." J Biol Chem 1996;271:28918-28924.

15 [2] Kochhar A, Khurana JP, Tyagi AK; Medline: 97191538 "Nucleotide sequence of the psbP gene encoding precursor of 23-kDa polypeptide of oxygen-evolving complex in *Arabidopsis thaliana* and its expression in the wild-type and a constitutively photomorphogenic mutant." DNA Res 1996;3:277-285.

869. (PUA)

25 The PUA domain named after PseudoUridine synthase and Archaeosine transglycosylase, was detected in archaeal and eukaryotic pseudouridine synthases, archaeal archaeosine synthases, a family of predicted ATPases that may be involved in RNA modification, a family of predicted archaeal and bacterial rRNA methylases. Additionally, the PUA domain was detected in a family of eukaryotic proteins that also contain a domain homologous to the translation initiation factor eIF1/SUI1; these proteins may comprise a novel type of

30 translation factors. Unexpectedly, the PUA domain was detected also in bacterial and yeast glutamate kinases; this is compatible with the demonstrated role of these enzymes in the regulation of the expression of other genes [1]. It is predicted that the PUA domain is an RNA binding domain.

Number of members: 48

[1] Aravind L, Koonin EV; Medline: 99193178 "Novel predicted RNA-binding domains associated with the translation machinery." J Mol Evol 1999;48:291-302.

870. (RF1)

eRF1-like proteins

Members of this family are peptide chain release factors. The eukaryotic Release Factor 1 proteins (eRF1s) are involved in termination of translation. The eRF1 protein is functional for all stop codons and appears to abolish read-through of these codons. This family also includes other proteins for which the precise molecular function is unknown. Many of them are from Archaeobacteria. These proteins may also be involved in translation termination but this awaits experimental verification. Number of members: 25

[1] Frolova L, Le Goff X, Rasmussen HH, Cheperegin S, Drugeon G, Kress M, Arman I, Haenni AL, Celis JE, Philippe M, et al; Medline: 95082951 "A highly conserved eukaryotic protein family possessing properties of polypeptide chain release factor" [see comments] Nature 1994;372:701-703.

[2] Drugeon G, Jean-Jean O, Frolova L, Le Goff X, Philippe M, Kisselev L, Haenni AL; Medline: 97315314 "Eukaryotic release factor 1 (eRF1) abolishes readthrough and competes with suppressor tRNAs at all three termination codons in messenger RNA." Nucleic Acids Res 1997;25:2254-2258.

871. (Ribosomal_L14e)Ribosomal protein L14

This family includes the eukaryotic ribosomal protein L14.

Number of members: 15

872. (Ribosomal_S27)

Ribosomal protein S27a

This family of ribosomal proteins consists mainly of the 40S ribosomal protein S27a which is synthesized as a C-terminal extension of ubiquitin (CEP). The S27a domain comprises the C-terminal half of the protein. The synthesis of ribosomal proteins as extensions of ubiquitin promotes their incorporation into nascent ribosomes by a transient metabolic stabilization and is required for efficient ribosome biogenesis [3]. The ribosomal extension protein S27a contains a basic region that is proposed to form a zinc finger; its fusion gene is proposed as a mechanism to maintain a fixed ratio between ubiquitin necessary for degrading proteins and ribosomes a source of proteins [2].

Number of members: 36

873. (Spermine_synth)

Spermine/spermidine synthase

Spermine and spermidine are polyamines. This family includes spermidine synthase that catalyses the fifth (last) step in the biosynthesis of spermidine from arginine, and spermine synthase.

Number of members: 39

[1] Mezquita J, Pau M, Mezquita C; Medline: 97449308 "Characterization and expression of two chicken cDNAs encoding ubiquitin fused to ribosomal proteins of 52 and 80 amino acids." Gene 1997;195:313-319.

[2] Redman KL, Rechsteiner M; Medline: 89181932 "Identification of the long ubiquitin extension as ribosomal protein S27a." Nature 1989;338:438-440.

[3] Finley D, Bartel B, Varshavsky A; Medline: 89181925 "The tails of ubiquitin precursors are ribosomal proteins whose fusion to ubiquitin facilitates ribosome biogenesis." Nature 1989;338:394-401.

874. (Surp)

Surp module

[1] Denhez F, Lafyatis R; Medline: 94266805 "Conservation of regulated alternative splicing and identification of functional domains in vertebrate homologs to the Drosophila splicing regulator, suppressor-of-white-apricot." J Biol Chem 1994;269:16170-16179.

This domain is also known as the SWAP domain. SWAP stands for Suppressor-of-White-APricot. It has been suggested that these domains may be RNA binding [1].

Number of members: 32

875. (TFIIE)

TFIIE alpha subunit

The general transcription factor TFIIE has an essential role in eukaryotic transcription initiation together with RNA polymerase II and other general factors. Human TFIIE consists of two subunits TFIIE-alpha Swiss:P29083 and TFIIE-beta Swiss:P29084 and joins the preinitiation complex after RNA polymerase II and TFIIF [1]. This family consists of the conserved amino terminal region of eukaryotic TFIIE-alpha [2] and proteins from archaeobacteria that are presumed to be TFIIE-alpha subunits also Swiss:O29501 [3].

Number of members: 12

[1] Ohkuma Y, Sumimoto H, Hoffmann A, Shimasaki S, Horikoshi M, Roeder RG; Medline: 92065982 "Structural motifs and potential sigma homologies in the large subunit of human general transcription factor TFIIE." Nature 1991;354:398-401.

[2] Ohkuma Y, Hashimoto S, Roeder RG, Horikoshi M; Medline: 93087200 Identification of two large subdomains in TFIIE-alpha on the basis of homology between Xenopus and human sequences. Nucleic Acids Res 1992;20:5838-5838.

[3] Klenk HP, Clayton RA, Tomb JF, White O, Nelson KE, Ketchum KA, Dodson RJ, Gwinn M, Hickey EK, Peterson JD, Richardson DL, Kerlavage AR, Graham DE, Kyrpides NC,

Fleischmann RD, Quackenbush J, Lee NH, Sutton GG, Gill S, Kirkness EF, Dougherty BA, McKenney K, Adams MD, Loftus B, Venter JC, et al; Medline: 98049343 "The complete genome sequence of the hyperthermophilic, sulphate- reducing archaeon *Archaeoglobus fulgidus*." Nature 1997;390:364-370.

5

876. (Transglut_core)

Cross-reference(s) PS00547; TRANSGLUTAMINASES

10

Transglutaminases (EC 2.3.2.13) (TGase) [1,2] are calcium-dependent enzymes that catalyze the cross-linking of proteins by promoting the formation of isopeptide bonds between the gamma-carboxyl group of a glutamine in one polypeptide chain and the epsilon-amino group of a lysine in a second polypeptide chain. TGases also catalyze the conjugation of polyamines to proteins. The best known transglutaminase is blood coagulation factor XIII, a plasma tetrameric protein composed of two catalytic A subunits and two non-catalytic B subunits. Factor XIII is responsible for cross-linking fibrin chains, thus stabilizing the fibrin clot. Other forms of transglutaminases are widely distributed in various organs, tissues and body fluids. Sequence data is available for the following forms of TGase:

15

- 20 - Transglutaminase K (Tgase K), a membrane-bound enzyme found in mammalian epidermis and important for the formation of the cornified cell envelope (gene TGM1).
- Tissue transglutaminase (TGase C), a monomeric ubiquitous enzyme located in the cytoplasm (gene TGM2).
- Transglutaminase 3, responsible for the later stages of cell envelope formation in the
- 25 epidermis and the hair follicle (gene TGM3).
- Transglutaminase 4 (gene TGM4).

A conserved cysteine is known to be involved in the catalytic mechanism of TGases. The erythrocyte membrane band 4.2 protein, which probably plays an important role in regulating the shape of erythrocytes and their mechanical properties, is evolutionary related to TGases. However the active site cysteine is substituted by an alanine and the 4.2 protein does not show TGase activity.

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726

Consensus pattern:[GT]-Q-[CA]-W-V-x-[SA]-[GA]-[IVT]-x(2)-T-x-[LMSC SEQ ID NO:547)]-R-[CSA]-[LV]-G [The first C is the active site residue] Sequences known to belong to this class detected by the patternALL. Other sequence(s) detected in SWISS-PROT NONE.

5

[1] Ichinose A., Bottenus R.E., Davie E.W. J. Biol. Chem. 265:13411-13414(1990).

[2] Greenberg C.S., Birckbichler P.J., Rice R.H. FASEB J. 5:3071-3077(1991).

10 877. (TruB_N)

TruB family pseudouridylate synthase (N terminal domain)

Members of this family are involved in modifying bases in RNA molecules. They carry out the conversion of uracil bases to pseudouridine. This family includes TruB, a pseudouridylate synthase that specifically converts uracil 55 to pseudouridine in most tRNAs. This family also includes Cbf5p that modifies rRNA [2].

15

Number of members: 33

20 [1] Nurse K, Wrzesinski J, Bakin A, Lane BG, Ofengand J; Medline: 96079944 "Purification, cloning, and properties of the tRNA psi 55 synthase from Escherichia coli." RNA 1995;1:102-112.

[2] Lafontaine DLJ, Bouisquet-Antonelli C, Henry Y, Caizergues-Ferrer M, Tollervey D; Medline: 98139521 "The box H + ACA snoRNAs carry Cbf5p, the putative rRNA pseudouridine synthase." Genes Dev 1998;12:527-537.

25

878. (UDPGP)

UTP--glucose-1-phosphate uridylyltransferase

30

This family consists of UTP--glucose-1-phosphate uridylyltransferases, EC:2.7.7.9. Also known as UDP-glucose pyrophosphorylase (UDPGP) and Glucose-1-phosphate uridylyltransferase. UTP--glucose-1-phosphate uridylyltransferase catalyses the

interconversion of MgUTP + glucose-1-phosphate and UDP-glucose + MgPPi [1]. UDP-glucose is an important intermediate in mammalian carbohydrate interconversion involved in various metabolic roles depending on tissue type [1]. In Dictyostelium (slime mold) mutants in this enzyme abort the development cycle [2]. Also within the family is UDP-N-acetylglucosamine Swiss:Q16222 or AGX1 [3] and two hypothetical proteins from Borrelia burgdorferi the lyme disease spirochaete Swiss:O51893 and Swiss:O51036.

Number of members: 18

[1] Duggleby RG, Chao YC, Huang JG, Peng HL, Chang HY; Medline: 96202932 "Sequence differences between human muscle and liver cDNAs for UDPglucose pyrophosphorylase and kinetic properties of the recombinant enzymes expressed in Escherichia coli." Eur J Biochem 1996;235:173-179.

[2] Ragheb JA, Dottin RP; Medline: 87231075 "Structure and sequence of a UDP glucose pyrophosphorylase gene of Dictyostelium discoideum." Nucleic Acids Res 1987;15:3891-3906.

[3] Mio T, Yabe T, Arisawa M, Yamada-Okabe H; Medline: 98269105 "The eukaryotic UDP-N-acetylglucosamine pyrophosphorylases. Gene cloning, protein expression, and catalytic mechanism. J Biol Chem 1998;273:14392-14397.

879. (UPF004)

Uncharacterized protein family UPF0044 signature

Cross-reference(s) PS01301; UPF0044

The following uncharacterized proteins have been shown [1] to be highly similar:

- Bacillus subtilis hypothetical protein yqeI.
- Escherichia coli hypothetical protein yhbY and HI1333, the corresponding Haemophilus influenzae protein.
- Methanococcus jannaschii hypothetical protein MJ0652.

These are small proteins of 10 to 15 Kd. They can be picked up in the database by the following pattern. This pattern is located in the N-terminal part of these proteins.

Consensus pattern: L-[ST]-x(3)-K-x(3)-[KR]-[SGA]-x-[GA]-H-x-L-x-P-[LIV]-x(2)- [LIV]-[GA]-x(2)-G Sequences known to belong to this class detected by the patternALL. Other sequence(s) detected in SWISS-PROT/NONE.

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880. (zf-A20)

A20-like zinc finger

10 A20- (an inhibitor of cell death)-like zinc fingers. The zinc finger mediates self-association in A20. These fingers also mediate IL-1-induced NF-kappa B activation.

Number of members: 22

15 [1] Heyninck K, Beyaert R; Medline: 99126071 "The cytokine-inducible zinc finger protein A20 inhibits IL-1-induced NF- kappaB activation at the level of TRAF6. FEBS Lett 1999;442:147-150.

[2] De Valck D, Heyninck K, Van Crielinge W, Contreras R, Beyaert R, Fiers W; Medline: 96390831 "A20, an inhibitor of cell death, self-associates by its
20 zinc finger domain." FEBS Lett 1996;384:61-64.

[3] Song HY, Rothe M, Goeddel DV; Medline: 96270609 "The tumor necrosis factor-inducible zinc finger protein A20 interacts with TRAF1/TRAF2 and inhibits NF-kappaB activation. Proc Natl Acad Sci U S A 1996;93:6721-6725.

[4] Opipari AW Jr, Boguski MS, Dixit VM; Medline: 90368626 "The A20 cDNA induced by
25 tumor necrosis factor alpha encodes a novel type of zinc finger protein." J Biol Chem 1990;265:14705-14708.

881. (zf-PARP)

30 Poly(ADP-ribose) polymerase zinc finger domain

Cross-reference(s) PS00347; PARP_ZN_FINGER_1 PS50064; PARP_ZN_FINGER_2

729

Poly(ADP-ribose) polymerase (EC 2.4.2.30) (PARP) [1,2] is a eukaryotic enzyme that catalyzes the covalent attachment of ADP-ribose units from NAD(+) to various nuclear acceptor proteins. This post-translational modification of nuclear proteins is dependent on DNA. It appears to be involved in the regulation of various important cellular processes such as differentiation, proliferation and tumor transformation as well as in the regulation of the molecular events involved in the recovery of the cell from DNA damage. Structurally, PARP, about 1000 amino-acids residues long, consists of three distinct domains: an N-terminal zinc-dependent DNA-binding domain, a central automodification domain and a C-terminal NAD-binding domain. The DNA-binding region contains a pair of zinc finger domains which have been shown to bind DNA in a zinc-dependent manner. The zinc finger domains of PARP seem to bind specifically to single-stranded DNA. DNA ligase III [3] contains, in its N-terminal section, a single copy of a zinc finger highly similar to those of PARP.

Consensus pattern: C-[KR]-x-C-x(3)-I-x-K-x(3)-[RG]-x(16,18)-W-[FYH]-H-x(2)-C [The three C's and the H are zinc ligands] Sequences known to belong to this class detected by the patternALL. Other sequence(s) detected in SWISS-PROT NONE. Sequences known to belong to this class detected by the profile ALL. Other sequence(s) detected in SWISS-PROT NONE.

Note: This documentation entry is linked to both signature patterns and a profile. As the profile is much more sensitive than the patterns, you should use it if you have access to the necessary software tools to do so.

[1] Althaus F.R., Richter C.R. Mol. Biol. Biochem. Biophys. 37:1-126(1987).

[2] de Murcia G., Menissier de Murcia J. Trends Biochem. Sci. 19:172-176(1994).

[3] Wei Y.-F., Robins P., Carter K., Caldecott K., Pappin D.J.C., Yu G.-L., Wang R.-P., Shell B.K., Nash R.A., Schar P., Barnes D.E., Haseltine W.A., Lindahl T. Mol. Cell. Biol. 15:3206-3216(1995).

882. Adenylylsulfate kinase (APS_kinase)

Enzyme that catalyses the phosphorylation of adenylylsulfate to 3'-phosphoadenylylsulfate. This domain contains an ATP binding P-loop motif. Number of members: 34

[1] MacRae IJ, Rose AB, Segel IH; Medline: 99003196 "Adenosine 5'-phosphosulfate kinase from *Penicillium chrysogenum*. site- directed mutagenesis at putative phosphoryl-accepting and ATP P-loop residues. *J Biol Chem* 1998;273:28583-28589.

5

883. DNA polymerase family B signature DNA_POLYMERASE_B (DNA_pol_B)

Replicative DNA polymerases (EC 2.7.7.7) are the key enzymes catalyzing the accurate replication of DNA. They require either a small RNA molecule or a protein as a primer for the de novo synthesis of a DNA chain. On the basis of sequence similarity, a number of DNA polymerases have been grouped [1 to 7] under the designation of DNA polymerase family B. These are:

10

- Higher eukaryotes polymerases alpha.
- Higher eukaryotes polymerases delta.
- 15 - Yeast polymerase I/alpha (gene POL1), polymerase II/epsilon (gene POL2), polymerase III/delta (gene POL3) and polymerase REV3.
- *Escherichia coli* polymerase II (gene *dinA* or *polB*).
- Archaeobacterial polymerases.
- Polymerases of viruses from the herpesviridae family.
- 20 - Polymerases from Adenoviruses.
- Polymerases from Baculoviruses.
- Polymerases from Chlorella viruses.
- Polymerases from Poxviruses.
- Bacteriophage T4 polymerase.
- 25 - Podoviridae bacteriophages Phi-29, M2 and PZA polymerase.
- Tectiviridae bacteriophage PRD1 polymerase.
- Polymerases encoded on mitochondrial linear DNA plasmids in various fungi and plants (*Kluyveromyces lactis* pGKL1 and pGKL2, *Agaricus bitorquis* pEM, *Ascobolus immersus* pAI2, *Claviceps purpurea* pCLK1, *Neurospora Kalilo* and *Maranhar*, maize S-1, etc).

30

Six regions of similarity (numbered from I to VI) are found in all or a subset of the above polymerases. The most conserved region (I) includes a conserved tetrapeptide with two aspartate residues. Its function is not yet known. However, it has been suggested [3] that it

may be involved in binding a magnesium ion. This conserved region was selected as a signature for this family of DNA polymerases.

Consensus pattern [YA]-[GLIVMSTAC SEQ ID NO:723)]-D-T-D-[SG]-[LIVMFTC SEQ ID NO:724)]-x-[LIVMSTAC SEQ ID NO:151)] Sequences known to belong to this class detected by the patternALL, except for yeast polymerase II/epsilon, *Agaricus bitorquis* pEM and *Sulfolobus solfataricus* polymerase II.

[1] Jung G., Leavitt M.C., Hsieh J.-C., Ito J. Proc. Natl. Acad. Sci. U.S.A. 84:8287-8291(1987).

[2] Bernad A., Zaballos A., Salas M., Blanco L. EMBO J. 6:4219-4225(1987).

[3] Argos P. Nucleic Acids Res. 16:9909-9916(1988).

[4] Wang T.S.-F., Wong S.W., Korn D. FASEB J. 3:14-21(1989).

[5] Delarue M., Poch O., Todro N., Moras D., Argos P. Protein Eng. 3:461-467(1990).

[6] Ito J., Braithwaite D.K. Nucleic Acids Res. 19:4045-4057(1991).

[7] Braithwaite D.K., Ito J. Nucleic Acids Res. 21:787-802(1993).

884. DNA polymerase family X signature - DNA_POLYMERASE_X (DNA_polymeraseX)

DNA polymerases (EC 2.7.7.7) can be classified, on the basis of sequence similarity [1], into at least four different groups: A, B, C and X. DNA polymerases that belong to family X are listed below [2]:

- Vertebrate polymerase beta, involved in DNA repair.

- Yeast polymerase IV (POL4) [3], an enzyme with similar characteristics to that of the mammalian polymerase beta.

- Terminal deoxynucleotidyltransferase (TdT) (EC 2.7.7.31). TdT catalyzes the elongation of polydeoxynucleotide chains by terminal addition. One of the functions of this enzyme is the addition of nucleotides at the junction of rearranged Ig heavy chain and T cell receptor gene segments during the maturation of B and T cells.

- African Swine Fever virus protein O174L [4].

- Fission yeast hypothetical protein SpAC2F7.06c.

These enzymes are small (about 40 Kd) compared with other polymerases and their reaction mechanism operates via a distributive mode, i.e. they dissociate from the template-primer after addition of each nucleotide.

- 5 As a signature pattern for this family of DNA polymerases, a highly conserved region that contains a conserved arginine and two conserved aspartic acid residues were selected. The latter together with the arginine have been shown [5] to be involved in primer binding in polymerase beta.
- 10 Consensus pattern G-[SG]-[LFY]-x-R-[GE]-x(3)-[SGCL SEQ ID NO:725)]-x-D-[LIVM SEQ ID NO:4)]-D- [LIVMFY SEQ ID NO:18)](3)-x(2)-[SAP] Sequences known to belong to this class detected by the patternALL.
- [1] Ito J., Braithwaite D.K. Nucleic Acids Res. 19:4045-4057(1991).
- 15 [2] Matsukage A., Nishikawa K., Ooi T., Seto Y., Yamaguchi M. J. Biol. Chem. 262:8960-8962(1987).
- [3] Prasad R., Widen S.G., Singhal R.K., Watkins J., Prakash L., Wilson S.H. Nucleic Acids Res. 21:5301-5307(1993).
- [4] Yanez R.J., Rodriguez J.M., Nogal M.L., Yuste L., Enriquez C., Rodriguez J.F., Vinuela
- 20 E. Virology 208:249-278(1995).
- [5] Date T., Yamamoto S., Tanihara K., Nishimoto Y., Matsukage A. Biochemistry 30:5286-5292(1991).

885. DUF14 - Domain of unknown function

- 25 This domain is found in glutamate synthase, tungsten formylmethanofuran dehydrogenase subunit c (FwdC) and molybdenum formylmethanofuran dehydrogenase subunit c (FmdC). It has no known function. Number of members: 52
- [1] Hochheimer A, Hedderich R, Thauer RK; Medline: 99035764. "The formylmethanofuran dehydrogenase isoenzymes in Methanobacterium wolfei and Methanobacterium
- 30 thermoautotrophicum: induction of the molybdenum isoenzyme by molybdate and constitutive synthesis of the tungsten isoenzyme." Arch Microbiol 1998;170:389-393.

886. DUF18-Domain of unknown function

This domain of unknown function is found in several *C. elegans* proteins. The domain is 120 amino acids long and rich in cysteine residues. There are 16 conserved cysteine positions in the domain. Number of members: 34

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887. DUF27-Domain of unknown function

This domain is found in a number of otherwise unrelated proteins. This domain is found at the C-terminus of the macro-H2A histone protein Swiss:Q02874. This domain is found in the non-structural proteins of several types of ssRNA viruses such as NSP2 from alphaviruses Swiss:P03317. This domain is also found on its own in a family of proteins from bacteria Swiss:P75918, archaeobacteria Swiss:O59182 and eukaryotes Swiss:Q17432, suggesting that it is involved in an important and ubiquitous cellular process. Number of members: 66

10

888. DUF37-Domain of unknown function

This domain is found in short (70 amino acid) hypothetical proteins from various bacteria. The domain contains three conserved cysteine residues. Swiss:Q44066 from *Aeromonas hydrophila* has been found to have hemolytic activity (unpublished). Number of members: 19

15

889. EGF-like domain signatures. (EGF-like)

A sequence of about thirty to forty amino-acid residues long found in the sequence of epidermal growth factor (EGF) has been shown [1 to 6] to be present, in a more or less conserved form, in a large number of other, mostly animal proteins. The proteins currently known to contain one or more copies of an EGF-like pattern are listed below.

20

- Adipocyte differentiation inhibitor (gene PREF-1) from mouse (6 copies).
- Agrin, a basal lamina protein that causes the aggregation of acetylcholine receptors on cultured muscle fibers (4 copies).
- Amphiregulin, a growth factor (1 copy).
- Betacellulin, a growth factor (1 copy).
- Blastula proteins BP10 and Span from sea urchin which are thought to be involved in pattern formation (1 copy).
- BM86, a glycoprotein antigen of cattle tick (7 copies).

25

30

- Bone morphogenic protein 1 (BMP-1), a protein which induces cartilage and bone formation and which expresses metalloendopeptidase activity (1-2 copies). Homologous proteins are found in sea urchin - suBMP (1 copy) - and in Drosophila - the dorsal-ventral patterning protein tolloid (2 copies).
- 5 - Caenorhabditis elegans developmental proteins lin-12 (13 copies) and glp-1 (10 copies).
- Caenorhabditis elegans APX-1 protein, a patterning protein (4.5 copies).
- Calcium-dependent serine proteinase (CASP) which degrades the extracellular matrix proteins type I and IV collagen and fibronectin (1 copy).
- Cartilage matrix protein CMP (1 copy).
- 10 - Cartilage oligomeric matrix protein COMP (4 copies).
- Cell surface antigen 114/A10 (3 copies).
- Cell surface glycoprotein complex transmembrane subunit ASGP-2 from rat (2 copies).
- Coagulation associated proteins C, Z (2 copies) and S (4 copies).
- Coagulation factors VII, IX, X and XII (2 copies).
- 15 - Complement C1r components (1 copy).
- Complement C1s components (1 copy).
- Complement-activating component of Ra-reactive factor (RARF) (1 copy).
- Complement components C6, C7, C8 alpha and beta chains, and C9 (1 copy).
- Crumbs, an epithelial development protein from Drosophila (29 copies).
- 20 - Epidermal growth factor precursor (7-9 copies).
- Exogastrula-inducing peptides A, C, D and X from sea urchin (1 copy).
- Fat protein, a Drosophila cadherin-related tumor suppressor (5 copies).
- Fetal antigen 1, a probable neuroendocrine differentiation protein, which is derived from the delta-like protein (DLK) (6 copies).
- 25 - Fibrillin 1 (47 copies) and fibrillin 2 (14 copies).
- Fibropellins IA (21 copies), IB (13 copies), IC (8 copies), II (4 copies) and III (8 copies) from the apical lamina - a component of the extracellular matrix - of sea urchin.
- Fibulin-1 and -2, two extracellular matrix proteins (9-11 copies).
- Giant-lens protein (protein Argos), which regulates cell determination and axon guidance in the Drosophila eye (1 copy).
- 30 - Growth factor-related proteins from various poxviruses (1 copy).
- Gurken protein, a Drosophila developmental protein (1 copy).

- Heparin-binding EGF-like growth factor (HB-EGF), transforming growth factor alpha (TGF-alpha), growth factors Lin-3 and Spitz (1 copy); the precursors are membrane proteins, the mature form is located extracellular.
- Hepatocyte growth factor (HGF) activator (EC 3.4.21.-) (2 copies).
- 5 - LDL and VLDL receptors, which bind and transport low-density lipoproteins and very low-density lipoproteins (3 copies).
- LDL receptor-related protein (LRP), which may act as a receptor for endocytosis of extracellular ligands (22 copies).
- Leucocyte antigen CD97 (3 copies), cell surface glycoprotein EMR1 (6 copies) and cell
- 10 surface glycoprotein F4/80 (7 copies).
- Limulus clotting factor C, which is involved in hemostasis and host defense mechanisms in japanese horseshoe crab (1 copy).
- Meprin A alpha subunit, a mammalian membrane-bound endopeptidase (1 copy).
- Milk fat globule-EGF factor 8 (MFG-E8) from mouse (2 copies).
- 15 - Neuregulin GGF-I and GGF-II, two human glial growth factors (1 copy).
- Neurexins from mammals (3 copies).
- Neurogenic proteins Notch, Xotch and the human homolog Tan-1 (36 copies), Delta (9 copies) and the similar differentiation proteins Lag-2 from *Caenorhabditis elegans* (2 copies), Serrate (14 copies) and Slit (7 copies) from *Drosophila*.
- 20 - Nidogen (also called entactin), a basement membrane protein from chordates (2-6 copies).
- Ookinete surface proteins (24 Kd, 25 Kd, 28 Kd) from *Plasmodium* (4 copies).
- Pancreatic secretory granule membrane major glycoprotein GP2 (1 copy).
- Perforin, which lyses non-specifically a variety of target cells (1 copy).
- Proteoglycans aggrecan (1 copy), versican (2 copies), perlecan (at least 2 copies), brevican
- 25 (1 copy) and chondroitin sulfate proteoglycan (gene PG-M) (2 copies).
- Prostaglandin G/H synthase 1 and 2 (EC 1.14.99.1) (1 copy), which is found in the endoplasmatic reticulum.
- S1-5, a human extracellular protein whose ultimate activity is probably modulated by the environment (5 copies).
- 30 - Schwannoma-derived growth factor (SDGF), an autocrine growth factor as well as a mitogen for different target cells (1 copy).
- Selectins. Cell adhesion proteins such as ELAM-1 (E-selectin), GMP-140 (P-selectin), or the lymph-node homing receptor (L-selectin) (1 copy).

- Serine/threonine-protein kinase homolog (gene Pro25) from *Arabidopsis thaliana*, which may be involved in assembly or regulation of light-harvesting chlorophyll A/B protein (2 copies).
- Sperm-egg fusion proteins PH-30 alpha and beta from guinea pig (1 copy).
- 5 - Stromal cell derived protein-1 (SCP-1) from mouse (6 copies).
- TDGF-1, human teratocarcinoma-derived growth factor 1 (1 copy).
- Tenascin (or neuronectin), an extracellular matrix protein from mammals (14.5 copies), chicken (TEN-A) (13.5 copies) and the related proteins human tenascin-X (18 copies) and tenascin-like proteins TEN-A and TEN-M from *Drosophila* (8 copies).
- 10 - Thrombomodulin (fetomodulin), which together with thrombin activates protein C (6 copies).
- Thrombospondin 1, 2 (3 copies), 3 and 4 (4 copies), adhesive glycoproteins that mediate cell-to-cell and cell-to-matrix interactions.
- Thyroid peroxidase 1 and 2 (EC 1.11.1.8) from human (1 copy).
- 15 - Transforming growth factor beta-1 binding protein (TGF-B1-BP) (16 or 18 copies).
- Tyrosine-protein kinase receptors Tek and Tie (EC 2.7.1.112) (3 copies).
- Urokinase-type plasminogen activator (EC 3.4.21.73) (UPA) and tissue plasminogen activator (EC 3.4.21.68) (TPA) (1 copy).
- Uromodulin (Tamm-horsfall urinary glycoprotein) (THP) (3 copies).
- 20 - Vitamin K-dependent anticoagulants protein C (2 copies) and protein S (4 copies) and the similar protein Z, a single-chain plasma glycoprotein of unknown function (2 copies).
- 63 Kd sperm flagellar membrane protein from sea urchin (3 copies).
- 93 Kd protein (gene nel) from chicken (5 copies).
- Hypothetical 337.6 Kd protein T20G5.3 from *Caenorhabditis elegans* (44 copies).

25

The functional significance of EGF domains in what appear to be unrelated proteins is not yet clear. However, a common feature is that these repeats are found in the extracellular domain of membrane-bound proteins or in proteins known to be secreted (exception: prostaglandin G/H synthase). The EGF domain includes six cysteine residues which have been shown (in

30 EGF) to be involved in disulfide bonds. The main structure is a two-stranded beta-sheet followed by a loop to a C-terminal short two-stranded sheet. Subdomains between the conserved cysteines strongly vary in length as shown in the following schematic representation of the EGF-like domain:

737

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      +-----+      +-----+      |      |      |
| x(4)-C-x(0,48)-C-x(3,12)-C-x(1,70)-C-x(1,6)-C-x(2)-G-a-x(0,21)-G-x(2)-C-x  |
| *****
      +-----+

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5

'C': conserved cysteine involved in a disulfide bond.

'G': often conserved glycine

'a': often conserved aromatic amino acid

'*': position of both patterns.

10 'x': any residue

The region between the 5th and 6th cysteine contains two conserved glycines of which at least one is present in most EGF-like domains. Two patterns were created for this domain, each including one of these C-terminal conserved glycine residues.

15

Consensus pattern: C-x-C-x(5)-G-x(2)-C [The 3 C's are involved in disulfide bonds]

Sequences known to belong to this class detected by the pattern A majority, but not those that have very long or very short regions between the last 3 conserved cysteines of their EGF-like domain(s). Other sequence(s) detected in SWISS-PROT87 proteins, of which 27 can be considered as possible candidates.

20

Consensus pattern: C-x-C-x(2)-[GP]-[FYW]-x(4,8)-C [The three C's are involved in disulfide bonds] Sequences known to belong to this class detected by the pattern A majority, but not those that have very long or very short regions between the last 3 conserved cysteines of their EGF-like domain(s). Other sequence(s) detected in SWISS-PROT83 proteins, of which 49 can be considered as possible candidates. Note The beta chain of the integrin family of proteins contains 2 cysteine- rich repeats which were said to be dissimilar with the EGF pattern [7].

25

30 Note Laminin EGF-like repeats (see <PDOC00961>) are longer than the average EGF module and contain a further disulfide bond C-terminal of the EGF-like region. Perlecan and agrin contain both EGF-like domains and laminin-type EGF-like domains. Note the pattern do not detect all of the repeats of proteins with multiple EGF-like repeats. Note see

<PDOC00913> for an entry describing specifically the subset of EGF- like domains that bind calcium.

[1] Davis C.G. New Biol. 2:410-419(1990).

5 [2] Blomquist M.C., Hunt L.T., Barker W.C. Proc. Natl. Acad. Sci. U.S.A. 81:7363-7367(1984).

[3] Barker W.C., Johnson G.C., Hunt L.T., George D.G. Protein Nucl. Acid Enz. 29:54-68(1986).

[4] Doolittle R.F., Feng D.F., Johnson M.S. Nature 307:558-560(1984).

10 [5] Appella E., Weber I.T., Blasi F. FEBS Lett. 231:1-4(1988).

[6] Campbell I.D., Bork P. Curr. Opin. Struct. Biol. 3:385-392(1993).

[7] Tamkun J.W., DeSimone D.W., Fonda D., Patel R.S., Buck C., Horwitz A.F., Hynes R.O. Cell 46:271-282(1986).

15

890. Ham1 family (Ham1p_like)

This family consists of the HAM1 protein Swiss:P47119 and hypothetical archaeal bacterial and C. elegans proteins. HAM1 controls 6-N-hydroxylaminopurine (HAP) sensitivity and mutagenesis in S. cerevisiae Swiss:P47119 [1]. The HAM1 protein protects the cell from
20 HAP, either on the level of deoxynucleoside triphosphate or the DNA level by a yet unidentified set of reactions [1]. Number of members: 19

[1] Noskov VN, Staak K, Shcherbakova PV, Kozmin SG, Negishi K, Ono BC, Hayatsu H, Pavlov YI; Medline: 96381244 "HAM1, the gene controlling 6-N-hydroxylaminopurine
25 sensitivity and mutagenesis in the yeast Saccharomyces cerevisiae." Yeast 1996;12:17-29.

891. (HCO3_cotransp)

Anion exchange is a cellular transport function which contributes to the regulation of cell pH
30 and volume. Anion exchangers are a family of functionally related proteins that contributes to these properties by maintaining the intracellular level of the two principal anions: chloride and HCO3-. The best characterized anion exchanger is the band 3 protein [1], which is an erythrocyte anion exchange membrane glycoprotein. Band 3 is a protein of about 900 amino

acids which consists of a cytoplasmic N-terminal domain of about 400 residues and an hydrophobic C-terminal section of about 500 residues that contains at least ten transmembrane regions. The cytoplasmic domain provides binding sites for cytoskeletal proteins, while the integral membrane domain is responsible for anion transport. Band 3 protein is specific to erythroid cells, at least two other proteins [2] structurally and functionally related to band 3, are found in nonerythroid tissues:

- AE2 (or B3 related protein; B3RP), a protein of 1200 residues, which seems to be present in a variety of cell types including lymphoid, kidney, and choroid plexus.
- AE3, a protein of 1200 residues, which is specific to neurons.

Structurally AE2 and AE3 are very similar to band 3, the main difference being an extension of some 300 residues of the N-terminal domain in AE2 and AE3.

Two signature patterns were developed for these proteins. The first pattern is based on a conserved stretch of sequence that contains four clustered positive charged residues and which is located at the C-terminal extremity of the cytoplasmic domain, just before the first transmembrane segment from the integral domain. The second pattern is based on the perfectly conserved sequence of the fifth transmembrane segment; this segment contains a lysine, which is the covalent binding site for the isothiocyanate group of DIDS, an inhibitor of anion exchange.

Consensus pattern F-G-G-[LIVM SEQ ID NO:4]](2)-[KR]-D-[LIVM SEQ ID NO:4]]-[RK]-R-R-Y Sequences known to belong to this class detected by the pattern ALL.

Consensus pattern [FI]-L-I-S-L-I-F-I-Y-E-T-F-x-K-L Sequences known to belong to this class detected by the pattern ALL.

[1] Jay D., Cantley L. Annu. Rev. Biochem. 55:511-538(1986).

[2] Reithmeier R.A.F. Curr. Opin. Struct. Biol. 3:515-523(1993).

892. ATP phosphoribosyltransferase signature (HisG)

ATP phosphoribosyltransferase (EC 2.4.2.17) is the enzyme that catalyzes the first step in the biosynthesis of histidine in bacteria, fungi and plants. It is a protein of about 23 to 32 Kd. As a signature pattern a region located in the C-terminal part of this enzyme was selected.

Consensus pattern E-x(5)-G-x-[SAG]-x(2)-[IV]-x-D-[LIV]-x(2)-[ST]-G-x-T-[LM]

Sequences known to belong to this class detected by the pattern ALL.

5

893. HNH endonuclease (HNH)

Number of members: 56

[1] Shub DA, Goodrich-Blair H, Eddy SR; Medline: 95117127 "Amino acid sequence motif of group I intron endonucleases is conserved in open reading frames of group II introns."

10 Trends Biochem Sci 1994;19:402-404.

[2] Dalgaard JZ, Klar AJ, Moser MJ, Holley WR, Chatterjee A, Mian IS; Medline: 98026854 "Statistical modeling and analysis of the LAGLIDADG family of site-specific endonucleases and identification of an intein that encodes a site-specific endonuclease of the HNH family." Nucleic Acids Res 1997;25:4626-4638.

15 [3] Gorbalenya AE; Medline: 95004046 "Self-splicing group I and group II introns encode homologous (putative) DNA endonucleases of a new family." Protein Sci 1994;3:1117-1120.

894. NEUROHYPOPHYS_HORM (hormone5)

Oxytocin (or ocytocin) and vasopressin [1] are small (nine amino acid residues), structurally and functionally related neurohypophysial peptide hormones. Oxytocin causes contraction of the smooth muscle of the uterus and of the mammary gland while vasopressin has a direct antidiuretic action on the kidney and also causes vasoconstriction of the peripheral vessels. Like the majority of active peptides, both hormones are synthesized as larger protein precursors that are enzymatically converted to their mature forms. Peptides belonging to this family are also found in birds, fish, reptiles and amphibians (mesotocin, isotocin, valitocin, glumitocin, aspargtocin, vasotocin, seritocin, asvatocin, phasvatocin), in worms (annetocin), octopi (cephalotocin), locust (locupressin or neuropeptide F1/F2) and in molluscs (conopressins G and S) [2]. The pattern developed to detect this category of peptides spans their entire sequence and includes four invariant amino acid residues.

30

Consensus pattern C-[LIFY SEQ ID NO:580)](2)-x-N-[CS]-P-x-G [The two C's are linked by a disulfide bond]. Sequences known to belong to this class detected by the pattern ALL.

[1] Acher R., Chauvet J. Biochimie 70:1197-1207(1988).

[2] Chauvet J., Michel G., Ouedraogo Y., Chou J., Chait B.T., Acher R. Int. J. Pept. Protein Res. 45:482-487(1995).

5

895. 7,8-dihydro-6-hydroxymethylpterin-pyrophosphokinase (HPPK)

All organisms require reduced folate cofactors for the synthesis of a variety of metabolites. Most microorganisms must synthesize folate de novo because they lack the active transport system of higher vertebrate cells which allows these organisms to use dietary folates.

10 Enzymes involved in folate biosynthesis are therefore targets for a variety of antimicrobial agents such as trimethoprim or sulfonamides. 7,8-dihydro-6-hydroxymethylpterin-pyrophosphokinase (EC 2.7.6.3) (HPPK) catalyzes the attachment of pyrophosphate to 6-hydroxymethyl-7,8-dihydropterin to form 6-hydroxymethyl-7,8-dihydropteridine pyrophosphate. This is the first step in a three-step pathway leading to 7,8-dihydrofolate.

15 Bacterial HPPK (gene folK or sulD) [1] is a protein of 160 to 270 amino acids. In the lower eukaryote *Pneumocystis carinii*, HPPK is the central domain of a multifunctional folate synthesis enzyme (gene fas) [2]. As a signature for HPPK, a conserved region located in the central section of these enzymes was selected.

20 Consensus pattern [KRHD SEQ ID NO:726)]-x-[GA]-[PSAE SEQ ID NO:727)]-R-x(2)-D-[LIV]-D-[LIVM SEQ ID NO:4)](2) Sequences known to belong to this class detected by the pattern ALL. Other sequence(s) detected in SWISS-PROT NONE.

[1] Talarico T.L., Ray P.H., Dev I.K., Merrill B.M., Dallas W.S. J. Bacteriol. 174:5971-5977(1992).

25 [2] Volpes F., Dyer M., Scaife J.G., Darby G., Stammers D.K., Delves C.J. Gene 112:213-218(1992).

30 896. Metalloenzyme superfamily (Metalloenzyme)

This family includes phosphopentomutase Swiss:P07651 and 2,3-bisphosphoglycerate-independent phosphoglycerate mutase, Swiss:P37689. This family is also related to

alk_phosphatase [1]. The alignment contains the most conserved residues that are probably involved in metal binding and catalysis. Number of members: 34

[1] Galperin MY, Bairoch A, Koonin EV; Medline: 99180418 "A superfamily of metalloenzymes unifies phosphopentomutase and cofactor- independent phosphoglycerate mutase with alkaline phosphatases and sulfatases." Protein Sci 1998;7:1829-1835.

897. Penicillin amidase (Penicil_amidase)

Penicillin amidase or penicillin acylase EC:3.5.1.11 catalyses the hydrolysis of benzylpenicillin to phenylacetic acid and 6-aminopenicillanic acid (6-APA) a key intermediate in the the synthesis of penicillins [1]. Also in the family is cephalosporin acylase Swiss:P07662 and Swiss:P29958 aculeacin A acylase which are involved in the synthesis of related peptide antibiotics. Number of members: 13

[1] Verhaert RM, Riemens AM, van der Laan JM, van Duin J, Quax WJ; Medline: 97438505 "Molecular cloning and analysis of the gene encoding the thermostable penicillin G acylase from *Alcaligenes faecalis*. Appl Environ Microbiol 1997;63:3412-3418.

[2] Duggleby HJ, Tolley SP, Hill CP, Dodson EJ, Dodson G, Moody PC; Medline: 95115804 "Penicillin acylase has a single-amino-acid catalytic centre." Nature 1995;373:264-268.

898. Phosphoribosyl-AMP cyclohydrolase (PRA-CH)

This enzyme catalyses the third step in the histidine biosynthetic pathway. It requires Zn ions for activity. Number of members: 13

[1] D'Ordine RL, Klem TJ, Davisson VJ; Medline: 99129952 "N1-(5'-phosphoribosyl)adenosine-5'-monophosphate cyclohydrolase: purification and characterization of a unique metalloenzyme. Biochemistry 1999;38:1537-1546.

899. Phosphoribosyl-ATP pyrophosphohydrolase (PRA-PH)

This enzyme catalyses the second step in the histidine biosynthetic pathway. Number of members: 32

[1] Keesey JK Jr, Bigelis R, Fink GR; Medline: 79216449 "The product of the his4 gene cluster in *Saccharomyces cerevisiae*. A trifunctional polypeptide." J Biol Chem 1979 Aug 10;254:7427-7433.

[2] Bruni CB, Carlomagno MS, Formisano S, Paoletta G; Medline: 86310274 "Primary and secondary structural homologies between the HIS4 gene product of *Saccharomyces cerevisiae* and the hisIE and hisD gene products of *Escherichia coli* and *Salmonella typhimurium*." Mol Gen Genet 1986;203:389-396.

900. Prokaryotic membrane lipoprotein lipid attachment site (PstS)

In prokaryotes, membrane lipoproteins are synthesized with a precursor signal peptide, which is cleaved by a specific lipoprotein signal peptidase (signal peptidase II). The peptidase recognizes a conserved sequence and cuts upstream of a cysteine residue to which a glyceride-fatty acid lipid is attached [1]. Some of the proteins known to undergo such processing currently include (for recent listings see [1,2,3]):

- Major outer membrane lipoprotein (murein-lipoproteins) (gene lpp).
- *Escherichia coli* lipoprotein-28 (gene nlpA).
- *Escherichia coli* lipoprotein-34 (gene nlpB).
- *Escherichia coli* lipoprotein nlpC.
- *Escherichia coli* lipoprotein nlpD.
- *Escherichia coli* osmotically inducible lipoprotein B (gene osmB).
- *Escherichia coli* osmotically inducible lipoprotein E (gene osmE).
- *Escherichia coli* peptidoglycan-associated lipoprotein (gene pal).
- *Escherichia coli* rare lipoproteins A and B (genes rplA and rplB).
- *Escherichia coli* copper homeostasis protein cutF (or nlpE).
- *Escherichia coli* plasmids traT proteins.
- *Escherichia coli* Col plasmids lysis proteins.
- A number of *Bacillus* beta-lactamases.
- *Bacillus subtilis* periplasmic oligopeptide-binding protein (gene oppA).
- *Borrelia burgdorferi* outer surface proteins A and B (genes ospA and ospB).

- *Borrelia hermsii* variable major protein 21 (gene vmp21) and 7 (gene vmp7).
- *Chlamydia trachomatis* outer membrane protein 3 (gene omp3).
- *Fibrobacter succinogenes* endoglucanase cel-3.
- *Haemophilus influenzae* proteins Pal and Pcp.
- 5 - *Klebsiella pullulunase* (gene pulA).
- *Klebsiella pullulunase* secretion protein pulS.
- *Mycoplasma hyorhinis* protein p37.
- *Mycoplasma hyorhinis* variant surface antigens A, B, and C (genes vlpABC).
- *Neisseria* outer membrane protein H.8.
- 10 - *Pseudomonas aeruginosa* lipopeptide (gene lppL).
- *Pseudomonas solanacearum* endoglucanase egl.
- *Rhodopseudomonas viridis* reaction center cytochrome subunit (gene cytC).
- *Rickettsia* 17 Kd antigen.
- *Shigella flexneri* invasion plasmid proteins mxiJ and mxiM.
- 15 - *Streptococcus pneumoniae* oligopeptide transport protein A (gene amiA).
- *Treponema pallidum* 34 Kd antigen.
- *Treponema pallidum* membrane protein A (gene tmpA).
- *Vibrio harveyi* chitinase (gene chb).
- *Yersinia* virulence plasmid protein yscJ.
- 20 - Halocyanin from *Natrobacterium pharaonis* [4], a membrane associated copper-binding protein. This is the first archaeobacterial protein known to be modified in such a fashion).
From the precursor sequences of all these proteins, a consensus pattern was derived and a set of rules to identify this type of post-translational modification.
- 25 Consensus pattern {DERK SEQ ID NO:354}(6)-[LIVMFWSTAG SEQ ID NO:352]](2)-[LIVMFYSTAGCQ SEQ ID NO:353)]-[AGS]-C [C is the lipid attachment site] Additional rules: 1) The cysteine must be between positions 15 and 35 of the sequence in consideration. 2) There must be at least one Lys or one Arg in the first seven positions of the sequence. Sequences known to belong to this class detected by the patternALL. Other sequence(s)
- 30 detected in SWISS-PROT some 100 prokaryotic proteins. Some of them are not membrane lipoproteins, but at least half of them could be.

[2] Klein P., Somorjai R.L., Lau P.C.K. Protein Eng. 2:15-20(1988).

[3] von Heijne G. Protein Eng. 2:531-534(1989).

[4] Mattar S., Scharf B., Kent S.B.H., Rodewald K., Oesterhelt D., Engelhard M. J. Biol. Chem. 269:14939-14945(1994).

5

901. Ribosome recycling factor (RRF)

The ribosome recycling factor (RRF / ribosome release factor) dissociates the ribosome from the mRNA after termination of translation, and is essential bacterial growth [1]. Thus
10 ribosomes are "recycled" and ready for another round of protein synthesis. Number of members: 27

[1] Janosi L, Shimizu I, Kaji A; Medline: 94240115 "Ribosome recycling factor (ribosome releasing factor) is essential for bacterial growth." Proc Natl Acad Sci U S A 1994;91:4249-
15 4253.

902. S-layer homology(SLH)

S-layers are paracrystalline mono-layered assemblies of (glyco)proteins which coat the
20 surface of bacteria [1]. Several S-layer proteins and some other cell wall proteins contain one or more copies of a domain of about 50-60 residues, which has been called SLH (for S-layer homology) [2]. There is strong evidence that this domain serves as an anchor to the peptidoglycan [3]. The SLH domain has been found in:

- S-layer glycoprotein of *Acetogenium kivui* (3 copies).

25 - S-layer 125 Kd protein of *Bacillus sphaericus* (3 copies).

- S-layer protein of *Bacillus anthracis* (3 copies).

- S-layer protein of *Bacillus licheniformis* (3 copies).

- S-layer protein (HWP) from *Bacillus brevis* strain HPD31 (3 copies).

- Middle cell wall protein (MWP) from *Bacillus brevis* strain 47 (3 copies).

30 - S-layer protein (p100) of *Thermus thermophilus* (1 copy).

- Outer membrane protein Omp-alpha from *Thermotoga maritima* (1 copy).

- Cellulosome anchoring protein (gene *ancA*), outer layer protein B (OlpB) and a further potential cell surface glycoprotein from *Clostridium thermocellum* (3 copies; the first copy is

missing its N-terminal third which is appended to the end of the third copy; may have arisen by circular permutation).

- Amylopullulanase (gene amyB) from *Thermoanaerobacter thermosulfurogenes* (3 copies)
- Amylopullulanase (gene aapT) from *Bacillus* strain XAL-601 (3 copies).
- 5 - Endoglucanase from *Bacillus* strain KSM-635 (3 copies).
- Exoglucanase (gene xynX) from *Clostridium thermocellum* (3 copies).
- Xylanase A (gene xynA) from *Thermoanaerobacter saccharolyticum* (2 copies; 3 copies if a frameshift is taken into account).
- Protein involved in butirosin production (ButB) from *Bacillus circulans* (2 incomplete
- 10 copies; 3 copies if three frameshifts are taken into account).
- Two hypothetical proteins from *Synechocystis* strain PCC 6803 (1 copy each).
- A hypothetical protein with sequence similarity to amylopullulanases found 3' of amylase gene from *Bacillus circulans* (fragment of 1 copy; 3 copies if two frameshifts are taken into account).

15 SLH domains are found at the N- or C-termini of mature proteins. They occur in single copy followed by a predicted coiled coil domain, or in three contiguous copies. Structurally, the SLH domain is predicted to contain two alpha-helices flanking a beta strand. The SLH sequences are fairly divergent with an average identity of about 25%. It is however possible to build a sequence pattern that starts at the second position of the domain and that spans 3/4

20 of its length.

Consensus pattern[LVFYT SEQ ID NO:728)]-x-[DA]-x(2,5)-[DNGSATPHY SEQ ID NO:729)]-[FYWPDA SEQ ID NO:730)]-x(4)-[LIV]-x(2)- [GTALV SEQ ID NO:731)]-x(4,6)-[LIVFYC SEQ ID NO:732)]-x(2)-G-x-[PGSTA SEQ ID NO:733)]-x(2,3)-[MFYA

25 SEQ ID NO:734)]-x- [PGAV SEQ ID NO:735)]-x(3,10)-[LIVMA SEQ ID NO:30)]-[STKR SEQ ID NO:152)]-[RY]-x-[EQ]-x-[STALIVM SEQ ID NO:736)] Sequences known to belong to this class detected by the pattern ALL. Other sequence(s) detected in SWISS-PROT/NONE.

- 30 [1] Beveridge T.J. Curr. Opin. Struct. Biol. 4:204-212(1994).
- [2] Lupas A., Engelhardt H., Peters J., Santarius U., Volker S., Baumeister W. J. Bacteriol. 176:1224-1233(1994).

[3] Lemaire M., Ohayon H., Gounon P., Fujino T., Beguin P. J. Bacteriol. 177:2451-2459(1995).

5 903. Queuine tRNA-ribosyltransferase (TGT)

This is a family of queuine tRNA-ribosyltransferases EC:2.4.2.29, also known as tRNA-guanine transglycosylase and guanine insertion enzyme. Queuine tRNA-ribosyltransferase modifies tRNAs for asparagine, aspartic acid, histidine and tyrosine with queuine. It catalyses the exchange of guanine-34 at the wobble position with 7-aminomethyl-7-deazaguanine, and
10 the addition of a cyclopentenediol moiety to 7-aminomethyl-7-deazaguanine-34 tRNA; giving a hypermodified base queuine in the wobble position [1,2]. The aligned region contains a zinc binding motif C-x-C-x2-C-x29-H, and important tRNA and 7-aminomethyl-7deazaguanine binding residues [1]. Number of members: 27

15 [1] Romier C, Reuter K, Suck D, Ficner R; Medline: 96256303 "Crystal structure of tRNA-guanine transglycosylase: RNA modification by base exchange." EMBO J 1996;15:2850-2857.

[2] Garcia GA, Koch KA, Chong S; Medline: 93287116 "tRNA-guanine transglycosylase from Escherichia coli. Overexpression, purification and quaternary structure." J Mol Biol
20 1993;231:489-497.

904. ThiC Family (ThiC)

ThiC is found within the thiamine biosynthesis operon. ThiC is involved in pyrimidine
25 biosynthesis [2]. ThiC catalyzes the substitution of the pyrophosphate of 2-methyl-4-amino-5-hydroxymethylpyrimidine pyrophosphate by 4-methyl-5-(beta-hydroxyethyl)thiazole phosphate to yield thiamine phosphate [3]. Number of members: 12

[1] Vander Horn PB, Backstrom AD, Stewart V, Begley TP; Medline: 93163063 "Structural
30 genes for thiamine biosynthetic enzymes (thiCEFGH) in Escherichia coli K-12." J Bacteriol 1993;175:982-992.

[2] Begley TP, Downs DM, Ealick SE, McLafferty FW, Van Loon AP, Taylor S, Campobasso N, Chiu HJ, Kinsland C, Reddick JJ, Xi J; Medline: 99311269 "Thiamin biosynthesis in prokaryotes." Arch Microbiol 1999;171:293-300.

5 [3] Zhang Y, Taylor SV, Chiu HJ, Begley TP; Medline: 97284509 "Characterization of the Bacillus subtilis thiC operon involved in thiamine biosynthesis." J Bacteriol 1997;179:3030-3035.

905. Putative tRNA binding domain (tRNA_bind)

10 This domain is found in prokaryotic methionyl-tRNA synthetases, prokaryotic phenylalanyl tRNA synthetases the yeast GU4 nucleic-binding protein (G4p1 or p42, ARC1) [2], human tyrosyl-tRNA synthetase [1], and endothelial-monocyte activating polypeptide II. G4p1 binds specifically to tRNA form a complex with methionyl-tRNA synthetases [2]. In human tyrosyl-tRNA synthetase this domain may direct tRNA to the active site of the enzyme [2].

15 This domain may perform a common function in tRNA aminoacylation [1]. Number of members: 12

[1] Kleeman TA, Wei D, Simpson KL, First EA; Medline: 97306356 "Human tyrosyl-tRNA synthetase shares amino acid sequence homology with a putative cytokine." J Biol Chem
20 1997;272:14420-14425.

[2] Simos G, Segref A, Fasiolo F, Hellmuth K, Shevchenko A, Mann M, Hurt EC; Medline: 97050848 "The yeast protein Arc1p binds to tRNA and functions as a cofactor for the methionyl-and glutamyl-tRNA synthetases." EMBO J 1996;15:5437-5448.

25

906. UbiA prenyltransferase family signature (UbiA)

The following prenyltransferases are evolutionary related [1,2]:

- Bacterial 4-hydroxybenzoate octaprenyltransferase (gene ubiA).
- Yeast mitochondrial para-hydroxybenzoate--polyprenyltransferase (gene COQ2).
- 30 - Protoheme IX farnesyltransferase (heme O synthase) from yeast and mammals (gene COX10) and from bacteria (genes cyoE or ctaB).

These proteins probably contain seven transmembrane segments. The best conserved region is located in a loop between the second and third of these segments and was used as a signature pattern.

- 5 Consensus pattern N-x(3)-[DE]-x(2)-[LIF]-D-x(2)-[VM]-x-R-[ST]-x(2)-R-x(4)-G Sequences known to belong to this class detected by the pattern ALL. Other sequence(s) detected in SWISS-PROT NONE.

[1] Melzer M., Heide L. Biochim. Biophys. Acta 1212:93-102(1994).

- 10 [2] Mogi T., Saiki K., Anraku Y. Mol. Microbiol. 14:391-398(1994).

907. Uncharacterized protein family UPF0044 signature (UPF0044)

The following uncharacterized proteins have been shown [1] to be highly similar:

- 15 - *Bacillus subtilis* hypothetical protein yqeI.
- *Escherichia coli* hypothetical protein yhbY and HI1333, the corresponding *Haemophilus influenzae* protein.
- *Methanococcus jannaschii* hypothetical protein MJ0652.

20 These are small proteins of 10 to 15 Kd. They can be picked up in the database by the following pattern. This pattern is located in the N-terminal part of these proteins.

Consensus pattern L-[ST]-x(3)-K-x(3)-[KR]-[SGA]-x-[GA]-H-x-L-x-P-[LIV]-x(2)-[LIV]-[GA]-x(2)-G Sequences known to belong to this class detected by the pattern ALL.

25

908. ATP synthase (C/AC39) subunit (vATP-synt_AC39)

This family includes the AC39 subunit from vacuolar ATP synthase Swiss:P32366 [1], and the C subunit from archaebacterial ATP synthase [2]. The family also includes subunit C from the Sodium transporting ATP synthase from *Enterococcus hirae* Swiss:P43456 [3].

30 Number of members: 12

[1] Bauerle C, Ho MN, Lindorfer MA, Stevens TH; Medline: 93286119 "The *Saccharomyces cerevisiae* VMA6 gene encodes the 36-kDa subunit of the vacuolar H(+)-ATPase membrane sector." J Biol Chem 1993;268:12749-12757.

[2] Wilms R, Freiberg C, Wegerle E, Meier I, Mayer F, Muller V; Medline: 96324968

5 "Subunit structure and organization of the genes of the A1A0 ATPase from the Archaeon *Methanosarcina mazei* Go1." J Biol Chem 1996;271:18843-18852.

[3] Takase K, Kakinuma S, Yamato I, Konishi K, Igarashi K, Kakinuma Y; Medline: 94209269 "Sequencing and characterization of the ntp gene cluster for vacuolar- type Na(+)-translocating ATPase of *Enterococcus hirae*." J Biol Chem 1994;269:11037-11044.

10
909. ATP synthase (E/31 kDa) subunit (vATP-synt_E)

This family includes the vacuolar ATP synthase E subunit [1], as well as the archaebacterial ATP synthase E subunit [2]. Number of members: 24

15 [1] Foury F; Medline: 91009356 "The 31-kDa polypeptide is an essential subunit of the vacuolar ATPase in *Saccharomyces cerevisiae*." J Biol Chem 1990;265:18554-18560.

[2] Wilms R, Freiberg C, Wegerle E, Meier I, Mayer F, Muller V; Medline: 96324968

20 "Subunit structure and organization of the genes of the A1A0 ATPase from the Archaeon *Methanosarcina mazei* Go1." J Biol Chem 1996;271:18843-18852.

910. (WW)

25 The WW domain [1-4,E1] (also known as rsp5 or WWP) has been originally discovered as a short conserved region in a number of unrelated proteins, among them dystrophin, the gene responsible for Duchenne muscular dystrophy. The domain, which spans about 35 residues, is repeated up to 4 times in some proteins. It has been shown [5] to bind proteins with particular proline- motifs, [AP]-P-P-[AP]-Y, and thus resembles somewhat SH3 domains. It appears to contain beta-strands grouped around four conserved aromatic positions; generally Trp. The
30 name WW or WWP derives from the presence of these Trp as well as that of a conserved Pro. It is frequently associated with other domains typical for proteins in signal transduction processes.

Proteins containing the WW domain are listed below.

- Dystrophin, a multidomain cytoskeletal protein. Its longest alternatively spliced form consists of an N-terminal actin-binding domain, followed by 24 spectrin-like repeats, a cysteine-rich calcium-binding domain and a C-terminal globular domain. Dystrophin forms tetramers and is thought to have multiple functions including involvement in membrane stability, transduction of contractile forces to the extracellular environment and organization of membrane specialization. Mutations in the dystrophin gene lead to muscular dystrophy of Duchenne or Becker type. Dystrophin contains one WW domain C-terminal of the spectrin-repeats.
- Utrophin, a dystrophin-like protein of unknown function.
- Vertebrate YAP protein is a substrate of an unknown serine kinase. It binds to the SH3 domain of the Yes oncoprotein via a proline-rich region. This protein appears in alternatively spliced isoforms, containing either one or two WW domains [6].
- Mouse NEDD-4 plays a role in the embryonic development and differentiation of the central nervous system. It contains 3 WW modules followed by a HECT domain. The human ortholog contains 4 WW domains, but the third WW domain is probably spliced resulting in an alternate NEDD-4 protein with only 3 WW modules [3].
- Yeast RSP5 is similar to NEDD-4 in its molecular organization. It contains an N-terminal C2 domain (see <PDOC00380>, followed by a histidine-rich region, 3 WW domains and a HECT domain.
- Rat FE65, a transcription-factor activator expressed preferentially in liver. The activator domain is located within the N-terminal 232 residues of FE65, which also contain the WW domain.
- Yeast ESS1/PTF1, a putative peptidyl prolyl cis-trans isomerase from family ppiC (see <PDOC00840>). A related protein, dodo (gene dod) exists in Drosophila and in mammals (gene PIN1).
- Tobacco DB10 protein. The WW domain is located N-terminal to the region with similarity to ATP-dependent RNA helicases.
- IQGAP, a human GTPase activating protein acting on ras. It contains an N-terminal domain similar to fly muscle mp20 protein and a C-terminal ras GTPase activator domain.
- Yeast pre-mRNA processing protein PRP40, Caenorhabditis elegans ZK1098.1 and fission yeast SpAC13C5.02 are related proteins with similarity to MYO2-type myosin, each containing two WW-domains at the N-terminus.

- *Caenorhabditis elegans* hypothetical protein C38D4.5, which contains one WW module, a PH domain (see <PDOC50003>) and a C-terminal phosphatidylinositol 3-kinase domain.

- Yeast hypothetical protein YFL010c.

For the sensitive detection of WW domains, a profile was developed which spans the whole
5 homology region as well as a pattern.

Consensus pattern W-x(9,11)-[VFY]-[FYW]-x(6,7)-[GSTNE SEQ ID NO:737]-[GSTQCR
SEQ ID NO:738]-[FYW]-x(2)-P Sequences known to belong to this class detected by the
10 pattern ALL. Other sequence(s) detected in SWISS-PROT8. Sequences known to belong to
this class detected by the profile ALL.

[1] Bork P., Sudol M. Trends Biochem. Sci. 19:531-533(1994).

[2] Andre B., Springael J.Y. Biochem. Biophys. Res. Commun. 205:1201-1205(1994).

[3] Hofmann K.O., Bucher P. FEBS Lett. 358:153-157(1995).

15 [4] Sudol M., Chen H.I., Bougeret C., Einbond A., Bork P. FEBS Lett. 369:67-71(1995).

[5] Chen H.I., Sudol M. Proc. Natl. Acad. Sci. U.S.A. 92:7819-7823(1995).

[6] Sudol M., Bork P., Einbond A., Kastury K., Druck T., Negrini M., Huebner K., Lehman
D. J. Biol. Chem. 270:14733-14741(1995).

20 911. Xeroderma pigmentosum (XP) [1] (XPG_1)

Xeroderma pigmentosum (XP) [1] is a human autosomal recessive disease, characterized by a
high incidence of sunlight-induced skin cancer. People's skin cells with this condition are
hypersensitive to ultraviolet light, due to defects in the incision step of DNA excision repair.

25 There are a minimum of seven genetic complementation groups involved in this pathway:
XP-A to XP-G. The defect in XP-G can be corrected by a 133 Kd nuclear protein called XPG
(or XPGC) [2].

XPG belongs to a family of proteins [2,3,4,5,6] that are composed of two main subsets:

30 - Subset 1, to which belongs XPG, RAD2 from budding yeast and rad13 from fission yeast.
RAD2 and XPG are single-stranded DNA endonucleases [7,8]. XPG makes the 3'incision in
human DNA nucleotide excision repair [9].

- Subset 2, to which belongs mouse and human FEN-1, rad2 from fission yeast, and RAD27 from budding yeast. FEN-1 is a structure-specific endonuclease.

In addition to the proteins listed in the above groups, this family also includes:

- 5 - Fission yeast exo1, a 5'→3' double-stranded DNA exonuclease that could act in a pathway that corrects mismatched base pairs.
- Yeast EXO1 (DHS1), a protein with probably the same function as exo1.
- Yeast DIN7.

10 Sequence alignment of this family of proteins reveals that similarities are largely confined to two regions. The first is located at the N-terminal extremity (N-region) and corresponds to the first 95 to 105 amino acids. The second region is internal (I-region) and found towards the C-terminus; it spans about 140 residues and contains a highly conserved core of 27 amino acids that includes a conserved pentapeptide (E-A-[DE]-A-[QS]). It is possible that the
15 conserved acidic residues are involved in the catalytic mechanism of DNA excision repair in XPG. The amino acids linking the N- and I-regions are not conserved; indeed, they are largely absent from proteins belonging to the second subset.

Two signature patterns were developed for these proteins. The first corresponds to the central
20 part of the N-region, the second to part of the I-region and includes the putative catalytic core pentapeptide.

Consensus pattern [VI]-[KRE]-P-x-[FYIL SEQ ID NO:644)]-V-F-D-G-x(2)-[PIL]-x-[LVC]-
K Sequences known to belong to this class detected by the patternALL. Other sequence(s)
25 detected in SWISS-PROTNONE.

Consensus pattern [GS]-[LIVM SEQ ID NO:4)]-[PER]-[FYS]-[LIVM SEQ ID NO:4)]-x-A-
P-x-E-A-[DE]-[PAS]-[QS]-[CLM] Sequences known to belong to this class detected by the
patternALL. Other sequence(s) detected in SWISS-PROTNONE.

30

[1] Tanaka K., Wood R.D. Trends Biochem. Sci. 19:83-86(1994).

[2] Scherly D., Nospikel T., Corlet J., Ucla C., Bairoch A., Clarkson S.G. Nature 363:182-185(1993).

- [3] Carr A.M., Sheldrick K.S., Murray J.M., Al-Harithy R., Watts F.Z., Lehmann A.R. Nucleic Acids Res. 21:1345-1349(1993).
- [4] Murray J.M., Tavassoli M., Al-Harithy R., Sheldrick K.S., Lehmann A.R., Carr A.M., Watts F.Z. Mol. Cell. Biol. 14:4878-4888(1994).
- 5 [5] Harrington J.J., Lieber M.R. Genes Dev. 8:1344-1355(1994).
- [6] Szankasi P., Smith G.R. Science 267:1166-1169(1995).
- [7] Habraken Y., Sung P., Prakash L., Prakash S. Nature 366:365-368(1993).
- [8] O'Donovan A., Scherly D., Clarkson S.G., Wood R.D. J. Biol. Chem. 269:15965-15968(1994).
- 10 [9] O'Donovan A., Davies A.A., Moggs J.G., West S.C., Wood R.D. Nature 371:432-435(1994).

912. 5-formyltetrahydrofolate cyclo-ligase (5-FTHF_cyc-lig)

15

5-formyltetrahydrofolate cyclo-ligase or methenyl-THF synthetase EC:6.3.3.2 catalyses the interchange of 5-formyltetrahydrofolate (5-FTHF) to 5-10-methenyltetrahydrofolate, this requires ATP and Mg²⁺ [1]. 5-FTHF is used in chemotherapy where it is clinically known as Leucovorin [2].

20 Number of members: 23

[1] Dayan A, Bertrand R, Beauchemin M, Chahla D, Mamo A, Filion M, Skup D, Massie B, Jolivet J; Medline: 96096540 "Cloning and characterization of the human 5,10-methenyltetrahydrofolate synthetase-encoding cDNA." Gene 1995;165:307-311.

25 [2] Maras B, Stover P, Valiante S, Barra D, Schirch V; Medline: 94308074 "Primary structure and tetrahydropteroylglutamate binding site of rabbit liver cytosolic 5,10-methenyltetrahydrofolate synthetase." J Biol Chem 1994;269:18429-18433.

913. Cytosolic long-chain acyl-CoA thioester hydrolase (Acyl-CoA_hydro)

30

This family consist of various cytosolic long-chain acyl-CoA thioester hydrolases including human and rat [1,2]. The aligned region is repeated with in the sequence of human and rat cytosolic long-chain acyl-CoA thioester hydrolases of this family. Long-chain acyl-CoA

hydrolases hydrolyse palmitoyl-CoA to CoA and palmitate, they also catalyse the hydrolysis of other long chain fatty acyl-CoA thioesters. Long-chain acyl-CoA hydrolases are present in all living organisms and they may provide a mechanism for the control of lipid metabolism [1].

5 Number of members: 24

[1] Yamada J, Furihata T, Iida N, Watanabe T, Hosokawa M, Satoh T, Someya A, Nagaoka I, Suga T; Medline: 97236308 "Molecular cloning and expression of cDNAs encoding rat brain and liver cytosolic long-chain acyl-CoA hydrolases." Biochem Biophys Res Commun
10 1997;232:198-203.

[2] Broustas CG, Larkins LK, Uhler MD, Hajra AK; Medline: 96209964 "Molecular cloning and expression of cDNA encoding rat brain cytosolic acyl-coenzyme A thioester hydrolase." J Biol Chem 1996;271:10470-10476.

15 914. Agglutinin

Lectin (probable mannose binding)

Members of this family are plant lectins. Many if not all are mannose specific.

Number of members: 87

20

[1] Wright CS, Hester G; Medline: 97094989 "The 2.0 Å structure of a cross-linked complex between snowdrop lectin and a branched mannopentaose: evidence for two unique binding modes." Structure 1996;4:1339-1352.

25 915. (ANF_RECEPTORS)

Natriuretic peptides are hormones involved in the regulation of fluid and electrolyte homeostasis. These hormones stimulate the intracellular production of cyclic GMP as a second messenger.

30

Currently, three types of natriuretic peptide receptors are known [1,2]. Two express guanylate cyclase activity: GC-A (or ANP-A) which seems specific to atrial natriuretic peptide (ANP), and GC-B (or ANP-B) which seems to be stimulated more effectively by brain natriuretic

peptide (BNP) than by ANP. The third receptor (ANP-C) is probably responsible for the clearance of ANP from the circulation and does not play a role in signal transduction.

GC-A and GC-B are plasma membrane-bound proteins that share the following topology: an N-terminal extracellular domain which acts as the ligand binding region, then a transmembrane domain followed by a large cytoplasmic C-terminal region that can be subdivided into two domains: a protein kinase-like domain (see <PDOC00100>) that appears important for proper signalling and a guanylate cyclase catalytic domain (see <PDOC00425>). The topology of ANP-C is different: like GC-A and -B it possesses an extracellular ligand-binding region and a transmembrane domain, but its cytoplasmic domain is very short.

A pattern was developed from the ligand-binding region of natriuretic peptide receptors based on a highly conserved region located in the N-terminal part of the domain.

Consensus pattern G-P-x-C-x-Y-x-A-A-x-V-x-R-x(3)-H-W Sequences known to belong to this class detected by the pattern ALL. Other sequence(s) detected in SWISS-PROT NONE.

[1] Garbers D.L. New Biol. 2:499-504(1990).

[2] Schulz S., Chinkers M., Garbers D.L. FASEB J. 2:2026-2035(1989).

916. (Apocytochrome)

Cytochrome c family heme-binding site signature

In proteins belonging to cytochrome c family [1], the heme group is covalently attached by thioether bonds to two conserved cysteine residues. The consensus sequence for this site is Cys-X-X-Cys-His and the histidine residue is one of the two axial ligands of the heme iron. This arrangement is shared by all proteins known to belong to cytochrome c family, which presently includes cytochromes c, c', c1 to c6, c550 to c556, cc3/Hmc, cytochrome f and reaction center cytochrome c.

Consensus pattern C-{CPWHF SEQ ID NO:193}}-{CPWR SEQ ID NO:194}}-C-H-{CFYW SEQ ID NO:195}} Sequences known to belong to this class detected by the pattern ALL,

except for four cytochrome c's which lack the first thioether bond. Other sequence(s) detected in SWISS-PROT454.

Note: some cytochrome c's have more than a single bound heme group c4 has 2, c7 has 3, c3 has 4, the reaction center has 4, and cc3/Hmc has 16 !

[1] Mathews F.S. Prog. Biophys. Mol. Biol. 45:1-56(1985).

917. ATP-synt_A-c. ATP synthase Alpha chain, C terminal

10 [1] Medline: 94344236. Structure at 2.8 A resolution of F1-ATPase from bovine heart mitochondria. Abrahams JP, Leslie AG, Lutter R, Walker JE; Nature 1994;370:621-628.
Number of members: 125

918. (Basic)

15 Myc-type, 'helix-loop-helix' dimerization domain signature
HELIX_LOOP_HELIX

A number of eukaryotic proteins, which probably are sequence specific DNA- binding proteins that act as transcription factors, share a conserved domain of 40 to 50 amino acid residues. It has been proposed [1] that this domain is formed of two amphipathic helices joined by a variable length linker region that could form a loop. This 'helix-loop-helix' (HLH) domain mediates protein dimerization and has been found in the proteins listed below [2,3,E1,E2]. Most of these proteins have an extra basic region of about 15 amino acid residues that is adjacent to the HLH domain and specifically binds to DNA. They are referred as basic helix-loop-helix proteins (bHLH), and are classified in two groups: class A (ubiquitous) and class B (tissue-specific). Members of the bHLH family bind variations on the core sequence 'CANNTG', also referred to as the E-box motif. The homo- or heterodimerization mediated by the HLH domain is independent of, but necessary for DNA binding, as two basic regions are required for DNA binding activity. The HLH proteins lacking the basic domain (Emc, Id) function as negative regulators since they form heterodimers, but fail to bind DNA. The hairy-related proteins (hairy, E(spl), deadpan) also repress transcription although they can bind DNA. The proteins of this subfamily act together with co-repressor proteins, like groucho, through their C-terminal motif WRPW.

- The myc family of cellular oncogenes [4], which is currently known to contain four members: c-myc [E3], N-myc, L-myc, and B-myc. The myc genes are thought to play a role in cellular differentiation and proliferation.

- Proteins involved in myogenesis (the induction of muscle cells). In mammals MyoD1 (Myf-3), myogenin (Myf-4), Myf-5, and Myf-6 (Mrf4 or herculin), in birds CMD1 (QMF-1), in *Xenopus* MyoD and MF25, in *Caenorhabditis elegans* CeMyoD, and in *Drosophila nautilus* (nau).

- Vertebrate proteins that bind specific DNA sequences ('E boxes') in various immunoglobulin chains enhancers: E2A or ITF-1 (E12/pan-2 and E47/pan-1), ITF-2 (tcf4), TFE3, and TFEB.

- Vertebrate neurogenic differentiation factor 1 that acts as differentiation factor during neurogenesis.

- Vertebrate MAX protein, a transcription regulator that forms a sequence- specific DNA-binding protein complex with myc or mad.

- Vertebrate Max Interacting Protein 1 (MXI1 protein) which acts as a transcriptional repressor and may antagonize myc transcriptional activity by competing for max.

- Proteins of the bHLH/PAS superfamily which are transcriptional activators. In mammals, AH receptor nuclear translocator (ARNT), single-minded homologs (SIM1 and SIM2), hypoxia-inducible factor 1 alpha (HIF1A), AH receptor (AHR), neuronal pas domain proteins (NPAS1 and NPAS2), endothelial pas domain protein 1 (EPAS1), mouse ARNT2, and human BMAL1. In *drosophila*, single-minded (SIM), AH receptor nuclear translocator (ARNT), trachealess protein (TRH), and similar protein (SIMA).

- Mammalian transcription factors HES, which repress transcription by acting on two types of DNA sequences, the E box and the N box.

- Mammalian MAD protein (max dimerizer) which acts as transcriptional repressor and may antagonize myc transcriptional activity by competing for max.

- Mammalian Upstream Stimulatory Factor 1 and 2 (USF1 and USF2), which bind to a symmetrical DNA sequence that is found in a variety of viral and cellular promoters.

- Human lyl-1 protein; which is involved, by chromosomal translocation, in T- cell leukemia.

- Human transcription factor AP-4.

- Mouse helix-loop-helix proteins MATH-1 and MATH-2 which activate E box- dependent transcription in collaboration with E47.

- Mammalian stem cell protein (SCL) (also known as tal1), a protein which may play an important role in hemopoietic differentiation. SCL is involved, by chromosomal translocation, in stem-cell leukemia.

- Mammalian proteins Id1 to Id4 [5]. Id (inhibitor of DNA binding) proteins lack a basic DNA-binding domain but are able to form heterodimers with other HLH proteins, thereby inhibiting binding to DNA.

- *Drosophila* extra-macrochaetae (emc) protein, which participates in sensory organ patterning by antagonizing the neurogenic activity of the achaete- scute complex. Emc is the homolog of mammalian Id proteins.

- Human Sterol Regulatory Element Binding Protein 1 (SREBP-1), a transcriptional activator that binds to the sterol regulatory element 1 (SRE-1) found in the flanking region of the LDLR gene and in other genes.

- *Drosophila* achaete-scute (AS-C) complex proteins T3 (l'sc), T4 (scute), T5 (achaete) and T8 (asense). The AS-C proteins are involved in the determination of the neuronal precursors in the peripheral nervous system and the central nervous system.

- Mammalian homologs of achaete-scute proteins, the MASH-1 and MASH-2 proteins.

- *Drosophila* atonal protein (ato) which is involved in neurogenesis.

- *Drosophila* daughterless (da) protein, which is essential for neurogenesis and sex-determination.

- *Drosophila* deadpan (dpn), a hairy-like protein involved in the functional differentiation of neurons.

- *Drosophila* delilah (dei) protein, which is plays an important role in the differentiation of epidermal cells into muscle.

- *Drosophila* hairy (h) protein, a transcriptional repressor which regulates the embryonic segmentation and adult bristle patterning.

- *Drosophila* enhancer of split proteins E(spl), that are hairy-like proteins active during neurogenesis. also act as transcriptional repressors.

- *Drosophila* twist (twi) protein, which is involved in the establishment of germ layers in embryos.

- Maize anthocyanin regulatory proteins R-S and LC.

- Yeast centromere-binding protein 1 (CPF1 or CBF1). This protein is involved in chromosomal segregation. It binds to a highly conserved DNA sequence, found in centromeres and in several promoters.

- 5

The schematic representation of the helix-loop-helix domain is shown here:

10

The signature pattern that had been developed to detect this domain spans completely the second amphipathic helix.

15

Consensus pattern[DENSTAP SEQ ID NO:306)]-[KR]-[LIVMAGSNT SEQ ID NO:307)]-
{FYWCPHKR SEQ ID NO:308)}-[LIVMT SEQ ID NO:1)]-[LIVM SEQ ID NO:4)]- x(2)-
[STAV SEQ ID NO:105)]-[LIVMSTACKR SEQ ID NO:309)]-x-[VMFYH SEQ ID
NO:310)]-[LIVMTA SEQ ID NO:311)]-{P}-{P}- [LIVMRKHQ SEQ ID NO:312)]

20

- 25

919. (Beta-lactamase)

30

Beta-lactamases (EC 3.5.2.6) [1,2] are enzymes which catalyze the hydrolysis of an amide bond in the beta-lactam ring of antibiotics belonging to the penicillin/cephalosporin

family. Four kinds of beta-lactamase have been identified [3]. Class-B enzymes are zinc containing proteins whilst class -A, C and D enzymes are serine hydrolases. The three classes of serine beta-

lactamases are evolutionary related and belong to a superfamily [4] that also includes DD-peptidases and a variety of other penicillin-binding proteins (PBP's). All these proteins contain a Ser-x-x-Lys motif, where the serine is the active site residue. Although clearly homologous, the sequences of the three classes of serine beta-lactamases exhibit a large degree of variability and only a small number of residues are conserved in addition to the catalytic serine.

Since a pattern detecting all serine beta-lactamases would also pick up many unrelated sequences, it was decided to provide specific patterns, centered on the active site serine, for each of the three classes.

Consensus pattern [FY]-x-[LIVMFY SEQ ID NO:18)]-x-S-[TV]-x-K-x(4)-[AGLM SEQ ID NO:739)]-x(2)-[LC] [S is the active site residue] Sequences known to belong to this class detected by the patternALL class-A beta-lactamases. Other sequence(s) detected in SWISS-PROT7.

Consensus pattern F-E-[LIVM SEQ ID NO:4)]-G-S-[LIVMG SEQ ID NO:202)]-[SA]-K [The first S is the active site residue] Sequences known to belong to this class detected by the patternALL class-C beta-lactamases. Other sequence(s) detected in SWISS-PROT NONE.

Consensus pattern [PA]-x-S-[ST]-F-K-[LIV]-[PAL]-x-[STA]-[LI] [S is the active site residue] Sequences known to belong to this class detected by the patternALL class-D beta-lactamases. Other sequence(s) detected in SWISS-PROT NONE.

[1] Ambler R.P. Philos. Trans. R. Soc. Lond., B, Biol. Sci. 289:321-331(1980).

[2] Pastor N., Pinero D., Valdes A.M., Soberon X. Mol. Microbiol. 4:1957-1965(1990).

[3] Bush K. Antimicrob. Agents Chemother. 33:259-263(1989).

[4] Joris B., Ghuysen J.-M., Dive G., Renard A., Dideberg O., Charlier P., Frere J.M., Kelly J.A., Boyington J.C., Moews P.C., Knox J.R. Biochem. J. 250:313-324(1988).

920. Biotin protein ligase (BPL)

Biotin is covalently attached at the active site of certain enzymes that transfer carbon dioxide from bicarbonate to organic acids to form cellular metabolites. Biotin protein ligase (BPL) is the enzyme responsible for attaching biotin to a specific lysine at the active site of biotin enzymes. Each organism probably has only one BPL. Biotin attachment is a two step reaction that results in the formation of an amide linkage between the carboxyl group of biotin and the epsilon-amino group of the modified lysine [2].

Number of members: 26

[1] Wilson KP, Shewchuk LM, Brennan RG, Otsuka AJ, Matthews BW; Medline: 93028443 "Escherichia coli biotin holoenzyme synthetase/bio repressor crystal structure delineates the biotin- and DNA-binding domains." Proc Natl Acad Sci USA 1992;89:9257-9261.

[2] Chapman-Smith A, Cronan JE Jr; Medline: 10470036 "The enzymatic biotinylation of proteins: a post-translational modification of exceptional specificity." Trends Biochem Sci 1999;24:359-363.

921. (BRCA2_repeat)

The alignment covers only the most conserved region of the repeat. Respiratory-chain NADH dehydrogenase 30 Kd subunit signature

[1] Bork P, Blomberg N, Nilges M; Medline: 96241568 "Internal repeats in the BRCA2 protein sequence." Nat Genet 1996;13:22-23.

Number of members: 63

922. (C6)

This domain of unknown function is found in the C. elegans protein Swiss:Q19522. It is presumed to be an extracellular domain. The C6 domain contains six conserved cysteine residues in most copies of the domain. However some copies of the domain are missing cysteine residues 1 and 3 suggesting that these form a disulphide bridge.

Number of members: 23

923. Cadherin cytoplasmic region (Cadherin_C_term)

5 Cadherins are vital in cell-cell adhesion during tissue differentiation. Cadherins are linked to the cytoskeleton by catenins. Catenins bind to the cytoplasmic tail of the cadherin. Cadherins cluster to form foci of homophilic binding units. A key determinant to the strength of the binding that it is mediated by cadherins is the juxtamembrane region of the cadherin. This region induces clustering and also binds to the protein p120ctn [1].

10 Number of members: 59

[1] Yap AS, Niessen CM, Gumbiner BM; Medline: 98234411 "The juxtamembrane region of the cadherin cytoplasmic tail supports lateral clustering, adhesive strengthening, and interaction with p120ctn." J Cell Biol 1998;141:779-789.

15 [2] Barth AI, Nathke IS, Nelson WJ; Medline: 97471931 "Cadherins, catenins and APC protein: interplay between cytoskeletal complexes and signaling pathways." Curr Opin Cell Biol 1997;9:683-690.

[3] Braga VM, Machesky LM, Hall A, Hotchin NA; Medline: 97327766 "The small GTPases Rho and Rac are required for the establishment of cadherin-dependent cell-cell contacts." J
20 Cell Biol 1997;137:1421-1431.

924. Clathrin propeller repeat (Clathrin_propel)

25 Clathrin is the scaffold protein of the basket-like coat that surrounds coated vesicles. The soluble assembly unit, a triskelion, contains three heavy chains and three light chains in an extended three-legged structure. Each leg contains one heavy and one light chain. The N-terminus of the heavy chain is known as the globular domain, and is composed of seven repeats which form a beta propeller [1].

Number of members: 61

30

[1] ter Haar E, Musacchio A, Harrison SC, Kirchhausen T; Medline: 99043510 "Atomic structure of clathrin: a beta propeller terminal domain joins an alpha zigzag linker." Cell. 1998;95:563-573.

925. Respiratory-chain NADH dehydrogenase 30 Kd subunit signature (complex1_30Kd)

Respiratory-chain NADH dehydrogenase (EC 1.6.5.3) [1,2] (also known as complex I or NADH-ubiquinone oxidoreductase) is an oligomeric enzymatic complex located in the inner mitochondrial membrane which also seems to exist in the chloroplast and in cyanobacteria (as a NADH-plastoquinone oxidoreductase). Among the 25 to 30 polypeptide subunits of this bioenergetic enzyme complex there is one with a molecular weight of 30 Kd (in mammals) which has been found to be:

- Nuclear encoded, as a precursor form with a transit peptide in mammals, and in *Neurospora crassa*.
- Mitochondrial encoded in *Paramecium* (protein P1), and in the slime mold *Dictyostelium discoideum* (ORF 209).
- Chloroplast encoded in various higher plants (ORF 159). It is also present in bacteria:
- In the cyanobacteria *Synechocystis* strain PCC 6803 (gene *ndhJ*).
- Subunit C of *Escherichia coli* NADH-ubiquinone oxidoreductase (gene *nuoC*).
- Subunit NQO5 of *Paracoccus denitrificans* NADH-ubiquinone oxidoreductase.

This protein, in its mature form, consists of from 157 to 266 amino acid residues. The best conserved region is located in the C-terminal section and can be used as a signature pattern.

Consensus pattern E-R-E-x(2)-[DE]-[LIVMFY SEQ ID NO:18)](2)-x(6)-[HK]-x(3)-[KRP]-x-[LIVM SEQ ID NO:4)]- [LIVMYS SEQ ID NO:740)] Sequences known to belong to this class detected by the patternALL. Other sequence(s) detected in SWISS-PROT NONE.

[1] Ragan C.I. Curr. Top. Bioenerg. 15:1-36(1987).

[2] Weiss H., Friedrich T., Hofhaus G., Preis D. Eur. J. Biochem. 197:563-576(1991).

926. Respiratory-chain NADH dehydrogenase 49 Kd subunit signature (complex1_49Kd)

Respiratory-chain NADH dehydrogenase (EC 1.6.5.3) [1,2] (also known as complex I or NADH-ubiquinone oxidoreductase) is an oligomeric enzymatic complex located in the inner mitochondrial membrane which also seems to exist in the chloroplast and in

cyanobacteria (as a NADH-plastoquinone oxidoreductase). Among the 25 to 30 polypeptide subunits of this bioenergetic enzyme complex there is one with a molecular weight of 49 Kd (in mammals), which is the third largest subunit of complex I and is a component of the iron-sulfur (IP) fragment of the enzyme. It seems to bind a 4Fe-4S iron-sulfur cluster. The 49 Kd subunit has been found to be:

- Nuclear encoded, as a precursor form with a transit peptide in mammals, and in *Neurospora crassa*.

- Mitochondrial encoded in protozoan such as *Paramecium* (ORF 400), *Leishmania* and *Trypanosoma* (MURF 3).

- Chloroplast encoded in various higher plants (ORF 392).

The 49 Kd subunit is highly similar to [3,4]:

- Subunit D of *Escherichia coli* NADH-ubiquinone oxidoreductase (gene *nuoD*).

- Subunit NQO4 of *Paracoccus denitrificans* NADH-ubiquinone oxidoreductase.

- Subunit 5 of *Escherichia coli* formate hydrogenlyase (gene *hycE*).

- Subunit G of *Escherichia coli* hydrogenase-4 (gene *hyfG*).

A highly conserved region was selected as signature pattern, located in the N-terminal section of this subunit.

Consensus pattern [LIVMH SEQ ID NO:703]-H-[RT]-[GA]-x-E-K-[LIVMTN SEQ ID

NO:280)]-x-E-x-[KRQ] Sequences known to belong to this class detected by the patternALL.

[1] Ragan C.I. Curr. Top. Bioenerg. 15:1-36(1987).

[2] Weiss H., Friedrich T., Hofhaus G., Preis D. Eur. J. Biochem. 197:563-576(1991).

[3] Fearnley I.M., Walker J.E. Biochim. Biophys. Acta 1140:105-134(1992).

[4] Weidner U., Geier S., Ptöck A., Friedrich T., Leif H., Weiss H. J. Mol. Biol. 233:109-122(1993).

927. (COX2)

Cytochrome c oxidase (EC 1.9.3.1) [1,2] is an oligomeric enzymatic complex which is a component of the respiratory chain and is involved in the transfer of electrons from cytochrome c to oxygen. In eukaryotes this enzyme complex is located in the mitochondrial

inner membrane; in aerobic prokaryotes it is found in the plasma membrane. The enzyme complex consists of 3-4 subunits (prokaryotes) to up to 13 polypeptides (mammals).

Subunit 2 (CO II) transfers the electrons from cytochrome c to the catalytic subunit 1. It contains two adjacent transmembrane regions in its N-terminus and the major part of the protein is exposed to the periplasmic or to the mitochondrial intermembrane space, respectively. CO II provides the substrate-binding site and contains a copper center called Cu(A), probably the primary acceptor in cytochrome c oxidase. An exception is the corresponding subunit of the cbb3-type oxidase which lacks the copper A redox-center. Several bacterial CO II have a C-terminal extension that contains a covalently bound heme c.

It has been shown [3,4] that nitrous oxide reductase (EC 1.7.99.6) (gene nosZ) of *Pseudomonas* has sequence similarity in its C-terminus to CO II. This enzyme is part of the bacterial respiratory system which is activated under anaerobic conditions in the presence of nitrate or nitrous oxide. NosZ is a periplasmic homodimer that contains a dinuclear copper center, probably located in a 3-dimensional fold similar to the cupredoxin-like fold that has been suggested for the copper-binding site of CO II [3].

The dinuclear purple copper center is formed by 2 histidines and 2 cysteines [5]. This region was used as a signature pattern. The conserved valine and the conserved methionine are said to be involved in stabilizing the copper-binding fold by interacting with each other.

Consensus pattern V-x-H-x(33,40)-C-x(3)-C-x(3)-H-x(2)-M [The two C's and two H's are copper ligands] Sequences known to belong to this class detected by the patternALL, except for *Paramecium primaurelia* as well as in some plants where the pattern ends with Thr; an RNA editing event at this position could change this Thr to Met.

Note: cytochrome cbb(3) subunit 2 does not belong to this family.

[1] Capaldi R.A., Malatesta F., Darley-USmar V.M. *Biochim. Biophys. Acta* 726:135-148(1983).

[2] Garcia-Horsman J.A., Barquera B., Rumbley J., Ma J., Gennis R.B. *J. Bacteriol.* 176:5587-5600(1994).

[3] van der Oost J., Lappalainen P., Musacchio A., Warne A., Lemieux L., Rumbley J., Gennis R.B., Aasa R., Pascher T., Malmstrom B.G., Saraste M. EMBO J. 11:3209-3217(1992).

[4] Zumft W.G., Dreutsch A., Loechelt S., Cuypers H., Friedrich B., Schneider B. Eur. J. Biochem. 208:31-40(1992).

928. Cytochrome C assembly protein (CytC_asm)

This family consists of various proteins involved in cytochrome c assembly from mitochondria and bacteria; CycK from *Rhizobium* [3], CcmC from *E. coli* and *Paracoccus denitrificans* [2,1] and orf240 from wheat mitochondria [4]. The members of this family are probably integral membrane proteins with six predicted transmembrane helices. It has been proposed that members of this family comprise a membrane component of an ABC (ATP binding cassette) transporter complex. It is also proposed that this transporter is necessary for transport of some component needed for cytochrome c assembly. One member CycK contains a putative heme-binding motif [3], orf240 also contains a putative heme-binding motif and is a proposed ABC transporter with c-type heme as its proposed substrate [4]. However it seems unlikely that all members of this family transport heme nor c-type apocytochromes because CcmC in the putative CcmABC transporter transports neither [1].

Number of members: 67

[1] Page D, Pearce DA, Norris HA, Ferguson SJ; Medline: 97195802 "The *Paracoccus denitrificans* ccmA, B and C genes: cloning and sequencing, and analysis of the potential of their products to form a haem or apo-c-type cytochrome transporter. MICROBIOLOGY 1997;143:563-576.

[2] Thoeny-meyer L, Fischer F, Kunzler P, Ritz D, Hennecke H; Medline: 95362656 "Escherichia coli genes required for cytochrome c maturation." J. BACTERIOL 1995;177:4321-4326.

[3] Delgado MJ, Yeoman KH, Wu G, Vargas C, Davies A, Poole RK, Johnston AWB, Downie JA; Medline: 95394794 "Characterization of the cychJKL genes involved in cytochrome c biogenesis and symbiotic nitrogen fixation in *Rhizobium leguminosarum*." J. BACTERIOL 1995;177:4927-4934.

[4] Bonnard G, Grienberger JM; Medline: 95124303 "A gene proposed to encode a transmembrane domain of an ABC transporter is expressed in wheat mitochondria." MOL. GEN. GENET 1995;246:91-99.

5 929. Cytochrome b559 subunits heme-binding site signature (cytochr_b559)

Cytochrome b559 [1] is an essential component of photosystem II complex from oxygenic photosynthetic organisms. It is an integral thylakoid membrane protein composed of two subunits, alpha (gene psbE) and beta (gene psbF), each of which contains a histidine residue
10 located in a transmembrane region. The two histidines coordinate the heme iron of cytochrome b559.

The region around the heme-binding residue of both subunits is very similar and can be used as a signature pattern.

15

Consensus pattern[LIV]-x-[ST]-[LIVF SEQ ID NO:127)]-R-[FYW]-x(2)-[IV]-H-[STGA SEQ ID NO:741)]-[LIV]-[STGA SEQ ID NO:741)]-[IV]-P [H is the heme iron ligand]
Sequences known to belong to this class detected by the patternALL. Other sequence(s) detected in SWISS-PROT NONE.

20

[1] Pakrasi H.B., de Ciechi P., Whitmarsh J. EMBO J. 10:1619-1627(1991).

930. Cytochrome b/b6 signatures (Cytochrome_b)

25

In the mitochondrion of eukaryotes and in aerobic prokaryotes, cytochrome b is a component of respiratory chain complex III (EC 1.10.2.2) - also known as the bc1 complex or ubiquinol-cytochrome c reductase. In plant chloroplasts and cyanobacteria, there is an analogous protein, cytochrome b6, a component of the plastoquinone-plastocyanin reductase (EC 1.10.99.1),
30 also known as the b6f complex.

Cytochrome b/b6 [1,2] is an integral membrane protein of approximately 400 amino acid residues that probably has 8 transmembrane segments. In plants and cyanobacteria,

cytochrome b6 consists of two subunits encoded by the petB and petD genes. The sequence of petB is colinear with the N-terminal part of mitochondrial cytochrome b, while petD corresponds to the C-terminal part. Cytochrome b/b6 non-covalently binds two heme groups, known as b562 and b566. Four conserved histidine residues are postulated to be the ligands of the iron atoms of these two heme groups.

Apart from regions around some of the histidine heme ligands, there are a few conserved regions in the sequence of b/b6. The best conserved of these regions includes an invariant P-E-W triplet which lies in the loop that separates the fifth and sixth transmembrane segments. It seems to be important for electron transfer at the ubiquinone redox site - called Qz or Qo (where o stands for outside) - located on the outer side of the membrane.

A schematic representation of the structure of cytochrome b/b6 is shown below.

```
+---Fe-b562---+ | +---Fe-b566--|+ |||
xxxxxxxxxxxxHxHxxxxxxxxxxxxHxHxxxxxxxxxxPEWxxxxxxxxxxxxxxxxxxxxx <-----
---Cytochrome-b-----> <----Cytochrome-b6-petB-----><---Cytochrome-
b6-petD----->
```

Two signature patterns were developed for cytochrome b/b6. The first includes the first conserved histidine of b/b6, which is a heme b562 ligand; the second includes the conserved PEW triplet.

Consensus pattern [DENQ SEQ ID NO:371]-x(3)-G-[FYWMQ SEQ ID NO:742])-x-[LIVMF SEQ ID NO:2])-R-x(2)-H [H is a heme b562 ligand] Sequences known to belong to this class detected by the patternALL, except for 5 sequences.

Consensus pattern P-[DE]-W-[FY]-[LFY](2) Sequences known to belong to this class detected by the patternALL, except for *Odocoileus hemionus* (mule deer) and *Paramecium tetraurelia* cytochrome b.

[1] Howell N. J. Mol. Evol. 29:157-169(1989).

[2] Esposti M.D., de Vries S., Crimi M., Ghelli A., Patarnello T., Meyer A. *Biochim. Biophys. Acta* 1143:243-271(1993).

931. Phorbol esters / diacylglycerol binding domain (DAG_PE-bind)

5

Diacylglycerol (DAG) is an important second messenger. Phorbol esters (PE) are analogues of DAG and potent tumor promoters that cause a variety of physiological changes when administered to both cells and tissues. DAG activates a family of serine/threonine protein kinases, collectively known as protein kinase C (PKC) [1]. Phorbol esters can directly stimulate PKC. The N- terminal region of PKC, known as C1, has been shown [2] to bind PE and DAG in a phospholipid and zinc-dependent fashion. The C1 region contains one or two copies (depending on the isozyme of PKC) of a cysteine-rich domain about 50 amino-acid residues long and essential for DAG/PE-binding. Such a domain has also been found in the following proteins:

10

15

- Diacylglycerol kinase (EC 2.7.1.107) (DGK) [3], the enzyme that converts DAG into phosphatidate. It contains two copies of the DAG/PE-binding domain in its N-terminal section. At least five different forms of DGK are known in mammals.

20

- N-chimaerin. A brain specific protein which shows sequence similarities with the BCR protein at its C-terminal part and contains a single copy of the DAG/PE-binding domain at its N-terminal part. It has been shown [4,5] to be able to bind phorbol esters.

25

- The raf/mil family of serine/threonine protein kinases. These protein kinases contain a single N-terminal copy of the DAG/PE-binding domain.

- The unc-13 protein from *Caenorhabditis elegans*. Its function is not known but it contains a copy of the DAG/PE-binding domain in its central section and has been shown to bind specifically to a phorbol ester in the presence of calcium [6].

30

- The vav oncogene. Vav was generated by a genetic rearrangement during gene transfer assays. Its expression seems to be restricted to cells of hematopoietic origin. Vav seems [5,7] to contain a DAG/PE-binding domain in the central part of the protein.

- The *Drosophila* GTPase activating protein rotund.

The DAG/PE-binding domain binds two zinc ions; the ligands of these metal ions are probably the six cysteines and two histidines that are conserved in this domain. A signature pattern was developed that spans completely the DAG/PE domain.

Consensus pattern H-x-[LIVMFYW SEQ ID NO:26)]-x(8,11)-C-x(2)-C-x(3)-[LIVMFC SEQ ID NO:90)]-x(5,10)- C-x(2)-C-x(4)-[HD]-x(2)-C-x(5,9)-C [All the C and H are involved in binding Zinc] Sequences known to belong to this class detected by the pattern ALL, except a few DGK's.

[1] Azzi A., Boscoboinik D., Hensey C. Eur. J. Biochem. 208:547-557(1992).

[2] Ono Y., Fujii T., Igarashi K., Kuno T., Tanaka C, Kikkawa U., Nishizuka Y. Proc. Natl. Acad. Sci. U.S.A. 86:4868-4871(1989).

[3] Sakane F., Yamada K., Kanoh H., Yokoyama C., Tanabe T. Nature 344:345-348(1990).

[4] Ahmed S., Kozma R., Monfries C., Hall C., Lim H.H., Smith P., Lim L. Biochem. J. 272:767-773(1990).

[5] Ahmed S., Kozma R., Lee J., Monfries C., Harden N., Lim L. Biochem. J. 280:233-241(1991).

[6] Ahmed S., Maruyama I.N., Kozma R., Lee J., Brenner S., Lim L. Biochem. J. 287:995-999(1992).

[7] Boguski M.S., Bairoch A., Attwood T.K., Michaels G.S. Nature 358:113-113(1992).

932. 3-dehydroquinate synthase (DHQ_synthase)

[1] Barten R, Meyer TF; Medline: 98273626 "Cloning and characterisation of the Neisseria gonorrhoeae aroB gene." Mol Gen Genet 1998;258:34-44.

[2] Hawkins AR, Lamb HK; Medline: 96048023 "The molecular biology of multidomain proteins. Selected examples." Eur J Biochem 1995;232:7-18.

The 3-dehydroquinate synthase EC:4.6.1.3 domain is present in isolation in various bacterial 3-dehydroquinate synthases and also present as a domain in the pentafunctional AROM polypeptide Swiss:P07547 [2]. 3-dehydroquinate (DHQ) synthase catalyses the formation of dehydroquinate (DHQ) and orthophosphate from 3-deoxy-D-arabino heptulosonic 7 phosphate [1]. This reaction is part of the shikimate pathway which is involved in the biosynthesis of aromatic amino acids.

Number of members: 25

933. Dihydrofolate reductase signature (DiHfolate_red)

Dihydrofolate reductases (EC 1.5.1.3) [1] are ubiquitous enzymes which catalyze the reduction of folic acid into tetrahydrofolic acid. They can be inhibited by a number of antagonists such as trimethoprim and methotrexate which are used as antibacterial or anticancerous agents. A signature pattern was derived from a region in the N-terminal part of these enzymes, which includes a conserved Pro-Trp dipeptide; the tryptophan has been shown [2] to be involved in the binding of substrate by the enzyme.

Consensus pattern[LVAGC SEQ ID NO:743)]-[LIF]-G-x(4)-[LIVMF SEQ ID NO:2)]-P-W-x(4,5)-[DE]-x(3)-[FYIV SEQ ID NO:744)]-x(3)-[STIQ SEQ ID NO:745)] Sequences known to belong to this class detected by the patternALL, except for type II bacterial, plasmid-encoded, dihydrofolate reductases which do not belong to the same class of enzymes.

[1] Harpers' Review of Biochemistry, Lange, Los Altos (1985).

[2] Bolin J.T., Filman D.J., Matthews D.A., Hamlin R.C., Kraut J. J. Biol. Chem. 257:13650-13662(1982).

934. (DIL)

[1] Ponting CP; Medline: 95397417 "AF-6/cno: neither a kinesin nor a myosin, but a bit of both." Trends Biochem Sci 1995;20:265-266.

Number of members: 31

935. (DNA_gyraseB_C)

DNA topoisomerase II signature (cross-reference = TOPOISOMERASE_II)

DNA topoisomerase I (EC 5.99.1.2) [1,2,3,4,E1] is one of the two types of enzyme that catalyze the interconversion of topological DNA isomers. Type II topoisomerases are ATP-dependent and act by passing a DNA segment through a transient double-strand break. Topoisomerase II is found in phages, archaebacteria, prokaryotes, eukaryotes, and in African

Swine Fever virus (ASF). In bacteriophage T4 topoisomerase II consists of three subunits (the product of genes 39, 52 and 60). In prokaryotes and in archaebacteria the enzyme, known as DNA gyrase, consists of two subunits (genes *gyrA* and *gyrB* [E2]). In some bacteria, a second type II topoisomerase has been identified; it is known as topoisomerase IV and is required for chromosome segregation, it also consists of two subunits (genes *parC* and *parE*). In eukaryotes, type II topoisomerase is a homodimer.

There are many regions of sequence homology between the different subtypes of topoisomerase II. The relation between the different subunits is shown in the following representation:

```
<-----About-1400-residues----->
[-----Protein 39-*-----][----Protein 52----] Phage T4
[-----gyrB-----*-----][-----gyrA-----] Prokaryote II
Archaeobacteria
[-----parE-----*-----][-----parD-----] Prokaryote IV
[-----*-----] Eukaryote and ASF
'*': Position of the pattern.
```

As a signature pattern for this family of proteins, a region was selected that contains a highly conserved pentapeptide. The pattern is located in *gyrB*, in *parE*, and in protein 39 of phage T4 topoisomerase.

Consensus pattern [LIVMA SEQ ID NO:30)]-x-E-G-[DN]-S-A-x-[STAG SEQ ID NO:20)]

Sequences known to belong to this class detected by the pattern ALL.

[1] Sternglanz R. Curr. Opin. Cell Biol. 1:533-535(1990).

[2] Bjornsti M.-A. Curr. Opin. Struct. Biol. 1:99-103(1991).

[3] Sharma A., Mondragon A. Curr. Opin. Struct. Biol. 5:39-47(1995).

[4] Roca J. Trends Biochem. Sci. 20:156-160(1995).

936. (DNA_topoisolIV)

DNA topoisomerase II signature (cross-reference = TOPOISOMERASE_II)

DNA topoisomerase I (EC 5.99.1.2) [1,2,3,4,E1] is one of the two types of enzyme that catalyze the interconversion of topological DNA isomers. Type II topoisomerases are ATP-dependent and act by passing a DNA segment through a transient double-strand break.

5 Topoisomerase II is found in phages, archaeobacteria, prokaryotes, eukaryotes, and in African Swine Fever virus (ASF). In bacteriophage T4 topoisomerase II consists of three subunits (the product of genes 39, 52 and 60). In prokaryotes and in archaeobacteria the enzyme, known as DNA gyrase, consists of two subunits (genes *gyrA* and *gyrB* [E2]). In some bacteria, a second type II topoisomerase has been identified; it is known as topoisomerase IV and is
10 required for chromosome segregation, it also consists of two subunits (genes *parC* and *parE*). In eukaryotes, type II topoisomerase is a homodimer.

There are many regions of sequence homology between the different subtypes of topoisomerase II. The relation between the different subunits is shown in the following
15 representation:

```
<-----About-1400-residues----->
[-----Protein 39-*-----][----Protein 52----] Phage T4
[-----gyrB-----*-----][-----gyrA-----] Prokaryote II Archaeobacteria
20 [-----parE-----*-----][-----parD-----] Prokaryote IV
[-----*-----] Eukaryote and ASF
'*: Position of the pattern.
```

As a signature pattern for this family of proteins, a region was selected that contains a highly
25 conserved pentapeptide. The pattern is located in *gyrB*, in *parE*, and in protein 39 of phage T4 topoisomerase.

Consensus pattern [LIVMA SEQ ID NO:30)]-x-E-G-[DN]-S-A-x-[STAG SEQ ID NO:20)]
Sequences known to belong to this class detected by the patternALL.

30

- [1] Sternglanz R. Curr. Opin. Cell Biol. 1:533-535(1990).
- [2] Bjornsti M.-A. Curr. Opin. Struct. Biol. 1:99-103(1991).
- [3] Sharma A., Mondragon A. Curr. Opin. Struct. Biol. 5:39-47(1995).

[4] Roca J. Trends Biochem. Sci. 20:156-160(1995).

937. Prolyl oligopeptidase family serine active site (DPPIV_N_term)

- 5 The prolyl oligopeptidase family [1,2,3] consist of a number of evolutionary related peptidases whose catalytic activity seems to be provided by a charge relay system similar to that of the trypsin family of serine proteases, but which evolved by independent convergent evolution. The known members of this family are listed below.
- 10 - Prolyl endopeptidase (EC 3.4.21.26) (PE) (also called post-proline cleaving enzyme). PE is an enzyme that cleaves peptide bonds on the C-terminal side of prolyl residues. The sequence of PE has been obtained from a mammalian species (pig) and from bacteria (*Flavobacterium meningosepticum* and *Aeromonas hydrophila*); there is a high degree of sequence conservation between these sequences.
 - 15 - *Escherichia coli* protease II (EC 3.4.21.83) (oligopeptidase B) (gene prtB) which cleaves peptide bonds on the C-terminal side of lysyl and arginyl residues.
 - Dipeptidyl peptidase IV (EC 3.4.14.5) (DPP IV). DPP IV is an enzyme that removes N-terminal dipeptides sequentially from polypeptides having unsubstituted N-termini provided that the penultimate residue is proline.
 - 20 - Yeast vacuolar dipeptidyl aminopeptidase A (DPAP A) (gene: STE13) which is responsible for the proteolytic maturation of the alpha-factor precursor.
 - Yeast vacuolar dipeptidyl aminopeptidase B (DPAP B) (gene: DAP2).
 - Acylamino-acid-releasing enzyme (EC 3.4.19.1) (acyl-peptide hydrolase). This enzyme catalyzes the hydrolysis of the amino-terminal peptide bond of an N-acetylated protein to generate a N-acetylated amino acid and a protein with a free amino-terminus.
 - 25
- A conserved serine residue has experimentally been shown (in *E.coli* protease II as well as in pig and bacterial PE) to be necessary for the catalytic mechanism. This serine, which is part of the catalytic triad (Ser, His, Asp), is generally located about 150 residues away from the C-terminal extremity of these enzymes (which are all proteins that contains about 700 to 800 amino acids).
- 30

776

Consensus pattern D-x(3)-A-x(3)-[LIVMFYW SEQ ID NO:26])-x(14)-G-x-S-x-G-G-[LIVMFYW SEQ ID NO:26)](2) [S is the active site residue] Sequences known to belong to this class detected by the pattern ALL, except for yeast DPAP A.

- 5 Note: these proteins belong to families S9A/S9B/S9C in the classification of peptidases [4,E1].

[1] Rawlings N.D., Polgar L., Barrett A.J. Biochem. J. 279:907-911(1991).

[2] Barrett A.J., Rawlings N.D. Biol. Chem. Hoppe-Seyler 373:353-360(1992).

- 10 [3] Polgar L., Szabo E. Biol. Chem. Hoppe-Seyler 373:361-366(1992).

[4] Rawlings N.D., Barrett A.J. Meth. Enzymol. 244:19-61(1994).

938. Deoxyhypusine synthase (DS)

- 15 Eukaryotic initiation factor 5A (eIF-5A) contains an unusual amino acid, hypusine [N epsilon-(4-aminobutyl-2-hydroxy)lysine]. The first step in the post-translational formation of hypusine is catalysed by the enzyme deoxyhypusine synthase (DS) EC:1.1.1.249. The modified version of eIF-5A, and DS, are required for eukaryotic cell proliferation [1].

- 20 Number of members: 9

[1] Liao DI, Wolff EC, Park MH, Davies DR; Medline: 98154315 "Crystal structure of the NAD complex of human deoxyhypusine synthase: an enzyme with a ball-and-chain mechanism for blocking the active site." Structure 1998;6:23-32.

25

939. (DUF21)

- 30 Many of the sequences in this family are annotated as hemolysins, however this is due to a similarity to Swiss:Q54318 that does not contain this domain. This domain is found in the N-terminus of the proteins adjacent to two intracellular CBS domains CBS.

Number of members: 42

940. (DUF59)

This family includes prokaryotic proteins of unknown function. The family also includes
5 PhaH Swiss:O84984 from *Pseudomonas putida*. PhaH forms a complex with PhaF
Swiss:O84982, PhaG Swiss:O84983 and PhaI Swiss:O84985, which hydroxylates
phenylacetic acid to 2-hydroxyphenylacetic acid [1]. So members of this family may all be
components of ring hydroxylating complexes.

Number of members: 15

10 [1] Olivera ER, Minambres B, Garcia B, Muniz C, Moreno MA, Ferrandez A, Diaz E, Garcia
JL, Luengo JM; Medline: 98263372 "Molecular characterization of the phenylacetic acid
catabolic pathway in *Pseudomonas putida* U: the phenylacetyl-CoA catabolon." Proc Natl
Acad Sci U S A 1998;95:6419-6424.

941. (DUF82)

The protein contains four conserved cysteines that may be involved in metal binding or
disulphide bridges.

20 Number of members: 4

942. Riboflavin kinase / FAD synthetase (FAD_Synth)

This family consists part of the bifunctional enzyme riboflavin kinase / FAD synthetase.

25 These enzymes have both ATP:riboflavin 5'-phospho transferase and ATP:FMN-
adenylyltransferase activities [1]. They catalyse the 5'-phosphorylation of riboflavin to FMN
and the adenylylation of FMN to FAD [1].

CAUTION: It is not clear if this region of the enzymes catalyses either or both of the
enzymatic reactions.

30 Number of members: 27

[1] Manstein DJ, Pai EF; Medline: 87057286 "Purification and characterization of FAD
synthetase from *Brevibacterium ammoniagenes*." J Biol Chem 1986;261:16169-16173.

943. [2Fe-2S] binding domain (fer2_2)

[1] Romao MJ, Archer M, Moura I, Moura JJ, LeGall J, Engh R, Schneider M, Hof P, Huber R; Medline: 96072968 "Crystal structure of the xanthine oxidase-related aldehyde oxidoreductase from *D. gigas*." Science 1995;270:1170-1176.

Number of members: 53

944. Filovirus glycoprotein (Filo_glycop)

This family includes an extracellular region from the envelope glycoprotein of Ebola and Marburg viruses. This region is also produced as a separate transcript that gives rise to a non-structural, secreted glycoprotein, which is produced in large amounts and has an unknown function [1]. Processing of this protein may be involved in viral pathogenicity [2].

Number of members: 23

[1] Volchkov VE, Feldmann H, Volchkova VA, Klenk HD; Medline: 98245155 "Processing of the Ebola virus glycoprotein by the proprotein convertase furin." Proc Natl Acad Sci U S A 1998;95:5762-5767.

[2] Sanchez A, Trappier SG, Mahy BW, Peters CJ, Nichol ST; Medline: 96195018 "The virion glycoproteins of Ebola viruses are encoded in two reading frames and are expressed through transcriptional editing." Proc Natl Acad Sci U S A 1996;93:3602-3607.

945. Frataxin-like domain (Frataxin_Cyay)

This family contains proteins that have a domain related to the globular C-terminus of Frataxin the protein that is mutated in Friedreich's ataxia. This domain is found in a family of bacterial proteins. The function of this domain is currently unknown.

Number of members: 12

[1] Gibson TJ, Koonin EV, Musco G, Pastore A, Bork P; Medline: 97084946 "Friedreich's ataxia protein: phylogenetic evidence for mitochondrial dysfunction." Trends Neurosci 1996;19:465-468.

946. (GAF)

Domain present in phytochromes and cGMP-specific phosphodiesterases.

5 Number of members: 296

[1] Aravind L, Ponting CP; Medline: 98094688 "The GAF domain: an evolutionary link between diverse phototransducing proteins." Trends Biochem Sci 1997;22:458-459.

10 947. Galaptin signature (Gal-bind_lectin)

All vertebrates synthesize soluble galactoside-binding lectins [1,2,3] (also known as galectins, galaptins or S-lectin). These carbohydrate-binding proteins are developmentally regulated. Although their exact physiological role is not yet clear they seem to be involved in differentiation, cellular regulation and tissue construction. The sequence of galactoside-binding lectins from electric eel (electrolectin), conger eel (congerin), chicken and a number of mammalian species is known. These lectins are proteins of about 130 to 140 amino acid residues (14 Kd to 16 Kd).

20 A number of other proteins are known to belong to this family:

- Galectin-3 (also known as MAC-2 antigen; CBP-35 or IgE-binding protein), a 35 Kd lectin which binds immunoglobulin E and which is composed of two domains: a N-terminal domain that consist of tandem repeats of a glycine/ proline-rich sequence and a C-terminal galaptin domain.

25 - Galectin-4 [4], which is composed of two galaptin domains.

- Galectin-5.

- Galectin-7 [5], a keratinocyte protein which could be involved in cell-cell and/or cell-matrix interactions necessary for normal growth control.

- Galectin-8 [6], which is composed of two galaptin domains.

30 - Galectin-9 [7], which is composed of two galaptin domains.

- Human eosinophil lysophospholipase (EC 3.1.1.5) [8] (Charcot-Leyden crystal protein), a protein that may have both an enzymatic and a lectin activities. It forms hexagonal

bipyramidal crystals in tissues and secretions from sites of eosinophil-associated inflammation.

- *Caenorhabditis elegans* 32 Kd lactose-binding lectin [9]. This lectin is composed of two galaptin domains.

5 - *Caenorhabditis elegans* lec-7 and lec-8.

One of the conserved regions of these lectins contains a tryptophan that has been shown [10] to be essential to the binding of galactosides. This region was used as a signature pattern for these proteins.

10 Consensus pattern W-[GEK]-x-[EQ]-x-[KRE]-x(3,6)-[PCTF SEQ ID NO:746)]-[LIVMF SEQ ID NO:2)]-[NQE GSKV SEQ ID NO:747)]-x- [GH]-x(3)-[DENKHS SEQ ID NO:748)]-[LIVMFC SEQ ID NO:90)] [W binds carbohydrate] Sequences known to belong to this class detected by the pattern ALL, except for pig galectin 4.

15 [1] Barondes S.H., Gitt M.A., Leffler H., Cooper D.N.W. *Biochimie* 70:1627-1632(1988).

[2] Hirabayashi J., Kasai K.-I. *J. Biochem.* 104:1-4(1988).

[3] Barondes S.H., Castronovo V., Cooper D.N.W., Cummings R.D., Drickamer K., Feizi T., Gitt M.A., Hirabayashi J., Hughes C., Kasai K.-I., Leffler H., Liu F.-T., Lotan R., Mercurio A.M., Monsigny M., Pillair S., Poirer F., Raz A., Rigby P.W.J., Rini J.M., Wang J.L. *Cell* 76:597-598(1994).

20 [4] Oda Y., Herrmann J., Gitt M., Turck C.W., Burlingame A.L., Barondes S.H., Leffler H. *J. Biol. Chem.* 268:5929-5939(1993).

[5] Madsen P., Rasmussen H.H., Flint T., Gromov P., Kruse T.A., Honore B., Vorum H., Celis J.E. *J. Biol. Chem.* 270:5823-5829(1995).

25 [6] Hadari Y.R., Paz K., Dekel R., Mestrovic T., Accili D., Zick Y. *J. Biol. Chem.* 270:3447-3453(1995).

[7] Wada J., Kanwar Y.S. *J. Biol. Chem.* 272:6078-6086(1997).

[8] Ackerman S.J., Corrette S.E., Rosenberg H.F., Bennett J.C., Mastrianni D.M., Nicholson-Weller A., Weller P.F., Chin D.T., Tenen D.G. *J. Immunol.* 150:456-468(1993).

30 [9] Hirabayashi J., Satoh M., Kasai K.-I. *J. Biol. Chem.* 267:15485-15490(1992).

[10] Abbott W.M., Feizi T. *J. Biol. Chem.* 266:5552-5557(1991).

948. (GARS) Phosphoribosylglycinamide synthetase signature (phosphoribosylamine glycine ligase)

PROSITE: PDOC00164; cross-reference(s): PS00184

- 5 [1] catalyzes the second step in the de novo biosynthesis of purine, the ATP-dependent addition of 5-phosphoribosylamine to glycine to form 5'phosphoribosylglycinamide.

In bacteria GARS is a monofunctional enzyme (encoded by the purD gene), in of a bifunctional enzyme (encoded by the ADE5,7 gene), in higher eukaryotes it is part, with AIRS and with phosphoribosylglycinamide formyltransferase (GART) of a trifunctional enzyme (GARS-AIRS-GART).

The sequence of GARS is well conserved. A highly conserved octapeptide was selected as a signature pattern.

Consensus patternR-F-G-D-P-E-x-[QM]

- 15 Sequences known to belong to this class detected by the patternALL.

[1]Aiba A., Mizobuchi K. J. Biol. Chem. 264:21239-21246(1989).

949. GLTT - GLTT repeat (12 copies)

- 20 This short repeat of unknown function is found in multiple copies in several C. elegans proteins. The repeat is five residues long and consists of XGLTT where X can be any amino acid. Number of members: 34.

950. Glu_synthase - Conserved region in glutamate synthase

- 25 This family represents a region of the glutamate synthase protein. This region is expressed as a separate subunit in the glutamate synthase alpha subunit from archaebacteria, or part of a large multidomain enzyme in other organisms. The aligned region of these proteins contains a putative FMN binding site and Fe-S cluster. Number of members: 44.

- 30 [1] Medline: 97082505. Sequence of the GLT1 gene from Saccharomyces cerevisiae reveals the domain structure of yeast glutamate synthase. Filetici P, Martegani MP, Valenzuela L, Gonzalez A, Ballario P; Yeast 1996;12:1359-1366.

951. (Glyco_hydro_2) Glycosyl hydrolases family 2 signatures

GLYCOSYL_HYDROL_F2_1; PS00608; GLYCOSYL_HYDROL_F2_2

It has been shown [1,2,E1] that the following glycosyl hydrolases can be, on the basis of sequence similarities, classified into a single family:

- 5 -Beta-galactosidases (EC 3.2.1.23) from bacteria such as *Escherichia coli* (genes *lacZ* and *ebgA*), *Clostridium acetobutylicum*, *Clostridium thermosulfurogenes*, *Klebsiella pneumoniae*, *Lactobacillus delbrueckii*, or *Streptococcus thermophilus* and from the fungi *Kluyveromyces lactis*.

-Beta-glucuronidase (EC 3.2.1.31) from *Escherichia coli* (gene *uidA*) and from mammals.

- 10 One of the conserved regions in these enzymes is centered on a conserved glutamic acid residue which has been shown [3], in *Escherichia coli lacZ*, to be the general acid/base catalyst in the active site of the enzyme. This region has been used as a signature pattern. A highly conserved region located some sixty residues upstream from the active site glutamate has been selected as a second signature pattern.

15

Consensus pattern N-x-[LIVMFYWD SEQ ID NO:299)]-R-[STACN SEQ ID NO:300)](2)-H-Y-P-x(4)-[LIVMFYWS SEQ ID NO:301)](2)-x(3)-[DN]-x(2)-G-[LIVMFYW SEQ ID NO:26)](4) Sequences known to belong to this class detected by the pattern ALL.

20

Consensus pattern [DENQLF SEQ ID NO:302)]-[KRVW SEQ ID NO:303)]-N-[HRY]-[STAPPV SEQ ID NO:749)]-[SAC]-[LIVMFS SEQ ID NO:132)](3)-W-[GS]-x(2,3)-N-E [E is the active site residue] Sequences known to belong to this class detected by the pattern ALL, except for *Rhizobium meliloti lacZ*.

25

[1]Henrissat B. *Biochem. J.* 280:309-316(1991).

[2]Schroeder C.J., Robert C., Lenzen G., McKay L.L., Mercenier A. *J. Gen. Microbiol.* 137:369-380(1991).

[3]Gebler J.C., Aebersold R., Withers S.G. *J. Biol. Chem.* 267:11126-11130(1992).

30

952. (Glyco_hydro_3) Glycosyl hydrolases family 3 active site

PROSITE: PDOC00621. PROSITE cross-reference(s)PS00775; GLYCOSYL_HYDROL_F3

It has been shown [1,2] that the following glycosyl hydrolases can be, on the basis of sequence similarities, classified into a single family:

-Beta glucosidases (EC 3.2.1.21) from the fungi *Aspergillus wentii* (A-3), *Hansenula anomala*, *Kluyveromyces fragilis*, *Saccharomycopsis fibuligera*, (BGL1 and BGL2), *Schizophyllum commune* and *Trichoderma reesei* (BGL1).

5 -Beta glucosidases from the bacteria *Agrobacterium tumefaciens* (Cbg1), *Butyrivibrio fibrisolvens* (bglA), *Clostridium thermocellum* (bglB), *Escherichia coli* (bglX), *Erwinia chrysanthemi* (bgxA) and *Ruminococcus albus*.

-Alteromonas strain O-7 beta-hexosaminidase A (EC 3.2.1.52).

-Bacillus subtilis hypothetical protein yzbA.

10 -Escherichia coli hypothetical protein ycfO and HI0959, the corresponding Haemophilus influenzae protein.

One of the conserved regions in these enzymes is centered on a conserved aspartic acid residue which has been shown [3], in *Aspergillus wentii* beta-glucosidase A3, to be implicated in the catalytic mechanism. This region was used as a signature pattern.

15 Consensus pattern[LIVM SEQ ID NO:4)](2)-[KR]-x-[EQK]-x(4)-G-[LIVMFT SEQ ID NO:282)]-[LIVT SEQ ID NO:165)]-[LIVMF SEQ ID NO:2)]-[ST]-D-x(2)-[SGADNI SEQ ID NO:283)] [D is the active site residue]

Sequences known to belong to this class detected by the patternALL.

20 [1]Henrissat B. Biochem. J. 280:309-316(1991).

[2]Castle L.A., Smith K.D., Morris R.O. J. Bacteriol. 174:1478-1486(1992).

[3]Bause E., Legler G. Biochim. Biophys. Acta 626:459-465(1980).

953. GP120 - Envelope glycoprotein GP120

25 The entry of HIV requires interaction of viral GP120 with Swiss:P01730 and a chemokine receptor on the cell surface. Number of members: 17891

[1]Medline: 98303379. Structure of an HIV gp120 envelope glycoprotein in complex with the CD4 receptor and a neutralizing human antibody. Kwong PD, Wyatt R, Robinson J, Sweet RW, Sodroski J, Hendrickson WA; Nature 1998;393:648-659.

30

954. (GSPII_E) Bacterial type II secretion system protein E signature

PROSITE: PDOC00567. PROSITE cross-reference(s) PS00662; T2SP_E

A number of bacterial proteins, some of which are involved in a general secretion pathway (GSP) for the export of proteins (also called the type II pathway) [1,2], have been found to be evolutionary related. These proteins are listed below:

- The 'E' protein from the GSP operon of: *Aeromonas* (gene *exeE*); *Erwinia* (gene *outE*);
- 5 *Escherichia coli* (gene *yheG*); *Klebsiella pneumoniae* (gene *pulE*); *Pseudomonas aeruginosa* (gene *xcpR*); *Vibrio cholerae* (gene *epsE*) and *Xanthomonas campestris* (gene *xpsE*).
- Agrobacterium tumefaciens* Ti plasmid *virB* operon protein 11. This protein is required for the transfer of T-DNA to plants.
- Bacillus subtilis* *comG* operon protein 1 which is required for the uptake of DNA by
- 10 competent *Bacillus subtilis* cells.
- Aeromonas hydrophila* *tapB*, involved in type IV pilus assembly.
- Pseudomonas* protein *pilB*, which is essential for the formation of the pili.
- Pseudomonas aeruginosa* protein twitching mobility protein *pilT*.
- Neisseria gonorrhoeae* type IV pilus assembly protein *pilF*.
- 15 -*Vibrio cholerae* protein *tcpT*, which is involved in the biosynthesis of the *tcp* pilus.
- Escherichia coli* protein *hofB* (*hopB*).
- Escherichia coli* hypothetical protein *ygcB*.
- Escherichia coli* hypothetical protein *yggR*.

20 These proteins have from 344 (*pilT* and *virB11*) to 568 (*tapB*) amino acids, they are probably cytoplasmically located and, on the basis of the presence of a conserved P-loop region (see <PDOC00017>), probably bind ATP. A region that overlaps the 'B' motif of ATP-binding proteins was selected as a signature pattern.

25 Consensus pattern[LIVM SEQ ID NO:4]-R-x(2)-P-D-x-[LIVM SEQ ID NO:4](3)-G-E-[LIVM SEQ ID NO:4]-R-D
Sequences known to belong to this class detected by the patternALL, except for *ygcB*.

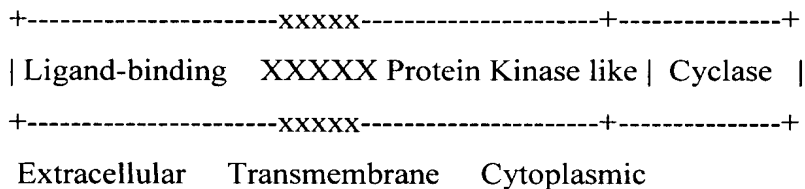
- [1]Salmond G.P.C., Reeves P.J. Trends Biochem. Sci. 18:7-12(1993).
- 30 [2]Hobbs M., Mattick J.S. Mol. Microbiol. 10:233-243(1993).

955. (guanylate_cyc) Guanylate cyclases signature

PROSITE: PDOC00425. PROSITE cross-reference(s) PS00452;

GUANYLATE_CYCLASES Guanylate cyclases (EC 4.6.1.2) [1 to 4] catalyze the formation of cyclic GMP (cGMP) from GTP. cGMP acts as an intracellular messenger, activating cGMP dependent kinases and regulating CGMP-sensitive ion channels. The role of cGMP as a second messenger in vascular smooth muscle relaxation and retinal photo-transduction is well established. Guanylate cyclase is found both in the soluble and particular fraction of eukaryotic cells. The soluble and plasma membrane-bound forms differ in structure, regulation and other properties.

Most currently known plasma membrane-bound forms are receptors for small polypeptides. The topology of such proteins is the following: they have a N-terminal extracellular domain which acts as the ligand binding region, then a transmembrane domain, followed by a large cytoplasmic C-terminal region that can be subdivided into two domains: a protein kinase-like domain that appears important for proper signalling and a cyclase catalytic domain. This topology is schematically represented below.



The known guanylate cyclase receptors are:

-The sea-urchins receptors for speract and resact, which are small peptides that stimulate sperm motility and metabolism.

-The receptors for natriuretic peptides (ANF). Two forms of ANF receptors with guanylate cyclase activity are currently known: GC-A (or ANP-A) which seems specific to atrial natriuretic peptide (ANP), and GC-B (or ANP-B) which seems to be stimulated more effectively by brain natriuretic peptide (BNP) than by ANP.

-The receptor for Escherichia coli heat-stable enterotoxin (GC-C). The endogenous ligand for this intestinal receptor seems to be a small peptide called guanylin.

-Retinal guanylate cyclase (retGC) which probably plays a specific functional role in the rods and/or cones of photoreceptors. It is not known if this protein acts as receptor, but its structure is similar to that of the other plasma membrane-bound GCs.

The soluble forms of guanylate cyclase are cytoplasmic heterodimers. The two subunits, alpha and beta are proteins of from 70 to 82 Kd which are highly related. Two forms of beta subunits are currently known: beta-1 which seems to be expressed in lung and brain, and beta-2 which is more abundant in kidney and liver.

The membrane and cytoplasmic forms of guanylate cyclase share a conserved domain which is probably important for the catalytic activity of the enzyme. Such a domain is also found twice in the different forms of membrane-bound adenylate cyclases (also known as class-III) [5,6] from mammals, slime mold or *Drosophila*. A consensus pattern was derived from the most conserved region in that domain.

Consensus pattern G-V-[LIVM SEQ ID NO:4)]-x(0,1)-G-x(5)-[FY]-x-[LIVM SEQ ID NO:4)]-[FYW]-[GS]-[DNTHKW SEQ ID NO:750)]-[DNT]-[IV]-[DNTA SEQ ID NO:751)]-x(5)-[DE]

Sequences known to belong to this class detected by the pattern ALL, except for the sea urchin *Arbacia punctulata* resact receptor which lack this domain.

Note this pattern will detect both domains of adenylate cyclases class-III.

[1] Koesling D., Boehme E., Schultz G. *FASEB J.* 5:2785-2791(1991).

[2] Garbers D.L. *New Biol.* 2:499-504(1990).

[3] Garbers D.L. *Cell* 71:1-4(1992).

[4] Yuen P.S.T., Garbers D.L. *Annu. Rev. Neurosci.* 15:193-225(1992).

[5] Iyengar R. *FASEB J.* 7:768-775(1993).

[6] Barzu O., Danchin A. *Prog. Nucleic Acid Res. Mol. Biol.* 49:241-283(1994).

956. Hemolysin-type calcium-binding region signature (HemolysinCabinD)

Gram-negative bacteria produce a number of proteins which are secreted into the growth medium by a mechanism that does not require a cleaved N-terminal signal sequence. These proteins, while having different functions, seem [1] to share two properties: they bind calcium and they contain a variable number of tandem repeats consisting of a nine amino acid motif rich in glycine, aspartic acid and asparagine. It has been shown [2] that such a domain is involved in the binding of calcium ions in a parallel beta roll structure. The proteins which are currently known to belong to this category are:

- Hemolysins from various species of bacteria. Bacterial hemolysins are exotoxins that attack blood cell membranes and cause cell rupture. The hemolysins which are known to contain such a domain are those from: *E. coli* (gene *hlyA*), *A. pleuropneumoniae* (gene *appA*), *A. actinomycetemcomitans* and *P. haemolytica* (leukotoxin) (gene *lktA*).

5 - Cyclolysin from *Bordetella pertussis* (gene *cyaA*). A multifunctional protein which is both an adenylate cyclase and a hemolysin.

- Extracellular zinc proteases: serralyisin (EC 3.4.24.40) from *Serratia*, *prtB* and *prtC* from *Erwinia chrysanthemi* and *aprA* from *Pseudomonas aeruginosa*.

- Nodulation protein *nodO* from *Rhizobium leguminosarum*.

10 A signature pattern was derived from conserved positions in the sequence of the calcium-binding domain.

Consensus pattern D-x-[LI]-x(4)-G-x-D-x-[LI]-x-G-G-x(3)-D Sequences known to belong to this class detected by the pattern ALL.

15

Note: This pattern is found once in *nodO* and the extracellular proteases but up to 5 times in some hemolysin/cyclolysins.

[1] Economou A., Hamilton W.D.O., Johnston A.W.B., Downie J.A. EMBO J. 9:349-354(1990).

20

[2] Baumann U., Wu S., Flaherty K.M., McKay D.B. EMBO J. 12:3357-3364(1993).

957. Hint module (Hint)

25 This is an alignment of the Hint module in the Hedgehog proteins. It does not include any Inteins which also possess the Hint module.

Number of members: 36

[1] Hall TM, Porter JA, Young KE, Koonin EV, Beachy PA, Leahy DJ; Medline: 97474313
30 "Crystal structure of a Hedgehog autoprocessing domain: homology between Hedgehog and self-splicing proteins." Cell 1997;91:85-97.

958. Hydantoinase/oxoprolinase (Hydantoinase)

This family includes the enzymes hydantoinase and oxoprolinase EC:3.5.2.9. Both reactions involve the hydrolysis of 5-membered rings via hydrolysis of their internal imide bonds [1].

Number of members: 14

5

[1] Ye GJ, Breslow EB, Meister A, Guo-jie GE\$[corrected to Ye GJ]; Medline: 97113037
“The amino acid sequence of rat kidney 5-oxo-L-prolinase determined by cDNA cloning”
[published erratum appears in J Biol Chem 1997 Feb 14;272(7):4646] J Biol Chem
1996;271:32293-32300.

10

959. IMP dehydrogenase / GMP reductase signature (IMPDH_N)

15

IMP dehydrogenase (EC 1.1.1.205) (IMPDH) catalyzes the rate-limiting reaction of de novo GTP biosynthesis, the NAD-dependent reduction of IMP into XMP [1]. Inhibition of IMP dehydrogenase activity results in the cessation of DNA synthesis. As IMP dehydrogenase is associated with cell proliferation, it is a possible target for cancer chemotherapy. Mammalian and bacterial IMPDHs are tetramers of identical chains. There are two IMP dehydrogenase isozymes in humans [2].

20

GMP reductase (EC 1.6.6.8) catalyzes the irreversible and NADPH-dependent reductive deamination of GMP into IMP [3]. It converts nucleobase, nucleoside and nucleotide derivatives of G to A nucleotides, and maintains intracellular balance of A and G nucleotides.

25

IMP dehydrogenase and GMP reductase share many regions of sequence similarity. One of these regions is centered on a cysteine residue thought [3] to be involved in binding IMP. This region was used as a signature pattern.

Consensus pattern[LIVM SEQ ID NO:4)]-[RK]-[LIVM SEQ ID NO:4)]-G-[LIVM SEQ ID NO:4)]-G-x-G-S-[LIVM SEQ ID NO:4)]-C-x-T [C is the putative IMP-binding residue]

30

Sequences known to belong to this class detected by the pattern ALL.

[1] Collart F.R., Huberman E. J. Biol. Chem. 263:15769-15772(1988).

[2] Natsumeda Y., Ohno S., Kawasaki H., Konno Y., Weber G., Suzuki K. J. Biol. Chem. 265:5292-5295(1990).

[3] Andrews S.C., Guest J.R. Biochem. J. 255:35-43(1988).

5 960. impB/mucB/samB family (IMS)

These proteins are involved in UV protection (Swiss).

Number of members: 38

10 961. Type II intron maturase (Intron_maturas2)

Group II introns use intron-encoded reverse transcriptase, maturase and DNA endonuclease activities for site-specific insertion into DNA [2]. Although this type of intron is self splicing in vitro they require a maturase protein for

15 splicing in vivo. It has been shown that a specific region of the aI2 intron is needed for the maturase function [1]. This region was found to be conserved in group II introns and called domain X [3].

Number of members: 335

20 [1] Moran JV, Mecklenburg KL, Sass P, Belcher SM, Mahnke D, Lewin A, Perlman P; Medline: 94301788 "Splicing defective mutants of the COXI gene of yeast mitochondrial DNA: initial definition of the maturase domain of the group II intron aI2. Nucleic Acids Res 1994;22:2057-2064.

25 [2] Guo H, Zimmerly S, Perlman PS, Lambowitz AM; Medline: 98031910 "Group II intron endonucleases use both RNA and protein subunits for recognition of specific sequences in double-stranded DNA." EMBO J 1997;16:6835-6848.

[3] Mohr G, Perlman PS, Lambowitz AM; Medline: 94077696 "Evolutionary relationships among group II intron-encoded proteins and identification of a conserved domain that may be related to maturase function." Nucleic Acids Res 1993;21:4991-4997.

30

962. LAGLIDADG endonuclease (Intron_maturase)

[1] Heath PJ, Stephens KM, Monnat RJ Jr, Stoddard BL; Medline: 97331323 "The structure of I-Crel, a group I intron-encoded homing endonuclease." Nat Struct Biol 1997;4:468-476.

[2] Belfort M, Roberts RJ; Medline: 97402526 "Homing endonucleases: keeping the house in order." Nucleic Acids Res 1997;25:3379-3388.

5 [3] Dalgaard JZ, Klar AJ, Moser MJ, Holley WR, Chatterjee A, Mian IS; Medline: 98026854 "Statistical modeling and analysis of the LAGLIDADG family of site-specific endonucleases and identification of an intein that encodes a site-specific endonuclease of the HNH family." Nucleic Acids Res 1997;25:4626-4638.

10 Number of members: 220

963. Isopentenyl transferase (IPT)

15 Isopentenyl transferase / dimethylallyl transferase synthesizes isopentenyladenosine 5'-monophosphate, a cytokinin that induces shoot formation on host plants infected with the Ti plasmid [1].

Number of members: 16

20 [1] Canaday J, Gerad JC, Crouzet P, Otten L; Medline: 93101133 "Organization and functional analysis of three T-DNAs from the vitopine Ti plasmid pTiS4." Mol Gen Genet 1992;235:292-303.

964. Laminin EGF-like (Domains III and V) (laminin_EGF)

25 This family is like EGF but has 8 conserved cysteines instead of 6.

Number of members: 501

[1] Engel J; Medline: 93041759 "Laminins and other strange proteins." Biochemistry 1992;31:10643-10651.

30

965. Legume lectins signatures (lectin_legA)

Leguminous plants synthesize sugar-binding proteins which are called legume lectins [1,2]. These lectins are generally found in the seeds. The exact function of legume lectins is not known but they may be involved in the attachment of nitrogen-fixing bacteria to legumes and in the protection against pathogens. Legume lectins bind calcium and manganese (or other transition metals).

Legume lectins are synthesized as precursor proteins of about 230 to 260 amino acid residues. Some legume lectins are proteolytically processed to produce two chains: beta (which corresponds to the N-terminal) and alpha (C-terminal). The lectin concanavalin A (conA) from jack bean is exceptional in that the two chains are transposed and ligated (by formation of a new peptide bond). The N-terminus of mature conA thus corresponds to that of the alpha chain and the C-terminus to the beta chain.

Two signature patterns were developed specific to legume lectins: the first is located in the C-terminal section of the beta chain and contains a conserved aspartic acid residue important for the binding of calcium and manganese; the second one is located in the N-terminal of the alpha chain.

Consensus pattern [LIV]-[STAG SEQ ID NO:20)]-V-[DEQV SEQ ID NO:358)]-[FLI]-D-[ST] [D binds manganese and calcium] Sequences known to belong to this class detected by the pattern ALL.

Consensus pattern [LIV]-x-[EDQ]-[FYWKR SEQ ID NO:359)]-V-x-[LIVF SEQ ID NO:127)]-G-[LF]-[ST] Sequences known to belong to this class detected by the pattern ALL.

[1] Sharon N., Lis H. FASEB J. 4:3198-320(1990).

[2] Lis H., Sharon N. Annu. Rev. Biochem. 55:33-37(1986).

966. Malate synthase signature (malate_synthase)

Malate synthase (EC 4.1.3.2) catalyzes the aldol condensation of glyoxylate with acetyl-CoA to form malate - the second step of the glyoxylate bypass, an alternative to the tricarboxylic acid cycle in bacteria, fungi and plants. Malate synthase is a protein of 530 to 570 amino

acids whose sequence is highly conserved across species [1]. As a signature pattern, a very conserved region was selected in the central section of the enzyme.

Consensus pattern[KR]-[DENQ SEQ ID NO:371)]-H-x(2)-G-L-N-x-G-x-W-D-Y-[LIVM
5 SEQ ID NO:4)]-F Sequences known to belong to this class detected by the pattern ALL.

[1] Bruinenberg P.G., Blaauw M., Kazemier B., Ab G. Yeast 6:245-254(1990).

967. MatK/TrnK amino terminal region (MatK_N)

10 [1] Mohr G, Perlman PS, Lambowitz AM; Medline: 94077696 "Evolutionary relationships among group II intron-encoded proteins and identification of a conserved domain that may be related to maturase function." Nucleic Acids Res 1993;21:4991-4997.

15 Number of members: 495

968. MOZ/SAS family (MOZ_SAS)

This region of these proteins has been suggested to be homologous to acetyltransferases [1].

20 However the similarity is not supported by standard sequence analysis.

Number of members: 15

[1] Kamine J, Elangovan B, Subramanian T, Coleman D, Chinnadurai G; Medline: 96182937

25 "Identification of a cellular protein that specifically interacts with the essential cysteine region of the HIV-1 Tat transactivator." Virology 1996;216:357-366.

[2] Reifsnyder C, Lowell J, Clarke A, Pillus L; Medline: 96376969 "Yeast SAS silencing genes and human genes associated with AML and HIV-1 Tat interactions are homologous with acetyltransferases" [see comments] [published erratum appears in Nat Genet 1997 May;16(1):109] Nat Genet 1996;14:42-49.

30 969. mRNA capping enzyme (mRNA_cap_enzyme)

[1] Hakansson K, Doherty AJ, Shuman S, Wigley DB; Medline: 97304383 "X-ray crystallography reveals a large conformational change during guanyl transfer by mRNA capping enzymes." Cell 1997;89:545-553.

5 Number of members: 7

970. DNA mismatch repair proteins mutS family signature (MutS_C)

Mismatch repair contributes to the overall fidelity of DNA replication [1]. It involves the
10 correction of mismatched base pairs that have been missed by the proofreading element of the DNA polymerase complex. The sequence of some proteins involved in mismatch repair in different organisms have been found to be evolutionary related [2,3]. One of these families is called mutS [4,E1], it consists of:

- Prokaryotic protein mutS protein (also called hexA in *Streptococcus pneumoniae*). Muts is
15 thought to carry out the mismatch recognition step of DNA repair.

- Eukaryotic MSH1, which is involved in mitochondrial DNA repair.

- Eukaryotic MSH2, which is involved in nuclear postreplication mismatch repair. MSH2 heterodimerizes with MSH6. In man, MSH2 is involved in a form of familial hereditary nonpolyposis colon cancer (HNPCC).

20 - Eukaryotic MSH3, which is probably involved in the repair of large loops.

- Eukaryotic MSH4, which is involved in meiotic recombination.

- Eukaryotic MSH5, which is involved in meiotic recombination.

- Eukaryotic MSH6 (also known as G/T mismatch binding protein), a DNA-repair protein that binds to G/T mismatches through heterodimerization with MSH2.

25 - Prokaryotic protein mutS2 whose function is not yet known.

- A coral (*Sarcophyton glaucum*) mitochondrial encoded mutS-like protein.

As a signature pattern for this class of mismatch repair proteins a region rich in glycine and negatively charged residues was selected This region is found
in the C-terminal section of these proteins; about 80 residues to the C-terminal of an ATP-
30 binding site motif 'A' (P-loop) (see <PDOC00017>).

Consensus pattern[ST]-[LIVMF SEQ ID NO:2)]-x-[LIVM SEQ ID NO:4)]-x-D-E-[LIVMFY
SEQ ID NO:18)]-[GC]-[RKH]-G-[GST]- x(4)-G Sequences known to belong to this class
detected by the pattern ALL, except for mutS2.

- 5 [1] Modrich P. Annu. Rev. Biochem. 56:435-466(1987).
[2] Haber L.T., Walker G.C. EMBO J. 10:2707-2715(1991).
[3] New L., Liu K., Crouse G.F. Mol. Gen. Genet. 239:97-108(1993).
[4] Eisen J.A. Nucleic Acids Res. 26:4291-4300(1998).

10 971. MutS family, N-terminal putative DNA binding domain (MutS_N)

This family consists of the N-terminal region of proteins in the mutS family of DNA
mismatch repair proteins and is found associated with MutS_C located in the C-terminal
region. The mutS family of proteins is named after the salmonella typhimurium MutS protein
involved in mismatch repair; other members of the family included the eukaryotic MSH
1,2,3,4,5 and 6 proteins. These have various roles in DNA repair and recombination. Human
MSH has been implicated in non-polyposis colorectal carcinoma (HNPCC) and is a
mismatch binding protein [2]. The aligned region corresponds in part with domains A1, A2
(which may bind DNA) and B (which binds dsDNA in vitro) from T. thermophilus MutS as
characterised in [1].

Number of members: 43

972. Domain in Myosin and Kinesin Tails (MyTH4)

25 Domain present twice in myosin-VIIa, and also present in 3 other myosins.

- [1] Chen ZY, Hasson T, Kelley PM, Schwender BJ, Schwartz MF, Ramakrishnan M,
Kimberling WJ, Mooseker MS, Corey DP; Medline: 97038686 "Molecular cloning and
domain structure of human myosin-VIIa, the gene product defective in Usher syndrome 1B."
Genomics 1996;36:440-448.

Number of members: 21

973. Sodium and potassium ATPases beta subunits signatures (Na₂K-ATPase)

The sodium pump (Na⁺,K⁺ ATPase), located in the plasma membrane of all animal cells [1], is an heterotrimer of a catalytic subunit (alpha chain), a glycoprotein subunit of about 34 Kd (beta chain) and a small hydrophobic protein of about 6 Kd. The beta subunit seems [2] to regulate, through the assembly of alpha/beta heterodimers, the number of sodium pumps transported to the plasma membrane.

Structurally the beta subunit is composed of a charged cytoplasmic domain of about 35 residues, followed by a transmembrane region, and a large extracellular domain that contains three disulfide bonds and glycosylation sites. This structure is schematically represented in the figure below.

+---+ +--+ +-----+ |||||

xxxxxxxxxxxxxxxxxxxxxxxxCxxxxCxCxxCxxxxxxxxCxxxxxxxxxxxxCxxxx

**** **<-Cyt-><TM><-----Extracellular----->

'C': conserved cysteine involved in a disulfide bond.

'*': position of the patterns.

Two isoforms of the beta subunit (beta-1 and beta-2) are currently known; they share about 50% sequence identity. Gastric (K⁺, H⁺) ATPase (proton pump) responsible for acid production in the stomach consist of two subunits [3]; the beta chain is highly similar to the sodium pump beta subunits. Two signature patterns were developed for beta subunits. The first is located in the cytoplasmic domain, while the second is found in the extracellular domain and contains two of the cysteines involved in disulfide bonds.

Consensus pattern [FYW]-x(2)-[FYW]-x-[FYW]-[DN]-x(6)-[LIVM SEQ ID NO:4)]-G-R-T-x(3)-W Sequences known to belong to this class detected by the pattern ALL.

Consensus pattern [RK]-x(2)-C-[RKQWI SEQ ID NO:752)]-x(5)-L-x(2)-C-[SA]-G [The two C's are involved in disulfide bonds] Sequences known to belong to this class detected by the patternALL, except for the beta subunit of the sodium pump of brine shrimp whose sequence is highly divergent in that region.

[1] Horisberger J.D., Lemas V., Krahenbul J.P., Rossier B.C. Annu. Rev. Physiol. 53:565-584(1991).

[2] McDonough A.A., Gerring K., Farley R.A. FASEB J. 4:1598-1605(1990).

- 5 [3] Toh B.-H., Gleeson P.A., Simpson R.J., Moritz R.L., Callaghan J.M., Goldkorn I., Jones C.M., Martinelli T.M., Mu F.-T., Humphris D.C., Pettitt J.M., Mori Y., Masuda T., Sobieszczuk P., Weinstock J., Mantamadiotis T., Baldwin G.S. Proc. Natl. Acad. Sci. U.S.A. 87:6418-6422(1990).

10 974. Respiratory-chain NADH dehydrogenase subunit 1 signatures (NADHdh)

Respiratory-chain NADH dehydrogenase (EC 1.6.5.3) [1,2] (also known as complex I or NADH-ubiquinone oxidoreductase) is an oligomeric enzymatic complex located in the inner mitochondrial membrane which also seems to exist in the chloroplast and in cyanobacteria
15 (as a NADH-plastoquinone oxidoreductase). Among the 25 to 30 polypeptide subunits of this bioenergetic enzyme complex there are fifteen which are located in the membrane part, seven of which are encoded by the mitochondrial and chloroplast genomes of most species. The most conserved of these organelle-encoded subunits is known as subunit 1 (gene ND1 in mitochondrion, and NDH1 in chloroplast) and seems to contain the ubiquinone binding site.

20

The ND1 subunit is highly similar to subunit 4 of *Escherichia coli* formate hydrogenlyase (gene hycD), subunit C of hydrogenase-4 (gene hyfC). *Paracoccus denitrificans* NQO8 and *Escherichia coli* nuoH NADH-ubiquinone oxidoreductase subunits also belong to this family [3]. Two signature patterns were developed based on conserved regions of this subunit.

25

Consensus pattern G-[LIVMFYKRS SEQ ID NO:753)]-[LIVMAGP SEQ ID NO:415)]-Q-x-[LIVMFY SEQ ID NO:18)]-x-D-[AGIM SEQ ID NO:754)]-[LIVMFTA SEQ ID NO:386)]-K-[LVMYST SEQ ID NO:755)]-[LIVMFYG SEQ ID NO:168)]-x-[KR]-[EQG] Sequences known to belong to this class detected by the patternALL, except for watermelon and
30 *Leishmania* ND1.

Consensus pattern P-F-D-[LIVMFYQ SEQ ID NO:188)]-[STAGPVM SEQ ID NO:756)]-E-[GAC]-E-x-[EQ]-[LIVMS SEQ ID NO:429)]-x(2)-G Sequences known to belong to this

class detected by the pattern ALL, except for *Chlamydomonas reinhardtii* and *Pisaster ochraceus* ND1, and tobacco NDH1.

[1] Ragan C.I. Curr. Top. Bioenerg. 15:1-36(1987).

5 [2] Weiss H., Friedrich T., Hofhaus G., Preis D. Eur. J. Biochem. 197:563-576(1991).

[3] Weidner U., Geier S., Ptock A., Friedrich T., Leif H., Weiss H. J. Mol. Biol. 233:109-122(1993).

975. Nickel-dependent hydrogenases large subunit signatures (NiFeSe_Hases)

10

Hydrogenases are enzymes that catalyze the reversible activation of hydrogen and which occur widely in prokaryotes as well as in some eukaryotes. There are various types of hydrogenases, but all of them seem to contain at least one iron-sulfur cluster. They can be broadly divided into two groups: hydrogenases containing nickel and, in some cases, also
15 selenium (the [NiFe] and [NiFeSe] hydrogenases) and those lacking nickel (the [Fe] hydrogenases).

20

The [NiFe] and [NiFeSe] hydrogenases are heterodimer that consist of a small subunit that contains a signal peptide and a large subunit. All the known large subunits seem to be evolutionary related [1]; they contain two Cys-x-x- Cys motifs; one at their N-terminal end; the other at their C-terminal end. These four cysteines are involved in the binding of nickel [2]. In the [NiFeSe] hydrogenases the first cysteine of the C-terminal motif is a selenocysteine which has experimentally been shown to be a nickel ligand [3]. Two patterns were developed which are centered on the Cys-x-x-Cys motifs.

25

Alcaligenes eutrophus possess a NAD-reducing cytoplasmic hydrogenase (hoxS) [4]; this enzyme is composed of four subunits. Two of these subunits (beta and delta) are responsible for the hydrogenase reaction and are evolutionary related to the large and small subunits of membrane-bound hydrogenases. The alpha subunit of coenzyme F420 hydrogenase (EC
30 1.12.99.1) (FRH) from archaeobacterial methanogens also belongs to this family.

Consensus pattern R-G-[LIVMF SEQ ID NO:2]-E-x(15)-[QESM SEQ ID NO:757]-R-x-C-G-[LIVM SEQ ID NO:4)]-C [The two C's are nickel ligands] Sequences known to belong to this class detected by the pattern ALL.

- 5 Consensus pattern [FY]-D-P-C-[LIM]-[ASG]-C-x(2,3)-H [The two C's are nickel ligands] Sequences known to belong to this class detected by the pattern ALL.

[1] Menon N.K., Robbins J., Peck H.D. Jr., Chatelus C.Y., Choi E.-S., Przybyla A.E. J. Bacteriol. 172:1969-1977(1990).

- 10 [2] Volbeda A., Charon M.-H., Piras C., Hatchikian E.C., Frey M., Fontecilla-Camps J.C. Nature 373:580-587(1995).

[3] Eidsness M.K., Scott R.A., Prickrill B., der Vartanian D.V., LeGall J., Moura I., Moura J.J.G., Peck H.D. Jr. Proc. Natl. Acad. Sci. U.S.A. 86:147-151(1989).

- 15 [4] Tran-Betcke A., Warnecke U., Boecker C., Zaborosch C., Friedrich B. J. Bacteriol. 172:2920-2929(1990).

976. NADH-Ubiquinone oxidoreductase (complex I), chain 5 C-terminus (oxidored_q1_C)

- 20 This sub-family represents a carboxyl terminal extension of oxidored_q1. Only NADH-Ubiquinone chain 5 from chloroplasts are in this family. This sub-family is part of complex I which catalyses the transfer of two electrons from NADH to ubiquinone in a reaction that is associated with proton translocation across the membrane.

Number of members: 572

- 25 [1] Walker JE; Medline: 93110040 "The NADH:ubiquinone oxidoreductase (complex I) of respiratory chains." Q Rev Biophys 1992;25:253-324.

977. NADH-Ubiquinone oxidoreductase (complex I), chain 5 N-terminus (oxidored_q1_N)

- 30 This sub-family represents an amino terminal extension of oxidored_q1. Only NADH-Ubiquinone chain 5 and eubacterial chain L are in this family. This sub-family is part of complex I which catalyses the transfer of two electrons from NADH to ubiquinone in a reaction that is associated with proton translocation across the membrane.

Number of members: 546

[1] Walker JE; Medline: 93110040 "The NADH:ubiquinone oxidoreductase (complex I) of respiratory chains." Q Rev Biophys 1992;25:253-324.

5

978. oxidored_q2. NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 4L (EC 1.6.5.3). ND4L OR NAD4L. Arabidopsis thaliana (Mouse-ear cress). Mitochondrion. OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

10

CATALYTIC ACTIVITY: NADH + UBIQUINONE = NAD(+) + UBIQUINOL.

[1] SEQUENCE FROM N.A. MEDLINE; 93156682. Brandt P., Sunkel S., Unseld M., Brennicke A., Knoop V.; "The nad4L gene is encoded between exon c of nad5 and orf25 in the Arabidopsis mitochondrial genome."; Mol. Gen. Genet. 236:33-38(1992).

15

[2] SEQUENCE FROM N.A. STRAIN=CV. COLUMBIA; MEDLINE; 97141919 Unseld M., Marienfeld J.R., Brandt P., Brennicke A.; "The mitochondrial genome of Arabidopsis thaliana contains 57 genes in 366,924 nucleotides."; Nat. Genet. 15:57-61(1997).

20

979. oxidored_q4. Protein name NADH-PLASTOQUINONE OXIDOREDUCTASE CHAIN 3, CHLOROPLAST. Synonym(s)EC 1.6.5.3. Gene name(s)NDHC OR NDH3 From Zea mays (Maize) Encoded on Chloroplast. Taxonomy Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Zea.

CATALYTIC ACTIVITY: NADH + PLASTOQUINONE = NAD(+) + PLASTOQUINOL.

25

SIMILARITY: BELONGS TO THE COMPLEX I SUBUNIT 3 FAMILY.

[1] SEQUENCE FROM N.A. MEDLINE; 89281491. Steinmueller K., Ley A.C., Steinmetz A.A., Sayre R.T., Bogorad L.; "Characterization of the ndhC-psbG-ORF157/159 operon of maize plastid DNA and of the cyanobacterium Synechocystis sp. PCC6803."; Mol. Gen.

30

Genet. 216:60-69(1989).

[2] SEQUENCE FROM N.A. MEDLINE; 95395841. Maier R.M., Neckermann K., Igloi G.L., Koessel H.; "Complete sequence of the maize chloroplast genome: gene content,

hotspots of divergence and fine tuning of genetic information by transcript editing."; J. Mol. Biol. 251:614-628(1995).

980. PAC: PAC motif

- 5 PAC motif occurs C-terminal to a subset of all known PAS motifs. It is proposed to contribute to the PAS domain fold [3]. Number of members: 181

[1] Medline: 97446881 PAS domain S-boxes in archaea, bacteria and sensors for oxygen and redox. Zhulin IB, Taylor BL, Dixon R; Trends Biochem Sci 1997;22:331-333.

- 10 [2] Medline: 95275818. 1.4 A structure of photoactive yellow protein, a cytosolic photoreceptor: unusual fold, active site, and chromophore. Borgstahl GE, Williams DR, Getzoff ED; Biochemistry 1995;34:6278-6287.

[3] Medline: 98044337. PAS: a multifunctional domain family comes to light. Ponting CP, Aravind L; Curr Biol 1997;7:674-677.

15

981. PARP: Poly(ADP-ribose) polymerase catalytic region.

Poly(ADP-ribose) polymerase catalyses the covalent attachment of ADP-ribose units from NAD⁺ to itself and to a limited number of other DNA binding proteins, which decreases their affinity for DNA. Poly(ADP-ribose) polymerase is a regulatory component induced by DNA

20 damage.

The carboxyl-terminal region is the most highly conserved region of the protein. Experiments have shown that a carboxyl 40 kDa fragment is still catalytically active [2]. Number of members: 19

25

[1] Medline: 96353841 Structure of the catalytic fragment of poly(AD-ribose) polymerase from chicken. Ruf A, Mennissier de Murcia J, de Murcia G, Schulz GE; Proc Natl Acad Sci U S A 1996;93:7481-7485.

- 30 [2] Medline: 93293867 The carboxyl-terminal domain of human poly(ADP-ribose) polymerase. Overproduction in Escherichia coli, large scale purification, and characterization. Simonin F, Hofferer L, Panzeter PL, Muller S, de Murcia G, Althaus FR; J Biol Chem 1993;268:13454-13461.

982. PC_rep: Proteasome/cyclosome repeat

[1] Medline: 97348748 A repetitive sequence in subunits of the 26S proteasome and 20S cyclosome (anaphase-promoting complex). Lupas A, Baumeister W, Hofmann K; Trends Biochem Sci 1997;22:195-196.

5 Number of members: 112

983. Peptidase_M1: Peptidase family M1

Members of this family are aminopeptidases. The members differ widely in specificity, hydrolysing acidic, basic or neutral N-terminal residues. This family includes leukotriene-A4 hydrolase Swiss:P09960, this enzyme also has an aminopeptidase activity [1]. Number of members: 72

10

[1] Medline: 95405261 Evolutionary families of metallopeptidases. Rawlings ND, Barrett AJ; Meth Enzymol 1995;248:183-228.

15

984. Neutral zinc metallopeptidases, zinc-binding region signature (Peptidase_M8)
PROSITE cross-reference(s) PS00142; ZINC_PROTEASE

The majority of zinc-dependent metallopeptidases (with the notable exception of the carboxypeptidases) share a common pattern of primary structure [1,2,3] in the part of their sequence involved in the binding of zinc, and can be grouped together as a superfamily, known as the metzincins, on the basis of this sequence similarity. They can be classified into a number of distinct families [4,E1] which are listed below along with the proteases which are currently known to belong to these families.

20

25 Family M1

- Bacterial aminopeptidase N (EC 3.4.11.2) (gene pepN).
- Mammalian aminopeptidase N (EC 3.4.11.2).
- Mammalian glutamyl aminopeptidase (EC 3.4.11.7) (aminopeptidase A). It may play a role in regulating growth and differentiation of early B-lineage cells.
- 30 - Yeast aminopeptidase yscII (gene APE2).
- Yeast alanine/arginine aminopeptidase (gene AAP1).
- Yeast hypothetical protein YIL137c.

- Leukotriene A-4 hydrolase (EC 3.3.2.6). This enzyme is responsible for the hydrolysis of an epoxide moiety of LTA-4 to form LTB-4; it has been shown that it binds zinc and is capable of peptidase activity.

Family M2

- 5 - Angiotensin-converting enzyme (EC 3.4.15.1) (dipeptidyl carboxypeptidase I) (ACE) the enzyme responsible for hydrolyzing angiotensin I to angiotensin II. There are two forms of ACE: a testis-specific isozyme and a somatic isozyme which has two active centers.

Family M3

- 10 - Thimet oligopeptidase (EC 3.4.24.15), a mammalian enzyme involved in the cytoplasmic degradation of small peptides.
- Neurolysin (EC 3.4.24.16) (also known as mitochondrial oligopeptidase M or microsomal endopeptidase).
- Mitochondrial intermediate peptidase precursor (EC 3.4.24.59) (MIP). It is involved the second stage of processing of some proteins imported in the mitochondrion.
- 15 - Yeast saccharolysin (EC 3.4.24.37) (proteinase yscD).
- Escherichia coli and related bacteria dipeptidyl carboxypeptidase (EC 3.4.15.5) (gene dcp).
- Escherichia coli and related bacteria oligopeptidase A (EC 3.4.24.70) (gene opdA or prlC).
- Yeast hypothetical protein YKL134c.

20 Family M4

- Thermostable thermolysins (EC 3.4.24.27), and related thermolabile neutral proteases (bacillolysins) (EC 3.4.24.28) from various species of Bacillus.
- Pseudolysin (EC 3.4.24.26) from Pseudomonas aeruginosa (gene lasB).
- Extracellular elastase from Staphylococcus epidermidis.
- 25 - Extracellular protease prt1 from Erwinia carotovora.
- Extracellular minor protease smp from Serratia marcescens.
- Vibriolysin (EC 3.4.24.25) from various species of Vibrio.
- Protease prtA from Listeria monocytogenes.
- Extracellular proteinase proA from Legionella pneumophila.

30

Family M5

- Mycolysin (EC 3.4.24.31) from Streptomyces cacaoi.

Family M6

- Immune inhibitor A from *Bacillus thuringiensis* (gene *ina*). Ina degrades two classes of insect antibacterial proteins, attacins and cecropins.

5 Family M7

- *Streptomyces* extracellular small neutral proteases

Family M8

10 - Leishmanolysin (EC 3.4.24.36) (surface glycoprotein gp63), a cell surface protease from various species of *Leishmania*.

Family M9

- Microbial collagenase (EC 3.4.24.3) from *Clostridium perfringens* and *Vibrio alginolyticus*.

15

Family M10A

- Serralysin (EC 3.4.24.40), an extracellular metalloprotease from *Serratia*.

- Alkaline metalloproteinase from *Pseudomonas aeruginosa* (gene *aprA*).

- Secreted proteases A, B, C and G from *Erwinia chrysanthemi*.

20

- Yeast hypothetical protein YIL108w.

Family M10B

25 - Mammalian extracellular matrix metalloproteinases (known as matrixins) [5]: MMP-1 (EC 3.4.24.7) (interstitial collagenase), MMP-2 (EC 3.4.24.24) (72 Kd gelatinase), MMP-9 (EC 3.4.24.35) (92 Kd gelatinase), MMP-7 (EC 3.4.24.23) (matrylisin), MMP-8 (EC 3.4.24.34) (neutrophil collagenase), MMP-3 (EC 3.4.24.17) (stromelysin-1), MMP-10 (EC 3.4.24.22) (stromelysin-2), and MMP-11 (stromelysin-3), MMP-12 (EC 3.4.24.65) (macrophage metalloelastase).

30

- Sea urchin hatching enzyme (envelysin) (EC 3.4.24.12). A protease that allows the embryo to digest the protective envelope derived from the egg extracellular matrix.

- Soybean metalloendoproteinase 1.

Family M11

- *Chlamydomonas reinhardtii* gamete lytic enzyme (GLE).

Family M12A

- Astacin (EC 3.4.24.21), a crayfish endoprotease.
- 5 - Meprin A (EC 3.4.24.18), a mammalian kidney and intestinal brush border metalloendopeptidase.
- Bone morphogenic protein 1 (BMP-1), a protein which induces cartilage and bone formation and which expresses metalloendopeptidase activity. The *Drosophila* homolog of BMP-1 is the dorsal-ventral patterning protein tolloid.
- 10 - Blastula protease 10 (BP10) from *Paracentrotus lividus* and the related protein SpAN from *Strongylocentrotus purpuratus*.
- *Caenorhabditis elegans* protein toh-2.
- *Caenorhabditis elegans* hypothetical protein F42A10.8.
- Choriolytins L and H (EC 3.4.24.67) (also known as embryonic hatching proteins LCE and HCE) from the fish *Oryzias latipes*. These proteases participate in the breakdown of the egg envelope, which is derived from the egg extracellular matrix, at the time of hatching.
- 15

Family M12B

- 20 - Snake venom metalloproteinases [6]. This subfamily mostly groups proteases that act in hemorrhage. Examples are: adamalysin II (EC 3.4.24.46), atrolysin C/D (EC 3.4.24.42), atrolysin E (EC 3.4.24.44), fibrolase (EC 3.4.24.72), trimereylisin I (EC 3.4.25.52) and II (EC 3.4.25.53).
- Mouse cell surface antigen MS2.

25

Family M13

- Mammalian neprilysin (EC 3.4.24.11) (neutral endopeptidase) (NEP).
- Endothelin-converting enzyme 1 (EC 3.4.24.71) (ECE-1), which process the precursor of endothelin to release the active peptide.
- 30 - Kell blood group glycoprotein, a major antigenic protein of erythrocytes. The Kell protein is very probably a zinc endopeptidase.
- Peptidase O from *Lactococcus lactis* (gene pepO).

Family M27

- Clostridial neurotoxins, including tetanus toxin (TeTx) and the various botulinum toxins (BoNT). These toxins are zinc proteases that block neurotransmitter release by proteolytic cleavage of synaptic proteins such as synaptobrevins, syntaxin and SNAP-25 [7,8].

Family M30

- *Staphylococcus hyicus* neutral metalloprotease.

Family M32

- Thermostable carboxypeptidase 1 (EC 3.4.17.19) (carboxypeptidase Taq), an enzyme from *Thermus aquaticus* which is most active at high temperature.

Family M34

- Lethal factor (LF) from *Bacillus anthracis*, one of the three proteins composing the anthrax toxin.

Family M35

- Deuterolysin (EC 3.4.24.39) from *Penicillium citrinum* and related proteases from various species of *Aspergillus*.

Family M36

- Extracellular elastinolytic metalloproteinases from *Aspergillus*.

From the tertiary structure of thermolysin, the position of the residues acting as zinc ligands and those involved in the catalytic activity are known. Two of the zinc ligands are histidines which are very close together in the sequence; C-terminal to the first histidine is a glutamic acid residue which acts as a nucleophile and promotes the attack of a water molecule on the carbonyl carbon of the substrate. A signature pattern which includes the two histidine and the glutamic acid residues is sufficient to detect this superfamily of proteins.

Consensus pattern[GSTALIVN SEQ ID NO:679]-x(2)-H-E-[LIVMFYW SEQ ID NO:26)]-
{DEHRKP SEQ ID NO:680})-H-x-[LIVMFYWGSPQ SEQ ID NO:681)]

[The two H's are zinc ligands] [E is the active site residue]

Sequences known to belong to this class detected by the patternALL, except
5 for members of families M5, M7 and M11.

Other sequence(s) detected in SWISS-PROT57; including *Neurospora crassa*
conidiation-specific protein 13 which could be a zinc-protease.

[1]Jongeneel C.V., Bouvier J., Bairoch A. FEBS Lett. 242:211-214(1989).

[2]Murphy G.J.P., Murphy G., Reynolds J.J. FEBS Lett. 289:4-7(1991).

10 [3]Bode W., Grams F., Reinemer P., Gomis-Rueth F.-X., Baumann U., McKay D.B.,
Stoecker W. Zoology 99:237-246(1996).

[4]Rawlings N.D., Barrett A.J. Meth. Enzymol. 248:183-228(1995).

[5]Woessner J. Jr. FASEB J. 5:2145-2154(1991).

[6]Hite L.A., Fox J.W., Bjarnason J.B. Biol. Chem. Hoppe-Seyler 373:381-385(1992).

15 [7]Montecucco C., Schiavo G. Trends Biochem. Sci. 18:324-327(1993).

[8]Niemann H., Blasi J., Jahn R. Trends Cell Biol. 4:179-185(1994).

985. PHO4: Phosphate transporter family

This family includes PHO-4 from *Neurospora crassa* which is a Na(+)-phosphate
20 symporter [1]. This family also contains the leukemia virus receptor Swiss:Q08344. Number
of members: 41

[1] Medline: 95249577 Repressible cation-phosphate symporters in *Neurospora crassa*.
Versaw WK, Metzenberg RL; Proc Natl Acad Sci U S A 1995;92:3884-3887.

25

986. Photosynthetic reaction center proteins signature (photoRC)

PROSITE cross-reference(s): PS00244; REACTION_CENTER

In the photosynthetic reaction center of purple bacteria, two homologous integral
30 membrane proteins, L(ight) and M(edium), are known to be essential to the light-mediated
water-splitting process. In the photosystem II of eukaryotic chloroplasts two related
proteins are involved: the D1 (psbA) and D2 proteins (psbD). These four types of protein
probably evolved from a common ancestor [see 1,2 for recent reviews].

A signature pattern was developed which include two conserved histidine residues. In L and M chains, the first histidine is a ligand of the magnesium ion of the special pair bacteriochlorophyll, the second is a ligand of a ferrous non-heme iron atom. In photosystem II these two histidines are thought to play a similar role.

Consensus pattern[NQH]-x(4)-P-x-H-x(2)-[SAG]-x(11)-[SAGC SEQ ID NO:758)]-x-H-[SAG](2)

[The first H is a magnesium ligand] [The second H is a iron ligand]

Sequences known to belong to this class detected by the patternALL, except for broad bean psbA which has Gln instead of the second His.

[1]Michel H., Deisenhofer J. Biochemistry 27:1-7(1988).

[2]Barber J. Trends Biochem. Sci. 12:321-326(1987).

987. phytochrome: Phytochrome region

This family contains a region specific to phytochrome proteins. Number of members:

145

988. PI3K_C2: C2 domain

Phosphoinositide 3-kinase region postulated to contain a C2 domain. Outlier of C2 family.

Number of members: 39

[1] Medline: 97388296 Using structure to define the function of phosphoinositide 3-kinase family members. Domin J, Waterfield MD; FEBS Lett 1997;410:91-95.

[2] Medline: 97398940 Phosphoinositide 3-kinases: a conserved family of signal transducers. Vanhaesebroeck B, Leever SJ, Panayotou G, Waterfield MD; Trends Biochem Sci 1997;22:267-272.

989. PI3Ka: Phosphoinositide 3-kinase family, accessory domain (PIK domain)

PIK domain is conserved in all PI3 and PI4-kinases. Its role is unclear but it has been suggested [2] to be involved in substrate presentation.

Number of members: 47

[1] Medline: 97388296 Using structure to define the function of phosphoinositide 3-kinase family members. Domin J, Waterfield MD; FEBS Lett 1997;410:91-95.

[2] Medline: 94069320 Phosphatidylinositol 4-kinase: gene structure and requirement for yeast cell viability. Flanagan CA, Schnieders EA, Emerick AW, Kunisawa R, Admon A, Thorner J; Science 1993;262:1444-1448.

990. P-II protein signatures

PROSITE cross-reference(s): PS00496; PII_GLNB_UMP, PS00638; PII_GLNB_CTER

The P-II protein (gene *glnB*) is a bacterial protein important for the control of glutamine synthetase [1,2,3]. In nitrogen-limiting conditions, when the ratio of glutamine to 2-ketoglutarate decreases, P-II is uridylylated on a tyrosine residue to form P-II-UMP. P-II-UMP allows the deadenylation of glutamine synthetase (GS), thus activating the enzyme. Conversely, in nitrogen excess, P-II-UMP is deuridylated and then promotes the adenylation of GS. P-II also indirectly controls the transcription of the GS gene (*glnA*) by preventing NR-II (*ntrB*) to phosphorylate NR-I (*ntrC*) which is the transcriptional activator of *glnA*. Once P-II is uridylylated, these events are reversed.

P-II is a protein of about 110 amino acid residues extremely well conserved. The tyrosine which is uridylylated is located in the central part of the protein.

In cyanobacteria, P-II seems to be phosphorylated on a serine residue rather than being uridylylated.

In methanogenic archaeobacteria, the nitrogenase iron protein gene (*nifH*) is followed by two open reading frames highly similar to the eubacterial P-II protein [4]. These proteins could be involved in the regulation of nitrogen fixation.

In the red alga, *Porphyra purpurea*, there is a *glnB* homolog encoded in the chloroplast genome.

Other proteins highly similar to *glnB* are:

- *Bacillus subtilis* protein nrgB [5].
- *Escherichia coli* hypothetical protein ybaI [6].

5 Two signature patterns were developed for P-II protein. The first one is a conserved stretch (in eubacteria) of six residues which contains the uridylated tyrosine, the other is derived from a conserved region in the C-terminal part of the P-II protein.

Consensus pattern Y-[KR]-G-[AS]-[AE]-Y [The second Y is uridylated]

10 Sequences known to belong to this class detected by the pattern ALL glnB's from eubacteria.

Consensus pattern [ST]-x(3)-G-[DY]-G-[KR]-[IV]-[FW]-[LIVM SEQ ID NO:4)]-x(2)-[LIVM SEQ ID NO:4)]

15 [1] Magasanik B. *Biochimie* 71:1005-1012(1989).

[2] Holtel A., Merrick M. *Mol. Gen. Genet.* 215:134-138(1988).

[3] Cheah E., Carr P.D., Suffolk P.M., Vasuvedan S.G., Dixon N.E., Ollis D.L. *Structure* 2:981-990(1994).

[4] Sibold L., Henriquet M., Possot O., Aubert J.-P. *Res. Microbiol.* 142:5-12(1991).

20 [5] Wray L.V. Jr., Atkinson M.R., Fisher S.H. *J. Bacteriol.* 176:108-114(1994).

[6] Allikmets R., Gerrard B.C., Court D., Dean M.C. *Gene* 136:231-236(1993).

991. PIP5K: Phosphatidylinositol-4-phosphate 5-Kinase

This family contains a region from the common kinase core found in the type I phosphatidylinositol-4-phosphate 5-kinase (PIP5K) family as described in [1]. The family consists of various type I, II and III PIP5K enzymes. PIP5K catalyses the formation of phosphoinositol-4,5-bisphosphate via the phosphorylation of phosphatidylinositol-4-phosphate a precursor in the phosphoinositide signaling pathway. Number of members: 33

30 [1] Medline: 98204859. Type I phosphatidylinositol-4-phosphate 5-kinases. Cloning of the third isoform and deletion/substitution analysis of members of this novel lipid kinase family. Ishihara H, Shibasaki Y, Kizuki N, Wada T, Yazaki Y, Asano T, Oka Y; *J Biol Chem* 1998;273:8741-8748.

[2] Medline: 97115834 Type I phosphatidylinositol-4-phosphate 5-kinases are distinct members of this novel lipid kinase family. Loijens JC, Anderson RA; J Biol Chem 1996 20;271:32937-32943.

5 992. PolyA_pol: Poly A polymerase family

This family includes nucleic acid independent RNA polymerases, such as Poly(A) polymerase, which adds the poly (A) tail to mRNA EC:2.7.7.19. This family also includes the tRNA nucleotidyltransferase that adds the CCA to the 3' of the tRNA EC:2.7.7.25. Number of members: 31

10

[1] Medline: 93066242 Identification of the gene for an Escherichia coli poly(A) polymerase. Cao GJ, Sarkar N; Proc Natl Acad Sci U S A 1992;89:10380-10384.

993. Photosystem I psaA and psaB proteins signature (psaA_psaB)

15 PROSITE cross-reference(s)PS00419; PHOTOSYSTEM_I_PSAAB

Photosystem I (PSI) [1] is an integral membrane protein complex that uses light energy to mediate electron transfer from plastocyanin to ferredoxin. PSI is found in the chloroplast of plants and cyanobacteria. The electron transfer components of the reaction center of PSI are a primary electron donor P-700 (chlorophyll dimer) and five electron acceptors: A0 (chlorophyll), A1 (a phylloquinone) and three 4Fe-4S iron-sulfur centers: Fx, Fa, and Fb.

20

PsaA and psaB, two closely related proteins, are involved in the binding of P700, A0, A1, and Fx. psaA and psaB are both integral membrane proteins of 730 to 750 amino acids that seem to contain 11 transmembrane segments. The Fx 4Fe-4S iron-sulfur center is bound by four cysteines; two of these cysteines are provided by the psaA protein and the two others by psaB. The two cysteines in both proteins are proximal and located in a loop between the ninth and tenth transmembrane segments. A leucine zipper motif seems to be present [2] downstream of the cysteines and could contribute to dimerization of psaA/psaB.

30

The signature pattern for these proteins is based on the perfectly conserved region that includes the two iron-sulfur binding cysteines.

Consensus pattern C-D-G-P-G-R-G-G-T-C [The two C's bind the iron-sulfur center]

[1]Golbeck J.H. Biochim. Biophys. Acta 895:167-204(1987).

[2]Webber A.N., Malkin R. FEBS Lett. 264:1-14(1990).

5 994. PSBH: Photosystem II 10 kDa phosphoprotein

This protein is phosphorylated in a light dependent reaction.

Number of members: 20

995. PsbJ

10 This family consists of the photosystem II reaction center protein PsbJ from plants and Cyanobacteria. In Synechocystis sp. PCC 6803 PsbJ regulates the number of photosystem II centers in thylakoid membranes, it is a predicted 4kDa protein with one membrane spanning domain [1]. Number of members: 20

15 [1] Medline: 93131892. Genetic and immunological analyses of the cyanobacterium Synechocystis sp. PCC 6803 show that the protein encoded by the psbJ gene regulates the number of photosystem II centers in thylakoid membranes. Lind LK, Shukla VK, Nyhus KJ, Pakrasi HB; J Biol Chem 1993;268:1575-1579.

20 996. PSBT: Photosystem II reaction centre T protein

The exact function of this protein is unknown. It probably consists of a single transmembrane spanning helix. The Swiss:P37256 protein, appears to be (i) a novel photosystem II subunit and (ii) required for maintaining optimal photosystem II activity under adverse growth conditions [1]. Number of members: 17

25 [1] Medline: 94298765. The chloroplast ycf8 open reading frame encodes a photosystem II polypeptide which maintains photosynthetic activity under adverse growth conditions. Monod C, Takahashi Y, Goldschmidt-Clermont M, Rochaix JD; EMBO J 1994;13:2747-2754.

30 997. PSI_8. PHOTOSYSTEM I REACTION CENTRE SUBUNIT VIII. Synonym(s)PSI-I. Gene name(s)PSAI. From Hordeum vulgare (Barley). Encoded on Chloroplast. Taxonomy

Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Hordeum.

MAY HELP IN THE ORGANIZATION OF THE PSAL SUBUNIT. BELONGS TO THE PSAL FAMILY.

5

[1] SEQUENCE FROM N.A. MEDLINE; 90036933. Scheller H.V., Okkels J.S., Hoej P.B., Svendsen I., Roepstorff P., Moeller B.L.; "The primary structure of a 4.0-kDa photosystem I polypeptide encoded by the chloroplast psal gene."; J. Biol. Chem. 264:18402-18406(1989).

10 998. PSI_PsaJ: Photosystem I reaction centre subunit IX / PsaJ

This family consists of the photosystem I reaction centre subunit IX or PsaJ from various organisms including *Synechocystis* sp. (strain pcc 6803), *Pinus thunbergii* (green pine) and *Zea mays* (maize). PsaJ Swiss:P19443 is a small 4.4kDa, chloroplastal encoded, hydrophobic subunit of the photosystem I reaction complex its function is not yet fully understood [1].

15

PsaJ can be cross-linked to PsaF Swiss:P12356 and has a single predicted transmembrane domain it has a proposed role in maintaining PsaF in the correct orientation to allow for fast electron transfer from soluble donor proteins to P700+ [1]. Number of members: 18

20

[1] Medline: 99238330. A large fraction of PsaF is nonfunctional in photosystem I complexes lacking the PsaJ subunit. Fischer N, Boudreau E, Hippler M, Drepper F, Haehnel W, Rochaix JD; Biochemistry 1999;38:5546-5552.

[2] Medline: 93252282. Genes encoding eleven subunits of photosystem I from the thermophilic cyanobacterium *Synechococcus* sp. Muhlenhoff U, Haehnel W, Witt H, Herrmann RG; Gene 1993;127:71-78.

25

999. PSII. Protein namePHOTOSYSTEM II P680 CHLOROPHYLL A APOPROTEIN.

Synonym(s)CP-47 PROTEIN. Gene name(s)PSBB. From *Hordeum vulgare* (Barley), Encoded on Chloroplast. Taxonomy Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Hordeum.

30

FUNCTION: THIS PROTEIN CONJUGATES WITH CHLOROPHYLL & CATALYZES THE PRIMARY LIGHT-INDUCED PHOTOCHEMICAL PROCESSES OF PHOTOSYSTEM II. SUBCELLULAR LOCATION: CHLOROPLAST THYLAKOID MEMBRANE. SIMILARITY: BELONGS TO THE PSBB / PSBC FAMILY.

[1] SEQUENCE FROM N.A. STRAIN=CV. SABARLIS; MEDLINE; 89240047. Andreeva A.V., Buryakova A.A., Reverdatto S.V., Chakhmakhcheva O.G., Efimov V.A.; "Nucleotide sequence of the 5.2 kbp barley chloroplast DNA fragment, containing psbB-psbH-petB-petD gene cluster."; Nucleic Acids Res. 17:2859-2860(1989).

[2] SEQUENCE FROM N.A. STRAIN=CV. SABARLIS; MEDLINE; 92207253. Efimov V.A., Andreeva A.V., Reverdatto S.V., Chakhmakhcheva O.G.; "Photosystem II of rye. Nucleotide sequence of the psbB, psbC, psbE, psbF, psbH genes of rye and chloroplast DNA regions adjacent to them."; Bioorg. Khim. 17:1369-1385(1991).

[3] SEQUENCE OF 411-420. Hinz U.G.; "Isolation of the photosystem II reaction center complex from barley. Characterization by circular dichroism spectroscopy and amino acid sequencing."; Carlsberg Res. Commun. 50:285-298(1985).

1000. QRPTase. Quinolinate phosphoribosyl transferase.

Quinolinate phosphoribosyl transferase (QRPTase) or nicotinate-nucleotide pyrophosphorylase EC:2.4.2.19 is involved in the de novo synthesis of NAD in both prokaryotes and eukaryotes. It catalyses the reaction of quinolinic acid with 5-phosphoribosyl-1-pyrophosphate (PRPP) in the presence of Mg^{2+} to give rise to nicotinic acid mononucleotide (NaMN), pyrophosphate and carbon dioxide [1,2]. Number of members: 26.

[1]Medline: 97169443. A new function for a common fold: the crystal structure of quinolinic acid phosphoribosyltransferase. Eads JC, Ozturk D, Wexler TB, Grubmeyer C, Sacchettini JC; Structure 1997;5:47-58.

[2]Medline: 96139309. The sequencing expression, purification, and steady-state kinetic analysis of quinolinate phosphoribosyl transferase from Escherichia coli. Bhatia R, Calvo KC; Arch Biochem Biophys 1996;325:270-278.

1001. R3H domain

The name of the R3H domain comes from the characteristic spacing of the most conserved arginine and histidine residues. The function of the domain is predicted to be binding ssDNA. Number of members: 28

[1]Medline: 99003905 The R3H motif: a domain that binds single-stranded nucleic acids.
Grishin NV; Trends Biochem Sci 1998;23:329-330.

1002. recF protein signatures (RecF)

5

The prokaryotic protein recF [1,2] is a single-stranded DNA-binding protein which also probably binds ATP. RecF is involved in DNA metabolism; it is required for recombinational DNA repair and for induction of the SOS response. RecF is a protein of about 350 to 370 amino acid residues; there is a conserved ATP-binding site motif 'A' (P-loop) in the N-terminal section of the protein as well as two other conserved regions, one located in the central section, and the other in the C-terminal section. Signature patterns were derived from these two regions.

10

Consensus pattern [LIVM SEQ ID NO:4)]-x(4)-[LIF]-x(6)-[LIF]-[LVF]-x-[GE]-[GSTAD
SEQ ID NO:759)]-[PA]- x(2)-R-R-x-[FYW]-[LIVMF SEQ ID NO:2)]-D Sequences known
to belong to this class detected by the pattern ALL.

15

Consensus pattern[LIVMFY SEQ ID NO:18)](2)-x-D-x(2,3)-[SA]-[EH]-L-D-x(2)-[KRH]-
x(3)-L Sequences known to belong to this class detected by the patternALL, except for T.
palidum recF.

20

[1] Sandler S.J., Chackerian B., Li J.T., Clark A.J. Nucleic Acids Res. 20:839-845(1992).
[2] Alonso J.C., Fisher L.M.; Mol. Gen. Genet. 246:680-686(1995).

1003. RibD C-terminal domain (RibD_C)

25

The function of this domain is not known, but it is thought to be involved in riboflavin biosynthesis. This domain is found in the C terminus of RibD/RibG Swiss:P25539, in combination with dCMP_cyt_deam, as well as in isolation in some archaeobacterial proteins Swiss:P95872.

30

Number of members: 21

1004. Ribosomal protein L16 signatures (Ribosomal_L16)

Ribosomal protein L16 is one of the proteins from the large ribosomal subunit. In *Escherichia coli*, L16 is known to bind directly the 23S rRNA and to be located at the A site of the peptidyltransferase center. It belongs to a family of ribosomal proteins which, on the basis of sequence similarities [1], groups:

- Eubacterial L16.
- Algal and plant chloroplast L16.
- Cyanelle L16.
- Plant mitochondrial L16.

L16 is a protein of 133 to 185 amino-acid residues. As signature patterns, we selected two conserved regions in the central section of these proteins.

Consensus pattern [KR](2)-x-[GSAC SEQ ID NO:93)]-[KRQVA SEQ ID NO:760)]-[LIVM SEQ ID NO:4)]-W-[LIVM SEQ ID NO:4)]-[KR]-[LIVM SEQ ID NO:4)]- [LFY]-[AP]

Sequences known to belong to this class detected by the pattern ALL.

Consensus pattern R-M-G-x-[GR]-K-G-x(4)-[FWKR SEQ ID NO:761)] Sequences known to belong to this class detected by the pattern ALL.

[1] Otaka E., Hashimoto T., Mizuta K., Suzuki K. Protein Seq. Data Anal. 5:301-313(1993).

1005. Ribosomal protein L32e signature (Ribosomal_L32E)

A number of eukaryotic and archaeobacterial ribosomal proteins can be grouped on the basis of sequence similarities. One of these families consists of:

- Mammalian L32 [1].
- *Drosophila* RP49 [2].
- *Trichoderma harzianum* L32 [3].
- Yeast L32e (YBL092w).
- Archaeobacterial L32e [4].

These proteins have 135 to 240 amino-acid residues. As a signature pattern, a stretch of about 20 residues located in the N-terminal part of these proteins was selected.

Consensus pattern F-x-R-x(4)-[KR]-x(2)-[KR]-[LIVMF SEQ ID NO:2)]-x(3,5)-W-R-[KR]-x(2)-G Sequences known to belong to this class detected by the pattern ALL.

[1] Jacks C.M., Powaser C.B., Hackett P.B. Gene 74:565-570(1988).

5 [2] Aguade M. Mol. Biol. Evol. 5:433-441(1988).

[3] Lora J.M., Garcia I., Benitez T., Llobell A., Pintor-Toro J.A. Nucleic Acids Res. 21:3319-3319(1993).

[4] Arndt E., Scholzen T., Kroemer W., Hatakeyama T., Kimura M. Biochimie 73:657-668(1991).

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1006. (Ribosomal_S3) Ribosomal protein S3 signature

PROSITE: PDOC00474. PROSITE cross-reference(s) PS00548; RIBOSOMAL_S3

Ribosomal protein S3 is one of the proteins from the small ribosomal subunit.

In Escherichia coli, S3 is known to be involved in the binding of initiator Met-tRNA. It

15 belongs to a family of ribosomal proteins which, on the basis of sequence similarities [1], groups:

-Eubacterial S3.

-Algal and plant chloroplast S3.

-Cyanelle S3.

20 -Archaeobacterial S3.

-Plant mitochondrial S3.

-Vertebrate S3.

-Insect S3.

-Caenorhabditis elegans S3 (C23G10.3).

25 -Yeast S3 (Rp13).

S3 is a protein of 209 to 559 amino-acid residues. A conserved region located in the C-terminal section was selected as a signature pattern.

Consensus pattern [GSTA SEQ ID NO:19)]-[KR]-x(6)-G-x-[LIVMT SEQ ID NO:1)]-x(2)-

30 [NQSCH SEQ ID NO:519)]-x(1,3)-[LIVFCA SEQ ID NO:520)]-x(3)-[LIV]-[DENQ SEQ ID NO:371)]-x(7)-[LMT]-x(2)-G-x(2)-[GS]. Sequences known to belong to this class detected by the pattern ALL, except for some mitochondrial S3.

[1]Otake E., Hashimoto T., Mizuta K. Protein Seq. Data Anal. 5:285-300(1993).

1007. RimM - RimM

The RimM protein is essential for efficient processing of 16S rRNA [1]. The RimM protein
5 was shown to have affinity for free ribosomal 30S subunits but not for 30S subunits in the
70S ribosomes [1]. Number of members: 14.

[1]Medline: 98083058. RimM and RbfA are essential for efficient processing of 16S rRNA in
Escherichia coli. Bylund GO, Wipemo LC, Lundberg LA, Wikstrom PM; J Bacteriol
10 1998;180:73-82.

1008. RNA_pol_A - RNA polymerase alpha subunit

-!- RNA polymerases catalyse the DNA dependent polymerisation of RNA. Prokaryotes
contain a single RNA polymerase compared to three in eukaryotes (not including
15 mitochondrial and chloroplast polymerases).

-!- Members of this family include: A subunit from eukaryotes, gamma subunit from
cyanobacteria, beta' subunit from eubacteria, A' subunit from archaeobacteria, B" from
chloroplasts. Number of members: 139.

[1]Medline: 97066998. Structural modules of the large subunits of RNA polymerase.
Introducing archaeobacterial and chloroplast split sites in the beta and beta' subunits of
Escherichia coli RNA polymerase. Severinov K, Mustaev A, Kukarin A, Muzzin O, Bass I,
20 Darst SA, Goldfarb A; J Biol Chem 1996;271:27969-27974.

25 1009. RuBisCO_large - Ribulose biphosphate carboxylase large chain active site
PROSITE: PDOC00142; PROSITE cross-reference(s) PS00157; RUBISCO_LARGE

Ribulose biphosphate carboxylase (EC 4.1.1.39) (RuBisCO) [1,2] catalyzes the
initial step in Calvin's reductive pentose phosphate cycle in plants as well as purple and green
bacteria. It consists of a large catalytic unit and a small subunit of undetermined function. In
30 plants, the large subunit is coded by the chloroplastic genome while the small subunit is
encoded in the nuclear genome. Molecular activation of RuBisCO by CO₂ involves the
formation of a carbamate with the epsilon-amino group of a conserved lysine residue. This
carbamate is stabilized by a magnesium ion. One of the ligands of the magnesium ion is an

aspartic acid residue close to the active site lysine [3]. A pattern was developed which includes both the active site residue and the metal ligand, and which is specific to RuBisCO large chains.

- 5 Consensus pattern G-x-[DN]-F-x-K-x-D-E [K is the active site residue] [The second D is a magnesium ligand]. Sequences known to belong to this class detected by the pattern ALL, except for *Cheilopleuria bicuspidis* RuBisCO.

[1] Miziorko H.M., Lorimer G.H. Annu. Rev. Biochem. 52:507-535(1983).

- 10 [2] Akazawa T., Takabe T., Kobayashi H. Trends Biochem. Sci. 9:380-383(1984).

[3] Andersson I., Knight S., Schneider G., Lindqvist Y., Lundqvist T., Branden C.-I., Lorimer G.H. Nature 337:229-234(1989).

1010. Rve - Integrase core domain

- 15 Integrase mediates integration of a DNA copy of the viral genome into the host chromosome. Integrase is composed of three domains. The amino-terminal domain is a zinc binding domain Integrase_Zn. This domain is the central catalytic domain. The carboxyl terminal domain that is a non-specific DNA binding domain integrase. The catalytic domain acts as an endonuclease when two nucleotides are removed from the 3' ends of the blunt-ended viral
- 20 DNA made by reverse transcription. This domain also catalyses the DNA strand transfer reaction of the 3' ends of the viral DNA to the 5' ends of the integration site [1]. Number of members: 694.

- [1] Medline: 95099322. Crystal structure of the catalytic domain of HIV-1 integrase: similarity to other polynucleotidyl transferases. Dyda F, Hickman AB, Jenkins TM, Engelman A, Craigie R, Davies DR; Science 1994;266:1981-1986.
- 25

1011. (SBP_bac_3) Bacterial extracellular solute-binding proteins, family 3 signature PROSITE: PDOC00798. PROSITE cross-reference(s) PS01039; SBP_BACTERIAL_3

- 30 Bacterial high affinity transport systems are involved in active transport of solutes across the cytoplasmic membrane. The protein components of these traffic systems include one or two transmembrane protein components, one or two membrane-associated ATP-binding proteins (ABC transporters; see <PDOC00185>) and a high affinity periplasmic

solute-binding protein. The later are thought to bind the substrate in the vicinity of the inner membrane, and to transfer it to a complex of inner membrane proteins for concentration into the cytoplasm.

In gram-positive bacteria which are surrounded by a single membrane and have therefore no periplasmic region the equivalent proteins are bound to the membrane via an N-terminal lipid anchor. These homolog proteins do not play an integral role in the transport process per se, but probably serve as receptors to trigger or initiate translocation of the solute through the membrane by binding to external sites of the integral membrane proteins of the efflux system.

In addition at least some solute-binding proteins function in the initiation of sensory transduction pathways.

On the basis of sequence similarities, the vast majority of these solute-binding proteins can be grouped [1] into eight families of clusters, which generally correlate with the nature of the solute bound.

Family 3 groups together specific amino acids and opine-binding periplasmic proteins and a periplasmic homolog with catalytic activity:

-Histidine-binding protein (gene *hisJ*) of *Escherichia coli* and related bacteria. An homologous lipoprotein exists in *Neisseria gonorrhoeae*.

-Lysine/arginine/ornithine-binding proteins (LAO) (gene *argT*) of *Escherichia coli* and related bacteria are involved in the same transport system than *hisJ*. Both solute-binding proteins interact with a common membrane-bound receptor *hisP* of the binding protein dependent transport system *HisQMP*.

-Glutamine-binding proteins (gene *glnH*) of *Escherichia coli* and *Bacillus stearothermophilus*.

-Glutamate-binding protein (gene *gluB*) of *Corynebacterium glutamicum*.

-Arginine-binding proteins *artI* and *artJ* of *Escherichia coli*.

-Nopaline-binding protein (gene *nocT*) from *Agrobacterium tumefaciens*.

-Octopine-binding protein (gene *occT*) from *Agrobacterium tumefaciens*.

-Major cell-binding factor (CBF1) (gene: *peb1A*) from *Campylobacter jejuni*.

-*Bacteroides nodosus* protein *aabA*.

-Cyclohexadienyl/arogenate dehydratase of *Pseudomonas aeruginosa*, a periplasmic enzyme which forms an alternative pathway for phenylalanine biosynthesis.

-*Escherichia coli* protein *fliY*.

- Vibrio harveyi protein patH.
- Escherichia coli hypothetical protein ydhW.
- Bacillus subtilis hypothetical protein yckB.
- Bacillus subtilis hypothetical protein yckK.

5

The signature pattern is located near the N-terminus of the mature proteins.

Consensus pattern G-[FYIL SEQ ID NO:644)]-[DE]-[LIVMT SEQ ID NO:1)]-[DE]-[LIVMF
SEQ ID NO:2)]-x(3)-[LIVMA SEQ ID NO:30)]-[VAGC SEQ ID NO:762)]-x(2)-
[LIVMAGN SEQ ID NO:763)]

10

Sequences known to belong to this class detected by the pattern ALL.

[1] Tam R., Saier M.H. Jr. Microbiol. Rev. 57:320-346(1993).

1012. Sec7 - Sec7 domain

15

The Sec7 domain is a guanine-nucleotide-exchange-factor (GEF) for the arf family [2].

Number of members: 32.

[1] Medline: 98169075. Structure of the Sec7 domain of the Arf exchange factor. ARNO.

Cherfils J, Menetrey J, Mathieu M, Le Bras G, Robineau S, Beraud-Dufour S, Antonny B,

20

Chardin P; Nature 1998;392:101-105.

[2] Medline: 97100951. A human exchange factor for ARF contains Sec7- and pleckstrin-
homology domains. Chardin P, Paris S, Antonny B, Robineau S, Beraud-Dufour S, Jackson
CL, Chabre M. Nature 1996;384:481-484.

25

1013. SecA_protein. SecA protein, amino terminal region

SecA protein binds to the plasma membrane where it interacts with proOmpA to support
translocation of proOmpA through the membrane. SecA protein achieves this translocation,
in association with SecY protein, in an ATP dependent manner. SecA possesses the ATPase
activity. The carboxyl terminus has similarity with the helicase carboxyl terminus. See

30

Ribosomal_L5. Number of members: 45.

[1]Medline: 98309858. Amino-terminal region of SecA is involved in the function of SecG for protein translocation into Escherichia coli membrane vesicles. Mori H, Sugiyama H, Yamanaka M, Sato K, Tagaya M, Mizushima S; J Biochem (Tokyo) 1998;124:122-129.

[2]Medline: 89251629. SecA protein hydrolyzes ATP and is an essential component of the protein translocation ATPase of Escherichia coli. Lill R, Cunningham K, Brundage LA, Ito K, Oliver D, Wickner W; EMBO J 1989;8:961-966.

1014. Seedstore_2S - 2S seed storage family

Members of this family are composed of two chains (both included in the alignment), these are co-translated and later cleaved. The two chains are disulphide linked together. Number of members: 27.

[1]Medline: 97121264. ¹H NMR assignment and global fold of napin BnIb, a representative 2S albumin seed protein. Rico M, Bruix M, Gonzalez C, Monsalve RI, Rodriguez R; Biochemistry 1996;35:15672-15682.

1015. Smr - Smr domain

This family includes the Smr (Small MutS Related) proteins, and the C-terminal region of the MutS2 protein. It has been suggested that this domain interacts with the MutS1 Swiss:P23909 protein in the case of Smr proteins and with the N-terminal MutS related region of MutS2 Swiss:P94545 [1]. Number of members: 14.

[1]Medline: 10431172. Smr: a bacterial and eukaryotic homologue of the C-terminal region of the MutS2 family. Moreira D, Philippe H; Trends Biochem Sci 1999;24:298-300.

1016. (SSF) Sodium:solute symporter family signatures and profile

PROSITE: PDOC00429. PROSITE cross-reference(s)PS00456; NA_SOLUT_SYMP_1 PS00457; NA_SOLUT_SYMP_2 PS50283; NA_SOLUTE_SYMP_3

It has been shown [1,2] that integral membrane proteins that mediate the intake of a wide variety of molecules with the concomitant uptake of sodium ions (sodium symporters) can be grouped, on the basis of sequence and functional similarities into a number of distinct families. One of these families is known as the sodium:solute symporter family (SSF) and currently consists of the following proteins:

- Mammalian Na⁺/glucose co-transporter.
- Mammalian Na⁺/myo-inositol co-transporter.
- Mammalian Na⁺/nucleoside co-transporter.
- Mammalian Na⁺/neutral amino acid co-transporter.
- 5 -Escherichia coli Na⁺/proline symporter (gene putP).
- Escherichia coli Na⁺/pantothenate symporter (gene panF).
- Escherichia coli hypothetical protein yidK.
- Escherichia coli hypothetical protein yjcG.
- Bacillus subtilis hypothetical protein ywcA (ipa-31R).

10 These integral membrane proteins are predicted to comprise at least ten membrane spanning domains. Two conserved regions were selected as signature patterns; the first one is located in the fourth transmembrane region and the second one in a loop between two transmembrane regions in the C-terminal part of these proteins.

15 Consensus pattern[GS]-x(2)-[LIY]-x(3)-[LIVMFYWSTAG SEQ ID NO:764])(10)-[LIY]-[TAV]-x(2)-G-G-[LMF]-x-[SAP]. Sequences known to belong to this class detected by the patternALL.

 Consensus pattern[GAST SEQ ID NO:179)]-[LIVM SEQ ID NO:4)]-x(3)-[KR]-x(4)-G-A-x(2)-[GAS]-[LIVMGS SEQ ID NO:765)]-[LIVMW SEQ ID NO:235)]-[LIVMGAT SEQ ID

20 NO:766)]-G-x-[LIVMGA SEQ ID NO:175)] Sequences known to belong to this class detected by the patternALL, except for E.coli yidK.

Note this documentation entry is linked to both a signature pattern and a profile. As the profile is much more sensitive than the pattern, you should use it if you have access to the necessary software tools to do so.

25

- [1]Reizer J., Reizer A., Saier M.H. Jr. Res. Microbiol. 141:1069-1072(1991).
- [2]Reizer J., Reizer A., Saier M.H. Jr. Biochim. Biophys. Acta 1197:133-136(1994).

1017. SurE - Survival protein SurE

30 E. coli cells with the surE gene disrupted are found to survive poorly in stationary phase [1]. It is suggested that SurE may be involved in stress response. Yeast also contains a member of the family Swiss:P38254. Swiss:P30887 can complement a mutation in acid phosphatase, suggesting that members of this family could be phosphatases. Number of members: 17.

[1]Medline: 95014035. A new gene involved in stationary-phase survival located at 59 minutes on the *Escherichia coli* chromosome. Li C, Ichikawa JK, Ravetto JJ, Kuo HC, Fu JC, Clarke S; *J Bacteriol* 1994;176:6015-6022.

- 5 [2]Medline: 93046805. Complementation of *Saccharomyces cerevisiae* acid phosphatase mutation by a genomic sequence from the yeast *Yarrowia lipolytica* identifies a new phosphatase. Treton BY, Le Dall MT, Gaillardin CM; *Curr Genet* 1992;22:345-355.

1018. Synuclein - Synuclein

- 10 There are three types of synucleins in humans, these are called alpha, beta and gamma. Alpha synuclein has been found mutated in families with autosomal dominant Parkinson's disease. A peptide of alpha synuclein has also been found in amyloid plaques in Alzheimer's patients. Number of members: 12.

- 15 [1]Medline: 98424410. The synuclein family. Lavedan C; *Genome Res* 1998;8:871-880.

1019. (T-box) T-box domain signatures

PROSITE: PDOC00972. PROSITE cross-reference(s) PS01283; TBOX_1 PS01264; TBOX_2

- 20 A number of eukaryotic DNA-binding proteins contain a domain of about 170 to 190 amino acids known as the T-box domain [1,2,3] and which probably binds DNA. The T-box has first been found in the mice T locus (Brachyury) protein, a transcription factor involved in mesoderm differentiation. It has since been found in the following proteins:

- Vertebrate and invertebrate homologs of the T protein.
- 25 -Mammalian proteins TBX1 to TBX6.
- Mammalian protein TBR1 which is expressed specifically in brain.
- Xenopus laevis* eomesodermin (eomes).
- Xenopus laevis* Vegt (or Antipodean), a transcription factor that activates the expression of wnt-8, eomes and Brachyury.
- 30 -Chicken TbxT.
- Drosophila* protein optomotor-blind (omb).
- Drosophila* protein brachyenteron (byn) (also known as Trg), which is required for the specification of the hindgut and anal pads.

-Drosophila protein H15.

-Caenorhabditis elegans protein tbx-12.

-Caenorhabditis elegans hypothetical proteins F21H11.3, F40H6.4, T07C4.2, T07C4.6 and ZK177.10.

5

Two conserved regions were selected as signature patterns for the T-domain. The first region corresponds to the N-terminal of the domain and the second one to the central part.

Consensus pattern L-W-x(2)-[FC]-x(3,4)-[NT]-E-M-[LIV](2)-T-x(2)-G-[RG]-[KRQ]

Sequences known to belong to this class detected by the pattern ALL, except for C.elegans

10

ZK177.10.

Consensus pattern [LIVMYW SEQ ID NO:767]-H-[PADH SEQ ID NO:768]-[DEN]-[GS]-

x(3)-G-x(2)-W-M-x(3)-[IVA]-x- F Sequences known to belong to this class detected by the pattern ALL, except for C.elegans tbx-12, ZK177.10 and Drosophila H15.

15

[1] Bollag R.J., Siegfried Z., Cebra-Thomas J.A., Garvey N., Davison E.M., Silver L.M. Nat. Genet. 7:383-389(1994).

[2] Agulnik S.I., Garvey N., Hancock S., Ruvinsky I., Chapman D.L., Agulnik I., Bollag R.J., Papaioannou V.E., Silver L.M. Genetics 144:249-254(1996).

[3] Papaioannou V.E. Trends Genet. 13:212-213(1997).

20

1020. Toprim - Toprim domain

This is a conserved region from DNA primase. This corresponds to the Toprim domain common to DnaG primases, topoisomerases, OLD family nucleases and RecR proteins [1].

Both DnaG motifs IV and V are present in the alignment, the Dx D (V) motif may be involved

25

in Mg²⁺ binding and mutations to the conserved glutamate (IV) completely abolish DnaG type primase activity [1]. DNA primase EC:2.7.7.6 is a nucleotidyltransferase it synthesizes the oligoribonucleotide primers required for DNA replication on the lagging strand of the replication fork; it can also prime the leading strand and has been implicated in cell division [2]. Number of members: 133.

30

[1] Medline: 98391745. Toprim--a conserved catalytic domain in type IA and II topoisomerases, DnaG-type primases, OLD family nucleases and RecR proteins. Aravind L, Leipe DD, Koonin EV; Nucleic Acids Res 1998;26:4205-4213.

[2]Medline: 97368180. Cloning and analysis of the dnaG gene encoding *Pseudomonas putida* DNA primase. Szafranski P, Smith CL, Cantor CR; *Biochim Biophys Acta* 1997;1352:243-248.

[3]Medline: 94124015. The *Haemophilus influenzae* dnaG sequence and conserved bacterial primase motifs. Versalovic J, Lupski JR; *Gene* 1993;136:281-286.

1021. TraB - TraB family

pAD1 is a hemolysin/bacteriocin plasmid originally identified in *Enterococcus faecalis* DS16. It encodes a mating response to a peptide sex pheromone, cAD1, secreted by recipient bacteria. Once the plasmid pAD1 is acquired, production of the pheromone ceases--a trait related in part to a determinant designated traB. However a related protein is found in *C. elegans* Swiss:Q94217, suggesting that members of the TraB family have some more general function. Number of members: 12.

[1]Medline: 94302142. Characterization of the determinant (traB) encoding sex pheromone shutdown by the hemolysin/bacteriocin plasmid pAD1 in *Enterococcus faecalis*. An FY, Clewell DB; *Plasmid* 1994;31:215-221.

1022. (Transpo_mutator) Transposases, Mutator family, signature PROSITE: PDOC00770. PROSITE cross-reference(s) PS01007; TRANSPOSASE_MUTATOR

Autonomous mobile genetic elements such as transposon or insertion sequences (IS) encode an enzyme, called transposase, required for excising and inserting the mobile element. On the basis of sequence similarities, transposases can be grouped into various families. One of these families has been shown [1,2,3,E1] to consist of transposases from the following elements:

- Mutator from Maize.
- Is1201 from *Lactobacillus helveticus*.
- Is905 from *Lactococcus lactis*.
- Is1081 from *Mycobacterium bovis*.
- Is6120 from *Mycobacterium smegmatis*.
- Is406 from *Pseudomonas cepacia*.
- IsRm3 from *Rhizobium meliloti*.

-IsRm5 from *Rhizobium meliloti*.

-Is256 from *Staphylococcus aureus*.

-IsT2 from *Thiobacillus ferrooxidans*.

5 The maize Mutator transposase (MudrA) is a protein of 823 amino acids; the bacterial transposases listed above are proteins of 300 to 420 amino acids. These proteins contain a conserved domain of about 130 residues; a signature pattern was derived from the most conserved part of this domain.

10 Consensus pattern D-x(3)-G-[LIVMF SEQ ID NO:2)]-x(6)-[STAV SEQ ID NO:105)]-[LIVMFYW SEQ ID NO:26)]-[PT]-x-[STAV SEQ ID NO:105)]-x(2)-[QR]-x-C-x(2)-H.
Sequences known to belong to this class detected by the pattern ALL.

[1]Eisen J.A., Benito M.-I., Walbot V. *Nucleic Acids Res.* 22:2634-2636(1994).

[2]Guilhot C., Gicquel B., Davies J., Martin C. *Mol. Microbiol.* 6:107-113(1992).

15 [3]Wood M.S., Byrne A., Lessie T.G. *Gene* 105:101-105(1991).

1023. Transposase_8 - Transposase

20 Transposase proteins are necessary for efficient DNA transposition. This family consists of various *E. coli* insertion elements and other bacterial transposases some of which are members of the IS3 family. Number of members: 58.

[1]Medline: 97324595. Genetic organization and transposition properties of IS511. D. A.

Mullin, D. L. Zies, A. H. Mullin, N. Caballera & B. Ely; *Mol Gen Genet* 1997;254:456-463.

25 [2]Medline: 97128810. The use of an improved transposon mutagenesis system for DNA sequencing leads to the characterization of a new insertion sequence of *Streptomyces lividans* 66. J. Fischer, H. Maier, P. Viell & J. Altenbuchner; *Gene* 1996;180:81-89.

[3]Medline: 97074647. Identification and nucleotide sequence of *Rhizobium meliloti* insertion sequence ISRm6, a small transposable element that belongs to the IS3 family. S. Zekri & N. Toro; *Gene* 1996;175:43-48.

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1024. tRNA_int_endo - tRNA intron endonuclease

Members of this family cleave pre tRNA at the 5' and 3' splice sites to release the intron
EC:3.1.27.9. Number of members: 8.

[1]Medline: 97344075. Properties of *H. volcanii* tRNA intron endonuclease reveal a relationship between the archaeal and eucaryal tRNA intron processing systems. Kleman-Leyer K, Armbruster DW, Daniels CJ; Cell 1997;89:839-847.

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1025. Urease - Urease signatures

PROSITE: PDOC00133PROSITE cross-reference(s) PS01120; UREASE_1 PS00145;
UREASE_2

10 Urease (EC 3.5.1.5) is a nickel-binding enzyme that catalyzes the hydrolysis of urea to carbon dioxide and ammonia [1]. Historically, it was the first enzyme to be crystallized (in 1926). It is mainly found in plant seeds, microorganisms and invertebrates. In plants, urease is a hexamer of identical chains. In bacteria [2], it consists of either two or three different subunits (alpha, beta and gamma).

15 Urease binds two nickel ions per subunit; four histidine, an aspartate and a carbamated-lysine serve as ligands to these metals; an additional histidine is involved in the catalytic mechanism [3].

As signatures for this enzyme, a region that contains two histidine that bind one of the nickel ions and the region of the active site histidine was selected.

20 Consensus pattern T-[AY]-[GA]-[GAT]-[LIVM SEQ ID NO:4])-D-x-H-[LIVM SEQ ID NO:4])-H-x(3)-P [The two H's bind nickel].Sequences known to belong to this class detected by the patternALL.

Consensus pattern[LIVM SEQ ID NO:4)](2)-[CT]-H-[HN]-L-x(3)-[LIVM SEQ ID NO:4)]-x(2)-D-[LIVM SEQ ID NO:4)]-x-F-A [H is the active site residue]. Sequences known to
25 belong to this class detected by the patternALL.

[1]Takishima K., Suga T., Mamiya G. Eur. J. Biochem. 175:151-165(1988).

[2]Mobley H.L.T., Husinger R.P. Microbiol. Rev. 53:85-108(1989).

[3]Jabri E., Carr M.B., Hausinger R.P., Karplus P.A. Science 268:998-1004(1995).

30

1026. Urease_beta - Urease beta subunit.

This subunit is known as alpha in *Helicobacter*. Number of members: 35.

[1]Medline: 95273988. The crystal structure of urease from *Klebsiella aerogenes*. Jabri E, Carr MB, Hausinger RP, Karplus PA; Science 1995;268:998-1004.

1027. UvrD-helicase - UvrD/REP helicase

5 The Rep family helicases are composed of four structural domains. The Rep family function as dimers. REP helicases catalyse ATP dependent unwinding of double stranded DNA to single stranded DNA. Swiss:P23478, Swiss:P08394 have large insertions near to the carboxy-terminus relative to other members of the family. Number of members: 52.

10 [1] Medline: 97433075. Major domain swiveling revealed by the crystal structures of complexes of *E. coli* Rep helicase bound to single-stranded DNA and ADP. Korolev S, Hsieh J, Gauss GH, Lohman TM, Waksman G; Cell 1997;90:635-647.

1028. V-type ATPase 116kDa subunit family (V_ATPase_sub_a)

15

This family consists of the 116kDa V-type ATPase (vacuolar (H⁺)-ATPases) subunits, as well as V-type ATP synthase subunit i. The V-type ATPases family are proton pumps that acidify intracellular compartments in eukaryotic cells for example yeast central vacuoles, clathrin-coated and synaptic vesicles. They have important roles in membrane trafficking processes [1]. The 116kDa subunit (subunit a) in the V-type ATPase is part of the V0 functional domain responsible for proton transport. The a subunit is a transmembrane glycoprotein with multiple putative transmembrane helices. It has a hydrophilic amino terminal and a hydrophobic carboxy terminal [1,2]. It has roles in proton transport and assembly of the V-type ATPase complex [1,2]. This subunit is encoded by two homologous gene in yeast VPH1 and STV1 [2].

20

25

Number of members: 27

[1] Forgac M; Medline: 99240666 "Structure and properties of the vacuolar (H⁺)-ATPases." J Biol Chem 1999;274:12951-12954.

30 [2] Forgac M; Medline: 99270697 "Structure and properties of the clathrin-coated vesicle and yeast vacuolar V-ATPases." J Bioenerg Biomembr 1999;31:57-65.

1029. Viral (Superfamily 1) RNA helicase (Viral_helicase1)

Number of members: 260

[1] Koonin EV, Dolja VV; Medline: 94094568 "Evolution and taxonomy of positive-strand RNA viruses: implications of comparative analysis of amino acid sequences." Crit Rev
5 Biochem Mol Biol 1993;28:375-430.

1030. Vesicular monoamine transporter (VMAT)

This family consists of various vesicular amine transporters with 12 transmembrane helices.
10 These included vesicular acetylcholine transporters (VACHT) [3], and vesicular monoamine transporters (VMATs) [1,2] isoforms 1 adrenal and 2 brain (VMAT1 and VMAT2).

These proteins transport biogenic amines into synaptic vesicles or chromaffin granules [4].
VMATs pack monoamine neurotransmitters into secretory vesicles for regulated exocytotic
15 release, they also protect against the parkinsonian neurotoxins MPP⁺ by transporting it into vesicles preventing it from acting on mitochondria [1].

Also in the family is *C. elegans* UNC-17 a putative vesicular acetylcholine transporter
mutations in UNC-17 cause impaired neuromuscular function, giving rise to jerky or
20 uncoordinated movement, [4].

Number of members: 15

[1] Krantz DE, Peter D, Liu Y, Edwards RH; Medline: 97197857 "Phosphorylation of a vesicular monoamine transporter by casein kinase II." J Biol Chem 1997;272:6752-6759.

25 [2] Erickson JD, Varoqui H, Schafer MK, Modi W, Diebler MF, Weihe E, Rand J, Eiden LE, Bonner TI, Usdin TB; Medline: 94350930 "Functional identification of a vesicular acetylcholine transporter and its expression from a 'cholinergic' gene locus." J Biol Chem 1994;269:21929-21932.

[3] Erickson JD, Schafer MK, Bonner TI, Eiden LE, Weihe E; Medline: 96209876 "Distinct
30 pharmacological properties and distribution in neurons and endocrine cells of two isoforms of the human vesicular monoamine transporter." Proc Natl Acad Sci U S A 1996;93:5166-5171.

[4] Alfonso A, Grundahl K, Duerr JS, Han HP, Rand JB; Medline: 3342494 "The *Caenorhabditis elegans* unc-17 gene: a putative vesicular acetylcholine transporter." *Science* 1993;261:617-619.

- 5 1031. WW/rsp5/WWP domain signature and profile. Cross-reference(s): PS01159; WW_DOMAIN_1; PS50020; WW_DOMAIN_2

The WW domain [1-4,E1] (also known as rsp5 or WWP) has been originally discovered as a short conserved region in a number of unrelated proteins, among them dystrophin, the gene responsible for Duchenne muscular dystrophy. The domain, which spans about 35 residues, is repeated up to 4 times in some proteins. It has been shown [5] to bind proteins with particular proline-motifs, [AP]-P-P-[AP]-Y, and thus resembles somewhat SH3 domains. It appears to contain beta-strands grouped around four conserved aromatic positions; generally Trp. The name WW or WWP derives from the presence of these Trp as well as that of a conserved Pro. It is frequently associated with other domains typical for proteins in signal transduction processes.

Proteins containing the WW domain are listed below.

- 20 --Dystrophin, a multidomain cytoskeletal protein. Its longest alternatively spliced form consists of an N-terminal actin-binding domain, followed by 24 spectrin-like repeats, a cysteine-rich calcium-binding domain and a C-terminal globular domain. Dystrophin form tetramers and is thought to have multiple functions including involvement in membrane stability, transduction of contractile forces to the extracellular environment and organization of membrane specialization. Mutations in the dystrophin gene lead to muscular dystrophy of Duchenne or Becker type. Dystrophin contains one WW domain C-terminal of the spectrin-repeats.
- 25 --Utrophin, a dystrophin-like protein of unknown function.
- Vertebrate YAP protein is a substrate of an unknown serine kinase. It binds to the SH3 domain of the Yes oncoprotein via a proline-rich region. This protein appears in alternatively spliced isoforms, containing either one or two WW domains [6].
- 30 --Mouse NEDD-4 plays a role in the embryonic development and differentiation of the central nervous system. It contains 3 WW modules followed by a HECT domain. The

human ortholog contains 4 WW domains, but the third WW domain is probably spliced resulting in an alternate NEDD-4 protein with only 3 WW modules [3].

--Yeast RSP5 is similar to NEDD-4 in its molecular organization. It contains an N-terminal C2 domain (see <PDOC00380>), followed by a histidine-rich region, 3 WW domains and a HECT domain.

--Rat FE65, a transcription-factor activator expressed preferentially in liver. The activator domain is located within the N-terminal 232 residues of FE65, which also contain the WW domain.

--Yeast ESS1/PTF1, a putative peptidyl prolyl cis-trans isomerase from family ppiC (see <PDOC00840>). A related protein, dodo (gene dod) exists in Drosophila and in mammals (gene PIN1).

--Tobacco DB10 protein. The WW domain is located N-terminal to the region with similarity to ATP-dependent RNA helicases.

--IQGAP, a human GTPase activating protein acting on ras. It contains an N-terminal domain similar to fly muscle mp20 protein and a C-terminal ras GTPase activator domain.

--Yeast pre-mRNA processing protein PRP40, Caenorhabditis elegans ZK1098.1 and fission yeast SpAC13C5.02 are related proteins with similarity to MYO2-type myosin, each containing two WW-domains at the N-terminus.

--Caenorhabditis elegans hypothetical protein C38D4.5, which contains one WW module, a PH domain (see <PDOC50003>) and a C-terminal phosphatidylinositol 3-kinase domain.

--Yeast hypothetical protein YFL010c.

For the sensitive detection of WW domains, a profile was developed which spans the whole homology region as well as a pattern.

Description of pattern(s) and/or profile(s):

Consensus pattern W-x(9,11)-[VFY]-[FYW]-x(6,7)-[GSTNE SEQ ID NO:737]-[GSTQCR SEQ ID NO:738]-[FYW]-x(2)-P.

[1] Bork P., Sudol M. Trends Biochem. Sci. 19:531-533(1994).

[2] Andre B., Springael J.Y. Biochem. Biophys. Res. Commun. 205:1201-1205(1994).

[3] Hofmann K.O., Bucher P. FEBS Lett. 358:153-157(1995).

- [4] Sudol M., Chen H.I., Bougeret C., Einbond A., Bork P. FEBS Lett. 369:67-71(1995).
 [5] Chen H.I., Sudol M. Proc. Natl. Acad. Sci. U.S.A. 92:7819-7823(1995).
 [6] Sudol M., Bork P., Einbond A., Kastury K., Druck T., Negrini M., Huebner K., Lehman D. J. Biol. Chem. 270:14733-14741(1995).

5

1032. XPA protein signatures. cross-reference(s): XPA_1 PROSITE PS00752;
 PS00753;XPA_2.

Xeroderma pigmentosum (XP) [1] is a human autosomal recessive disease, characterized by a high incidence of sunlight-induced skin cancer. People's skin cells with this condition are hypersensitive to ultraviolet light, due to defects in the incision step of DNA excision repair. There are a minimum of seven genetic complementation groups involved in this pathway: XP-A to XP-G. XP-A is the most severe form of the disease and is due to defects in a 30 Kd nuclear protein called XPA (or XPAC) [2].

15

The sequence of the XPA protein is conserved from higher eukaryotes [3] to yeast (gene RAD14) [4]. XPA is a hydrophilic protein of 247 to 296 amino-acid residues which has a C4-type zinc finger motif in its central section.

20

Two signature were developed patterns for XPA proteins. The first corresponds to the zinc finger region, the second to a highly conserved region located some 12 residues after the zinc finger region.

25

Consensus patternC-x-[DE]-C-x(3)-[LIVMF SEQ ID NO:2)]-x(1,2)-D-x(2)-L-x(3)-F-x(4)-C-x(2)-C
 Consensus pattern[LIVM SEQ ID NO:4)](2)-T-[KR]-T-E-x-K-x-[DE]-Y-[LIVMF SEQ ID NO:2)](2)-x-D-x-[DE]

30

- [1] Tanaka K., Wood R.D. Trends Biochem. Sci. 19:83-86(1994).
 [2] Miura N., Miyamoto I., Asahina H., Satokata I., Tanaka K., Okada Y. J. Biol. Chem. 266:19786-19789(1991).
 [3] Shimamoto T., Kohno K., Tanaka K., Okada Y. Biochem. Biophys. Res. Commun. 181:1231-1237(1991).

[4] Bankmann M., Prakash L., Prakash S. Nature 355:555-558(1992).

1033. YCF9

This family consists of the hypothetical protein product of the YCF9 gene from
5 chloroplasts and cyanobacteria. Number of members: 16

1034. (DUF15)

It is highly conserved between eubacteria and eukaryotes.

10 Number of members: 30

1035. Luminal portion of Cytochrome b559, alpha (gene psbE) subunit. (cytochr_b559a)

15 This family is the luminal portion of cytochrome b559 alpha chain, matches to this family
should be accompanied by a match to the cytochr_b559 family also. The Prosite pattern
pattern matches the transmembrane region of the cytochrome b559 alpha and beta subunits.
Number of members: 16

20 A. Asparaginase 2

Asparaginase II (L-asparagine aminohydrolase II) is an extracellular protein that may be
25 associated with the cell wall and whose expression is affected by the availability of nitrogen.
Asparaginase II catalyzes the reaction of L-Asparagine + H₂O = L-Aspartate + NH₃. As
many leukemias have high requirements for aspartic acid, asparaginase II proteins are useful
as reagents for screening compounds for activity as leukemia chemotherapy products.
Asparaginase II protein can also be over- or under-expressed to alter amino acid content in
30 plant tissues or to modify nitrogen fixation and/or nitrogen metabolism in plants.

Ref: Bon et al. (1997) Appl Biochem Biotechnol 63-65: 203-12

B. Chloro a-b-bind

Chlorophyll a-b binding proteins are located in the thylakoid membranes of the chloroplast and bind chlorophyll a and chlorophyll b, thereby triggering a chemical reaction (photosynthesis). These proteins are useful in controlling the rate, efficiency and/or output of photosynthesis. Overexpression of chlorophyll a-b binding proteins is expected to increase the rate of photosynthesis.

Ref: Leutwiler et al. (1986) Nucleic Acids Res 14: 4051-64

Brandt et al. (1992) Plant Mol Biol 19: 699-703

C. DMRL synthase

DMRL Synthase (6,7-Dimethyl-8-Ribityllumazine Synthase) catalyzes the last step in riboflavin (Vitamin B₂) synthesis, condensing 5-amino-6-(1'-D)-ribityl-amino-2,4(1H, 3H)-Pyrimidinedione with L-3,4-Dihydroxy-2-Butanone 4-Phosphate producing 6,7-Dimethyl-8-(1-D-Ribityl)Luminazine. The enzyme forms a homopentamer. Engineering of these proteins or those with homologous sequences/structures may allow control of the amounts of vitamin B₂ available in plants and/or accumulation of pigment, as well as altering reactions requiring hydrogen ion carriers/transmitters.

Ref: Garcia-Ramirez et al. (1995) J Biol Chem 270: 23801-7

D. E1_N

These proteins are ATP-dependent DNA helicases that are required for initiation of viral DNA replication. They form a complex with the viral E2 protein. The E1-E2 complex binds to the replication origin that contains binding sites for both proteins. The majority of sequences known for this group of proteins are from various papillomaviruses, a type of double stranded DNA virus. In plants, the prototype double stranded DNA virus is Cauliflower Mosaic virus (CaMV). Manipulation of these proteins, especially to produce variant proteins that form non-productive complexes, enables production of plants that are resistant to infection by double stranded DNA viruses.

Ref: Yang et al. (1993) PNAS USA **90**: 5086-90

Ustav and Stenlund (1991) EMBO J **10**: 449-57

Callaway et al. (1996) Mol Plant Microbe Interact **9**: 810-8

5

E. EF1_G

Elongation Factor-1 is composed of four subunits: alpha, beta, delta and gamma. Gamma subunits are presumed to play a role in anchoring the complex to other cellular components.

10

Studies of EF-1 genes in plants suggests that different forms of the EF-1 subunits may be expressed in particular organs or in response to stress. Manipulation of the activity of these proteins, either by altered expression level or by structural mutation, may result in the accumulation of a particular protein in a chosen organ or allow production of particular proteins during stress conditions.

15

Ref: Kinzy et al. (1994) NAR **22**: 2703-7

Dunn et al. (1993) Plant Mol Biol **23**: 221-5

Aguilar et al. (1991) Plant Mol Biol **17**: 351-60

20

F. ENV_polyprotein

This family comprises the envelope or coat proteins known from a number of different retroviruses. In mammalian species, retroviruses are responsible for diseases such as leukemia and HIV. In plants, retroviruses are known in both monocot (e.g. Zeon-1) and dicot (e.g. Arabidopsis and tobacco) species and have been shown to induce mutant alleles at new loci. Engineering of plant ENV proteins may allow mobilization or targeting of endogenous or introduced retroviruses, in essence generating a new method for mutant production, gene tagging and the like.

25

30 Ref: Mamoun et al (1990) J Virol **64**: 4180-8

Grandbastien et al. (1989) Nature **337**: 376-80

Wright and Voytas (1998) Genetics **149**: 703-15

G. Glycosyl_hydr9

Proteins having this domain (previously known as the glycosyl hydrolase family 5 domain) catalyze the endohydrolysis of 1,4- β -D-glucosidic linkages in cellulose. Numerous plant proteins with this domain exist and are expressed in an organ specific manner. They are involved in the fruit ripening process, in cell elongation and plant reproduction. Modulation of the activity of these proteins, either by over- or under-expression or by mutation of the polypeptide, could be used to affect post-harvest physiology (e.g. rate of ripening) or for engineering reproductive sterility.

Ref: Giorda et al. (1990) Biochemistry 29: 7264-9
Tucker et al. (1988) Plant Physiol 88: 1257-62
Shani et al. (1997) 43: 837-42
Milligan and Gasser (1995) Plant Mol Biol 28: 691-711

H. Glycosyl_hydr14

The β -amylases (family 14 of glycosyl hydrolases) catalyze the hydrolysis of 1,4- α -glucosidic linkages in polysaccharides and remove successive maltose units from the non-reducing ends of the chains. Mutants of β -amylase in Arabidopsis exhibited altered degradation of starch throughout the diurnal cycle. In addition, the mutant phenotypes indicated that these enzymes not only affect carbohydrate metabolism/catabolism, but also influence the amount of pigment stored within particular cells. Manipulation of the β -amylase genes enables control of plant pigmentation (for example, fibre pigment in cotton) as well as carbohydrate synthesis and degradation.

Ref: Zeeman et al. (1998) Plant J 15: 357-65
Hirano and Nakamura (1997) Plant Physiol 114: 5675-82
Kitamoto et al. (1988) J Bacteriol 170: 5848-54

I. Glycosyl_hydr15

Glycosyl hydrolases from family 15 (such as 1,4-Alpha-D-Glucan glucohydrolase,) catalyze the hydrolysis of terminal 1,4-linked alpha-D-glucose residues successively from the non-reducing ends of the chains resulting in the release of β -D-Glucose. In plants these proteins have been tied to the mobilization of the xyloglucan stored in the cotyledonary cell walls. Proteins such as these could be varied to affect the rate of plant growth (for example during germination), storage and/or use of glucose and other sugars by plant tissues and alteration of the properties, such as elasticity, of plant cell walls.

Ref: Crombie et al. (1998) Plant J 15: 27-38
Hata et al. (1991) Agric Biol Chem 55: 941-9

J. Glycosyl_hydr20

Members of the family 20 glycosyl hydrolases catalyze the hydrolysis of terminal non-reducing N-acetyl-D-hexosamine residues in N-acetyl- β -D-hexosaminides. N-acetyl- β -glucosaminidase belongs to this family and exists in several different forms (consisting of various combinations of alpha and beta chains) depending on the organism. Family 20 glycosyl hydrolases have been implicated in lysosomal storage diseases (such as Sandhoff disease) and glycogen storage disease in humans. These types of proteins are also responsible for the hydrolysis of chitin. In plants, these proteins could be useful in controlling carbohydrate catabolism, thereby influencing the amount of sugars available for storage and/or use in other metabolic pathways. In addition, it is possible that such proteins could be used to engineer an endogenous insect protection mechanism, e.g. by secretion of a chitin-hydrolyzing composition by the plant.

Ref: Graham et al (1988) J Biol Chem 263: 16823-9
O'Dowd et al. (1988) Biochemistry 27: 5216-26

K. HMG box

The HMG box is a novel type of DNA-binding domain found in a diverse group of proteins. Numerous plant proteins contain this domain, such as the HMG1/2-like proteins. The expression of some of these HMG proteins appears to be regulated by circadian rhythms and in a light dependent manner, occurring at higher levels in roots, for example and lower levels in light-grown tissues such as cotyledons. Generally, HMG proteins are thought to influence transcription regulation. In plants, HMGs are believed to have a role in maintaining patterns of circadian-regulated expression for other genes, suggesting that these proteins could be exploited to control growth and development.

- 10 Ref: Laudet et al. (1993) Nucleic Acids Res 21: 2493-501
Zheng et al. (1993) Plant Mol Biol 23: 813-23
Grasser et al. (1993) Plant Mol Biol 23: 619-25

L. IL2

15

Interleukin-2 (IL-2) is produced in mammals by T cells in response to antigenic or mitogenic stimulation and is crucial for proper regulation and functioning of the immune response. IL-2 is capable of stimulating B cells, monocytes, lymphokine-activated killer cells, natural killer cells and glioma cells. Plant extracts have also been shown to stimulate the immune system (for example, mistletoe therapy for human cancer). It is known that IL-2 is involved in feedback inhibition pathways that impact the inflammatory response as well as the growth inhibition of tumor reactive T cells. Plant proteins containing IL-2-like sequences are useful as immunity-based therapeutics, acting in a manner similar to IL-2 in mammals.

- 20
25 Ref: Heike et al. (1997) Scand J Immunol 45: 221-6
Ariel et al. (1998) J Immunol 161: 2465-72
Schink (1997) Anticancer Drugs 8 Suppl 1: S47-51

M. Oxidored_FMN

30

NADPH dehydrogenases catalyze the reaction $\text{NADPH} + \text{acceptor} = \text{NADP}(+) + \text{reduced acceptor}$. One member of this family is yeast "old yellow enzyme" (OYE) and is thought to be involved in oxylipin metabolism. A second yeast family member is a protein that binds

estrogen binding protein (EBP) in addition to exhibiting oxidoreductase activity. An Arabidopsis homolog to OYE has been described and estrogen binding proteins in plants have been reported. Plant proteins from this class have the potential to be used to modify lipid metabolism/catabolism. These proteins may also have use as therapeutics for breast and prostate cancer, and other abnormal growth in steroid-sensitive tissues.

Ref: Baker et al. (1998) Proc Soc Exp Biol Med 217: 317-21
Schaller and Weiler (1997) J Biol Chem 272: 28066-72
Mandani et al. (1994) PNAS USA 91: 922-6

N. Oxidored_q2

The NADH-plastoquinone oxidoreductases catalyze the reaction $\text{NADH} + \text{plastoquinone} = \text{NAD}(+) + \text{plastoquinol}$. In plants these reactions occur in the chloroplast and are believed to participate in a chloroplast respiratory system. Here, the NDH complex is postulated to act as a valve to remove excess reduction equivalents in the chloroplasts. Manipulation of these proteins may improve the rate or efficiency of photosynthesis.

Ref: Burrows et al. (1998) EMBO J 17: 868-76
Kofer et al (1998) Mol Gen Genet 258: 166-73
Maier et al. (1995) J Mol Biol 251: 614-28

O. PABP

Polyadenylate binding proteins bind the poly (A) tail of mRNA. Plants, as exemplified by Arabidopsis, contain numerous PABP genes that are expressed in an organ-specific manner. For example, PABP2 is functional in roots and shoots, while PABP5 is expressed predominantly in immature flowers. The PABP proteins are implicated in numerous aspects of posttranscriptional regulation including mRNA turnover and translational initiation. Control of activity of PABP proteins provides the ability to control the expression of various genes in particular organs during development.

Ref: Hilson et al (1993) Plant Physiol 103: 525-33

Belostotsky and Meagher (1993) PNAS USA 90: 6686-90

P. Parvo coat

5 Parvoviruses are linear single-stranded DNA viruses that are encapsulated by three capsid proteins. Plants are susceptible to infection by single stranded DNA viruses such as Maize streak virus (MSV) and various Gemini viruses. The coat proteins in these plant viruses are critical to the virus life cycle within the plant. For example, the coat protein of MSV is thought to be involved in intra- and inter-cellular movement within the plant. Engineering of
10 proteins having similarity to parvoviral coat proteins, especially to produce proteins that interfere with maturation of the virus particle, enables the production of plants having better resistance to natural plant single-stranded DNA viruses.

Ref: Liu et al. (1997) J Gen Virol 78: 1265-70

15 Rohde et al. (1990) Virology 176: 648-51

Q. Pkinase_C

Plant serine/threonine protein kinases possessing this domain are expressed in all tissues and
20 are known to undergo serine-specific autophosphorylation and specifically phosphorylate two ribosomal proteins, P14 and P16. During development, these proteins predominate during high metabolic activity in growing buds, root tips, leaf margins and germinating seeds. They are thought to be involved in the control of plant growth and development. In addition, two genes encoding proteins from this family have been described that help plant cells adapt
25 during cold or high salt stresses. Consequently, engineering Pkinase C proteins provides a way to control general growth/development of the plant as well as a means to provide endogenous protection against environmental stresses.

Ref: Zhang et al. (1994) J Biol Chem 269: 17586-92

30 Mizoguchi et al. (1995) FEBS Lett 358: 199-204

R. REV

The REV proteins act post-transcriptionally to relieve negative repression of GAG and ENV production in retroviruses such as Human Immunodeficiency Virus type I (HIV-1). Plants contain retrovirus-like viruses such as pararetroviruses and retrotransposons (i.e. transposons having long terminal repeats). Plant retrotransposons in particular have been used to create mutations at various loci, thereby permitting gene isolation, gene tagging and the like. Manipulation of plant REV proteins enables control of transposition frequencies of corresponding transposable elements and provides a new tool for genetic engineering of plants.

- 10 Ref: Sodroski et al. (1986) Nature 321: 412-7
Franchini et al. (1989) PNAS USA 86: 2433-7
Marquet et al. (1995) 77: 113-24
Grandbastien et al. (1989) Nature 337: 376-80
Wright and Voytas (1998) Genetics 149: 703-15

15

S. RuBisCo small

Ribulose 1,5-bisphosphate carboxylase/oxygenase (RuBisCo) catalyzes the initial step in the C3 photosynthetic carbon reduction cycle, adding carbon dioxide to D-ribulose 1,5-bisphosphate to form two molecules of 3-phospho-D-glycerate. RuBisCo is comprised of two subunits, one large which is synthesized in the chloroplast, and one small which is synthesized in the cytoplasm and then transported in to the chloroplast. The expression of the small subunit of RuBisCo is light regulated. Manipulation of these proteins could increase the efficiency of photosynthesis or allow alterations in developmental timing.

25

- Ref: Giuliano et al. (1988) PNAS USA 85: 7089-93
Dedonder et al. (1993) Plant Physiol 101: 801-8

T. Sialyltransf

30

Members of the CMP-N-acetylneuraminate- β -galactosamide- α -2,3-sialyltransferase family catalyze the following reaction:

CMP-N-acetylneuraminate + β -D-galactosyl-1,3-N-acetyl- α -D-galactosaminyl-R = CMP + α -N-acetylneuraminyl-2,3- β -D-galactosyl-1,3-N-acetyl- α -D-galactosaminyl-R. These proteins are thought to be responsible for the synthesis of the sequence neurac- α -2,3-gal- β -1,3-galnac- found on sugar chains)-linked to threonine or serine and also as a terminal sequence on certain gangliosides in mammalian cells. In plants, glycosyltransferases in the Golgi apparatus synthesize cell wall polysaccharides and elaborate the complex glycans of glycoproteins. Engineering of plant sialyltransferases allows targeting of proteins to particular cellular locations or enables the making of changes in cell wall structure.

- 10 Ref: Wee et al. (1998) Plant Cell 10: 1759-68
Lee et al. (1994) J Biol Chem 269: 10028-33
Kitagawa and Paulson (1994) J Biol Chem 269: 1394-401

U. Signal

15

Many plant proteins in this family contain sequences similar to those found in both components of the prokaryotic family of signal transducers known as the two-component systems. This suggests that activation may require a transfer of a phosphate group between the transmitter domain and the receiver domain. One family member in Arabidopsis appears to be involved in ethylene (a plant hormone) signal transduction. Other proteins in this family appear to be involved in the regulation of gene transcription under conditions of environmental stress. Signal proteins can be exploited to affect plant growth and development and/or control plant responses to stress conditions such as cold, nutrient availability, etc.

- 25 Ref: Chang et al. (1993) Science 262: 539-44
Nagaya et al. (1993) Gene 131: 119-124
Gottfert et al. (1990) PNAS USA 87: 2680-4

V. vMSA

30

vMSA proteins are major surface antigens presenting on the envelope of various retroviruses. Surface antigens of retroviruses are often involved in tropism of the virus. Plants contain retrovirus-like viruses such as pararetroviruses and retrotransposons (i.e.

transposons having long terminal repeats). Plant retrotransposons in particular have been used to create mutants at various loci, thereby permitting gene isolation, gene tagging and the like. Manipulation of plant vMSA proteins enables control of tropism of plant retroviruses that might be used for genetic engineering tools, thus enabling targeting of the virus to particular species and/or tissues of plants.

Ref: Okamoto et al. (1988) J Gen Virol 69: 2575-83

Grandbastien et al. (1989) Nature 337: 376-80

Wright and Voytas (1998) Genetics 149: 703-15

W. zf-CCCH

This family of proteins is defined by having two CX(8)CX(5)CX(3)H-type zinc finger domains. These proteins cover a broad range of functions. For example, the COP1 protein acts as a repressor of photomorphogenesis in darkness; light stimuli abolish this suppressive action. In addition, COP1 protein can function as a negative transcriptional regulator capable of direct interaction with components of the G-protein signaling pathway. As a second example, a zf-CCCH protein identified in Arabidopsis appears to be involved in the resistance to DNA damage induced by UV light and chemical DNA-damaging agents.

Overexpression of this class of proteins permits production of plants that are better suited to adverse environments. Manipulation of expression of zf-CCCH proteins functioning as transcriptional regulators, such as COP1, enables manipulation of some signal transduction pathways.

Ref: Pang et al. (1993) Nucleic Acids Res 21: 1647-53

Deng et al. (1992) Cell 71: 791-801

X. zf-RanBP

Proteins falling within this category contain many X-X-F-G and X-F-X-F-G repeats, and may contain RANBP1-like or PPIase domains. Plant proteins having domains similar to these include PAS1 and GMSTI. PAS1 has been shown to have dramatic developmental affects that appear to be correlated with both cell division and cell wall elongation. GMSTI has high

identity to the yeast STI stress-inducible gene and has been shown to be heat inducible. Proteins such as these may be useful for controlling growth and form of development.

Ref: Vittorioso et al. (1998) Mol Cell Biol 18: 3034-43

5 Hernandez Torres et al. (1995) 27: 1221-6

Y. Peptidase M48.

10 Proteins belonging to this peptidase family are metalloproteases that bind zinc as a cofactor and are located in the membranes of the endoplasmic reticulum. They function in NH₂-terminal proteolytic processing, as shown for the yeast STE24 gene product. This gene is required for the correct processing of α -factor, a yeast pheromone. Family M48 peptidases also appear to be required for some prenylation reactions, mediating COOH-terminal CAAX processing. Prenylation reactions are believed to be involved in the regulation of protein-

15 protein and protein-membrane interactions. As an example, RAS GTPase activity is regulated in part by localization to the inner side of the plasma membrane upon prenylation. In plants, proteins from this family could be involved in pollen-stigma interactions such as those mediating self-pollination vs. outcrossing, or could be members of several secondary metabolism pathways.

20

Ref: Fujimura-Kamada et al. (1997) J Cell Biol. 136: 271-85. Tam et al. (1998) J Cell Biol. 142: 635-49.

Z. DNA Pol Viral N

25 The DNA pol Viral N domain is located at the N-terminal region of DNA polymerase isolated from several retroid viruses such as the Cauliflower Mosaic Virus. The domain motif has also been found in numerous other species from humans to cyanobacteria. In these organisms, this motif seems to be associated with two types of sequences; retrotransposons and mitochondrial genes. In the mitochondrial sequences this domain is potentially involved

30 in the self-splicing conducted by group II introns. Various manipulations of this gene in plants allows control of the numerous retrotransposons endogenous to plant genomes or allows engineering of mitochondrial function, especially to increase efficiency of energy utilization by cells.

REF: Chapdelaine and Bonen (1991) Cell 65: 465-72
Ferat and Miche (1993) Nature 364: 358-61
Wilson et al. (1994) 368: 32-8
5 Cambareri et al. (1994) 242: 658-65
Gaardner et al. (1981) NAR 9: 2871-2888
Cummings et al. (1990) Curr Genet 17: 375-402
Hattori et al. (1986) Nature 321: 625-8

10 Aa. Calpain inhib

This domain is found in calpastatin, an inhibitor protein specific for calpain. Calpain is a non-lysosomal calcium-dependent intracellular protease that appears to be involved in the dynamic changes of the cytoskeleton, especially actin-related structures, during early *Drosophila* embryogenesis [1]. Calpastatins co-exist in cells with calpains and the subcellular
15 distribution of calpastatin is thought to be important to calpain regulation [2]. In plants calpains and calpastatins could be involved in embryogenesis and non-embryogenic organ reiteration. Mutations occurring in calpain inhibitor repeat domains would produce developmental abnormalities such as abnormal leaf, root or flower development.

20 Refs

- 1 Emori Y and Saigo K (1994) J Biol Chem 269: 25137-42.
- 2 Mellgren RL, Lane RD, Mericle MT (1989) Biochim Biophys Acta 999: 71-77.

Ab. chorismate bind

25 Chorismate binding domains are present in plant anthranilate synthase (AS) genes. AS genes catalyze the first step in the biosynthesis of tryptophan by converting chorismate and L-glutamine to anthranilate, pyruvate and L-glutamate. Some of these genes are involved in feedback inhibition by tryptophan [1] while some are feedback insensitive [2]. In Arabidopsis, two AS genes have overlapping, but different distributions. One of these AS
30 genes is induced by wounding and bacterial pathogen infiltration [1]. Mutations in the chorismate binding domain would affect the production of tryptophan and could influence the plant's defense system. AS gene products can be used for *in vitro* synthesis of tryptophan and tryptophan derivatives.

Refs

- 1 Niyogi KK, Fink GR (1992) Plant Cell 4: 721-33.
- 2 Song HS, Brotherton JE, Gonzales RA, Wilholm JM (1998) Plant Physiol 117:533-43.

Ac. late protein L2

Papillomaviruses are encapsulated double stranded DNA viruses. Plants are susceptible to infection by double stranded DNA viruses such as Cauliflower Mosaic virus (CaMV). The coat proteins in these plant viruses are critical to the virus life cycle within the plant. For example, the coat protein of CaMV is thought to be involved in intra- and inter-cellular movement within the plant [1]. Engineering of proteins having similarity to papillomavirus coat proteins may enable the production of plants having better resistance to natural plant double stranded DNA viruses.

Refs

- 1 Thompson SR, Melcher U (1993) J Gen Virol 74: 1141-8.

Ad. Peptidase M41

Proteins belonging to this peptidase family are metalloproteases that bind zinc as a cofactor and are integral membrane proteins. They seem to be involved in the degradation of carboxy-terminal-tagged cytoplasmic proteins. In plants, these proteins are located in the thylakoid membranes of the chloroplasts, their expression is light regulated and they are thought to be involved in degradation of soluble stromal proteins and turn-over of thylakoid proteins [1]. Manipulation of expression and structure of these proteins would have effects on the efficiency of photosynthesis and the development of chloroplasts.

Refs

- 1 Lindahl M, Tabak s, Cseke L, Pichersky E, Andersson B, Adam Z (1996) J Biol Chem 271: 29329-34.

Ae. UPF0051

There is some evidence that, in plants, proteins in this family are involved in ATP synthesis in chloroplasts [1, 2]. Mutations in these proteins or altering their expression would affect the efficiency of photosynthesis and energy production.

5 Refs

- 1 Kostrzewa M, Zetsche K (1992) J Mol Biol 227: 961-70.
- 2 Kostrzewa M, Zetsche K (1993) Plant Mol Biol 23: 67-76

Af. E7

10 Papillomaviruses are encapsulated double stranded DNA viruses. The Papillomavirus early protein 7 (E7) is known as a potent immortalizing and transforming agent. Transformation by E7 is thought to be mediated by the physical association of E7 with cellular proteins regulating entry into the cell cycle [1]. The result is entry into the cell cycle and suppression of terminal differentiation in mammalian cells. Thus, engineering of proteins having
15 similarity to papillomavirus E7 protein enables the production of plants having altered cellular proliferation characteristics and possibly altered morphology. For example, overexpression of E7-like proteins would be expected to result in proliferation of cells of the tissue in which the E7 protein is expressed, perhaps with suppression of differentiation events. Thus, for example, overexpression of E7-like proteins in meristem cells can result in
20 taller plants and suppression of leafing and/or flowering.

Refs

- 1 Zwerschke W, Jansen-Durr P Adv Cancer Res 2000;78:1-29

25 Ag. Peptidase U7

This protein is known to be an integral membrane protein in the cyanobacterium Synechocystis where it functions to digest cleaved signal peptides [1]. This activity is necessary to maintain proper secretion of mature proteins across the membrane. In higher plants this protein may be present in the plastid or chloroplast membranes where it would
30 function by enabling protein movement into and out of the chloroplasts. Mutations in this protein would be expected to affect the development of plastids, including chloroplasts, or alter the energy transfer system within the chloroplasts, thereby affecting growth and development.

Refs

- 1 Kaneko T, Sato S, Kotani H, Tanaka A, Asamizu E, Nakamura Y, Miyajima N,
Hirosawa M, Sugiura M, Sasamoto S, Kimura T, Hosouchi T, Matsuno A, Muraki A,
Nakazaki N, Naruo K, Okumura S, Shimpo S, Takeuchi C, Wada T, Watanabe A,
5 Yamada M, Yasuda M, Tabata S (1996) DNA Res 3:109-36.

Ah. 5'-3' Exonuclease

The 5'-3' exonuclease domain is one found in bacterial DNA polymerases I and in yeast DNA
repair enzymes such as Exonuclease I. Yeast Exo I is involved in mitotic recombination and
10 also includes a domain that interacts with the mismatch repair protein MSH2. The 5'-3'
exonuclease domain is also present in XPG DNA repair enzymes in humans and in yeast
RAD9 protein. Defects in XPG proteins result in Xeroderma Pigmentosum. Thus defects in
5'-3' exonuclease domain-containing proteins in plants are expected to lead to defects in DNA
repair and corresponding high spontaneous and inducible mutation rates. Consensus sequence
15 (SEQ ID NO: 769):

IMKKKLLLVDGSSLAFFALPPLTNSAGEPTNAVYGFLKMLIKLIEQEQPHTIAVV
FDAKAKTFRHEL YEGYKAGRAP
TPDELREQUIPLIKELLDALGIPLLEVAGYEADDVIGTLAKLAEKEGYEVLIVTGDRDLL
20 QLVSDHVTVIITKKGIAEFTL
FTPEAVIEKYGLTPEQIHDYKALMGDSSDNIPGVKGIGEKTA AKLLQEYGSLEGIYANL
DKLKGKKLREKLLAHKEDAKL
SRDLATIKTDVPLDLTLDDLRLPDPDRDALDLLFDE

25 Ref:

- Fiorentini P. et al. RT. Mol. Cell. Biol. 17:2764-2773(1997).
Tishkoff et al. Cancer Res. 0:0-0(1998).
Macinnes M.A. et al. Mol. Cell. Biol. 13:6393-6402(1993).

AA. Activities of Polypeptides Comprising Signal Peptides

Polypeptides comprising signal peptides are a family of proteins that are typically targeted to (1) a particular organelle or intracellular compartment, (2) interact with a particular molecule or (3) for secretion outside of a host cell. Example of polypeptides comprising signal peptides include, without limitation, secreted proteins, soluble proteins, receptors, proteins retained in the ER, etc.

These proteins comprising signal peptides are useful to modulate ligand-receptor interactions, cell-to-cell communication, signal transduction, intracellular communication, and activities and/or chemical cascades that take part in an organism outside or within of any particular cell.

One class of such proteins are soluble proteins which are transported out of the cell. These proteins can act as ligands that bind to receptor to trigger signal transduction or to permit communication between cells.

Another class is receptor proteins which also comprise a retention domain that lodges the receptor protein in the membrane when the cell transports the receptor to the surface of the cell. Like the soluble ligands, receptors can also modulate signal transduction and communication between cells.

In addition the signal peptide itself can serve as a ligand for some receptors. An example is the interaction of the ER targeting signal peptide with the signal recognition particle (SRP). Here, the SRP binds to the signal peptide, halting translation, and the resulting SRP complex then binds to docking proteins located on the surface of the ER, prompting transfer of the protein into the ER.

A description of signal peptide residue composition is described below in Subsection IV.C.1.

III. Methods of Modulating Polypeptide Production

It is contemplated that polynucleotides of the invention can be incorporated into a host cell or in-vitro system to modulate polypeptide production. For instance, the SDFs prepared as described herein can be used to prepare expression cassettes useful in a number of techniques for suppressing or enhancing expression.

An example are polynucleotides comprising sequences to be transcribed, such as coding sequences, of the present invention can be inserted into nucleic acid constructs to modulate polypeptide production. Typically, such sequences to be transcribed are heterologous to at least one element of the nucleic acid construct to generate a chimeric gene or construct.

Another example of useful polynucleotides are nucleic acid molecules comprising regulatory sequences of the present invention. Chimeric genes or constructs can be generated when the regulatory sequences of the invention linked to heterologous sequences in a vector construct. Within the scope of invention are such chimeric gene and/or constructs.

Also within the scope of the invention are nucleic acid molecules, whereof at least a part or fragment of these DNA molecules are presented in TABLE 1 of the present application, and wherein the coding sequence is under the control of its own promoter and/or its own regulatory elements. Such molecules are useful for transforming the genome of a host cell or an organism regenerated from said host cell for modulating polypeptide production.

Additionally, a vector capable of producing the oligonucleotide can be inserted into the host cell to deliver the oligonucleotide.

More detailed description of components to be included in vector constructs are described both above and below.

Whether the chimeric vectors or native nucleic acids are utilized, such polynucleotides can be incorporated into a host cell to modulate polypeptide production. Native genes and/or nucleic acid molecules can be effective when exogenous to the host cell.

Methods of modulating polypeptide expression includes, without limitation:

Suppression methods, such as

Antisense

Ribozymes

Co-suppression

Insertion of Sequences into the Gene to be Modulated

Regulatory Sequence Modulation.

as well as Methods for Enhancing Production, such as
Insertion of Exogenous Sequences; and
5 Regulatory Sequence Modulation.

III.A. Suppression

Expression cassettes of the invention can be used to suppress expression of
endogenous genes which comprise the SDF sequence. Inhibiting expression can be useful,
for instance, to tailor the ripening characteristics of a fruit (Oeller et al., *Science* 254:437
10 (1991)) or to influence seed size_(WO98/07842) or to provoke cell ablation (Mariani et al.,
Nature 357: 384-387 (1992)).

As described above, a number of methods can be used to inhibit gene expression in
plants, such as antisense, ribozyme, introduction of exogenous genes into a host cell,
insertion of a polynucleotide sequence into the coding sequence and/or the promoter of the
15 endogenous gene of interest, and the like.

III.A.1. Antisense

An expression cassette as described above can be transformed into host cell or
plant to produce an antisense strand of RNA. For plant cells, antisense RNA inhibits gene
expression by preventing the accumulation of mRNA which encodes the enzyme of interest, *see*,
20 e.g., Sheehy et al., *Proc. Nat. Acad. Sci. USA*, 85:8805 (1988), and Hiatt et al., U.S. Patent No.
4,801,340.

III.A.2. Ribozymes

Similarly, ribozyme constructs can be transformed into a plant to cleave mRNA
and down-regulate translation.

III.A.3. Co-Suppression

25 Another method of suppression is by introducing an exogenous copy of the gene
to be suppressed. Introduction of expression cassettes in which a nucleic acid is configured in
the sense orientation with respect to the promoter has been shown to prevent the accumulation of
mRNA. A detailed description of this method is described above.

III.A.4. Insertion of Sequences into the Gene to be Modulated

Yet another means of suppressing gene expression is to insert a polynucleotide into the gene of interest to disrupt transcription or translation of the gene.

Homologous recombination could be used to target a polynucleotide insert to a gene using the Cre-Lox system (A.C. Vergunst et al., *Nucleic Acids Res.* 26:2729 (1998), A.C. Vergunst et al., *Plant Mol. Biol.* 38:393 (1998), H. Albert et al., *Plant J.* 7:649 (1995)).

In addition, random insertion of polynucleotides into a host cell genome can also be used to disrupt the gene of interest. Azpiroz-Leehan et al., *Trends in Genetics* 13:152 (1997). In this method, screening for clones from a library containing random insertions is preferred for identifying those that have polynucleotides inserted into the gene of interest. Such screening can be performed using probes and/or primers described above based on sequences from TABLE 1, fragments thereof, and substantially similar sequence thereto. The screening can also be performed by selecting clones or any transgenic plants having a desired phenotype.

III.A.5. Regulatory Sequence Modulation

The SDFs described in Table 1, and fragments thereof are examples of nucleotides of the invention that contain regulatory sequences that can be used to suppress or inactivate transcription and/or translation from a gene of interest as discussed in I.C.5.

III.A.6. Genes Comprising Dominant-Negative Mutations

When suppression of production of the endogenous, native protein is desired it is often helpful to express a gene comprising a dominant negative mutation. Production of protein variants produced from genes comprising dominant negative mutations is a useful tool for research. Genes comprising dominant negative mutations can produce a variant polypeptide which is capable of competing with the native polypeptide, but which does not produce the native result. Consequently, over expression of genes comprising these mutations can titrate out an undesired activity of the native protein. For example, The product from a gene comprising a dominant negative mutation of a receptor can be used to constitutively activate or suppress a signal transduction cascade, allowing examination of the phenotype and thus the trait(s) controlled by that receptor and pathway. Alternatively, the protein arising from the gene comprising a dominant-negative mutation can be an inactive enzyme still capable

of binding to the same substrate as the native protein and therefore competes with such native protein.

Products from genes comprising dominant-negative mutations can also act upon the native protein itself to prevent activity. For example, the native protein may be active only as a homo-multimer or as one subunit of a hetero-multimer. Incorporation of an inactive subunit into the multimer with native subunit(s) can inhibit activity.

Thus, gene function can be modulated in host cells of interest by insertion into these cells vector constructs comprising a gene comprising a dominant-negative mutation.

III.B. Enhanced Expression

Enhanced expression of a gene of interest in a host cell can be accomplished by either (1) insertion of an exogenous gene; or (2) promoter modulation.

III.B.1. Insertion of an Exogenous Gene

Insertion of an expression construct encoding an exogenous gene can boost the number of gene copies expressed in a host cell.

Such expression constructs can comprise genes that either encode the native protein that is of interest or that encode a variant that exhibits enhanced activity as compared to the native protein. Such genes encoding proteins of interest can be constructed from the sequences from TABLE 1, fragments thereof, and substantially similar sequence thereto.

Such an exogenous gene can include either a constitutive promoter permitting expression in any cell in a host organism or a promoter that directs transcription only in particular cells or times during a host cell life cycle or in response to environmental stimuli.

III.B.2. Regulatory Sequence Modulation

The SDFs of Table 1, and fragments thereof, contain regulatory sequences that can be used to enhance expression of a gene of interest. For example, some of these sequences contain useful enhancer elements. In some cases, duplication of enhancer elements or insertion of exogenous enhancer elements will increase expression of a desired gene from a particular promoter. As other examples, all II promoters require binding of a regulatory protein to be activated, while some promoters may need a protein that signals a promoter binding protein to expose a polymerase binding site. In either case, over-production of such proteins can be used to enhance expression of a gene of interest by increasing the activation time of the promoter.

Such regulatory proteins are encoded by some of the sequences in TABLE 1, fragments thereof, and substantially similar sequences thereto.

Coding sequences for these proteins can be constructed as described above.

5 IV. Gene Constructs and Vector Construction

To use isolated SDFs of the present invention or a combination of them or parts and/or mutants and/or fusions of said SDFs in the above techniques, recombinant DNA vectors which comprise said SDFs and are suitable for transformation of cells, such as plant cells, are usually prepared. The SDF construct can be made using standard recombinant DNA techniques
10 (Sambrook et al. 1989) and can be introduced to the species of interest by *Agrobacterium*-mediated transformation or by other means of transformation (e.g., particle gun bombardment) as referenced below.

The vector backbone can be any of those typical in the art such as plasmids, viruses, artificial chromosomes, BACs, YACs and PACs and vectors of the sort described by

- 15 (a) **BAC:** Shizuya et al., Proc. Natl. Acad. Sci. USA 89: 8794-8797 (1992);
Hamilton et al., Proc. Natl. Acad. Sci. USA 93: 9975-9979 (1996);
- (b) **YAC:** Burke et al., Science 236:806-812 (1987);.
- (c) **PAC:** Sternberg N. et al., Proc Natl Acad Sci U S A. Jan;87(1):103-7 (1990);
- (d) **Bacteria-Yeast Shuttle Vectors:** Bradshaw et al., Nucl Acids Res 23: 4850-
20 4856 (1995);
- (e) **Lambda Phage Vectors:** Replacement Vector, e.g.,
Frischauf et al., J. Mol Biol 170: 827-842 (1983); or Insertion vector, e.g.,
Huynh et al., In: Glover NM (ed) DNA Cloning: A practical Approach, Vol.1 Oxford: IRL
Press (1985);
- 25 (f) **T-DNA gene fusion vectors :**Walden et al., Mol Cell Biol 1: 175-194 (1990);
and
- (g) **Plasmid vectors:** Sambrook et al., infra.

Typically, a vector will comprise the exogenous gene, which in its turn comprises an SDF of the present invention to be introduced into the genome of a host cell, and which gene
30 may be an antisense construct, a ribozyme construct chimera, or a coding sequence with any desired transcriptional and/or translational regulatory sequences, such as promoters, UTRs,

and 3' end termination sequences. Vectors of the invention can also include origins of replication, scaffold attachment regions (SARs), markers, homologous sequences, introns, etc.

A DNA sequence coding for the desired polypeptide, for example a cDNA sequence encoding a full length protein, will preferably be combined with transcriptional and translational initiation regulatory sequences which will direct the transcription of the sequence from the gene in the intended tissues of the transformed plant.

For example, for over-expression, a plant promoter fragment may be employed that will direct transcription of the gene in all tissues of a regenerated plant. Alternatively, the plant promoter may direct transcription of an SDF of the invention in a specific tissue (tissue-specific promoters) or may be otherwise under more precise environmental control (inducible promoters).

If proper polypeptide production is desired, a polyadenylation region at the 3'-end of the coding region is typically included. The polyadenylation region can be derived from the natural gene, from a variety of other plant genes, or from T-DNA.

The vector comprising the sequences from genes or SDF or the invention may comprise a marker gene that confers a selectable phenotype on plant cells. The vector can include promoter and coding sequence, for instance. For example, the marker may encode biocide resistance, particularly antibiotic resistance, such as resistance to kanamycin, G418, bleomycin, hygromycin, or herbicide resistance, such as resistance to chlorosulfuron or phosphinotricin.

IV.A. Coding Sequences

Generally, the sequence in the transformation vector and to be introduced into the genome of the host cell does not need to be absolutely identical to an SDF of the present invention. Also, it is not necessary for it to be full length, relative to either the primary transcription product or fully processed mRNA. Furthermore, the introduced sequence need not have the same intron or exon pattern as a native gene. Also, heterologous non-coding segments can be incorporated into the coding sequence without changing the desired amino acid sequence of the polypeptide to be produced.

IV.B. Promoters

As explained above, introducing an exogenous SDF from the same species or an orthologous SDF from another species can modulate the expression of a native gene

corresponding to that SDF of interest. Such an SDF construct can be under the control of either a constitutive promoter or a highly regulated inducible promoter (*e.g.*, a copper inducible promoter). The promoter of interest can initially be either endogenous or heterologous to the species in question. When re-introduced into the genome of said species, such promoter becomes exogenous to said species. Over-expression of an SDF transgene can lead to co-suppression of the homologous endogeneous sequence thereby creating some alterations in the phenotypes of the transformed species as demonstrated by similar analysis of the chalcone synthase gene (Napoli et al., *Plant Cell* 2:279 (1990) and van der Krol et al., *Plant Cell* 2:291 (1990)). If an SDF is found to encode a protein with desirable characteristics, its over-production can be controlled so that its accumulation can be manipulated in an organ- or tissue-specific manner utilizing a promoter having such specificity.

Likewise, if the promoter of an SDF (or an SDF that includes a promoter) is found to be tissue-specific or developmentally regulated, such a promoter can be utilized to drive or facilitate the transcription of a specific gene of interest (*e.g.*, seed storage protein or root-specific protein). Thus, the level of accumulation of a particular protein can be manipulated or its spatial localization in an organ- or tissue- specific manner can be altered.

IV. C Signal Peptides

SDFs of the present invention containing signal peptides are indicated in Table 1. In some cases it may be desirable for the protein encoded by an introduced exogenous or orthologous SDF to be targeted (1) to a particular organelle intracellular compartment, (2) to interact with a particular molecule such as a membrane molecule or (3) for secretion outside of the cell harboring the introduced SDF. This will be accomplished using a signal peptide.

Signal peptides direct protein targeting, are involved in ligand-receptor interactions and act in cell to cell communication. Many proteins, especially soluble proteins, contain a signal peptide that targets the protein to one of several different intracellular compartments. In plants, these compartments include, but are not limited to, the endoplasmic reticulum (ER), mitochondria, plastids (such as chloroplasts), the vacuole, the Golgi apparatus, protein storage vessicles (PSV) and, in general, membranes. Some signal peptide sequences are conserved, such as the Asn-Pro-Ile-Arg amino acid motif found in the N-terminal propeptide signal that targets proteins to the vacuole (Marty (1999) *The Plant Cell* 11: 587-599). Other signal peptides do not have a consensus sequence *per se*, but are largely composed of

hydrophobic amino acids, such as those signal peptides targeting proteins to the ER (Vitale and Denecke (1999) *The Plant Cell* 11: 615-628). Still others do not appear to contain either a consensus sequence or an identified common secondary sequence, for instance the chloroplast stromal targeting signal peptides (Keegstra and Cline (1999) *The Plant Cell* 11: 557-570). Furthermore, some targeting peptides are bipartite, directing proteins first to an organelle and then to a membrane within the organelle (e.g. within the thylakoid lumen of the chloroplast; see Keegstra and Cline (1999) *The Plant Cell* 11: 557-570). In addition to the diversity in sequence and secondary structure, placement of the signal peptide is also varied. Proteins destined for the vacuole, for example, have targeting signal peptides found at the N-terminus, at the C-terminus and at a surface location in mature, folded proteins. Signal peptides also serve as ligands for some receptors.

These characteristics of signal proteins can be used to more tightly control the phenotypic expression of introduced SDFs. In particular, associating the appropriate signal sequence with a specific SDF can allow sequestering of the protein in specific organelles (plastids, as an example), secretion outside of the cell, targeting interaction with particular receptors, etc. Hence, the inclusion of signal proteins in constructs involving the SDFs of the invention increases the range of manipulation of SDF phenotypic expression. The nucleotide sequence of the signal peptide can be isolated from characterized genes using common molecular biological techniques or can be synthesized in vitro.

In addition, the native signal peptide sequences, both amino acid and nucleotide, described in Table 1 can be used to modulate polypeptide transport. Further variants of the native signal peptides described in Table 1 are contemplated. Insertions, deletions, or substitutions can be made. Such variants will retain at least one of the functions of the native signal peptide as well as exhibiting some degree of sequence identity to the native sequence.

Also, fragments of the signal peptides of the invention are useful and can be fused with other signal peptides of interest to modulate transport of a polypeptide.

V. Transformation Techniques

A wide range of techniques for inserting exogenous polynucleotides are known for a number of host cells, including, without limitation, bacterial, yeast, mammalian, insect and plant cells.

Techniques for transforming a wide variety of higher plant species are well known and described in the technical and scientific literature. See, e.g. Weising et al., *Ann. Rev. Genet.* 22:421 (1988); and Christou, *Euphytica*, v. 85, n.1-3:13-27, (1995).

DNA constructs of the invention may be introduced into the genome of the desired plant host by a variety of conventional techniques. For example, the DNA construct may be introduced directly into the genomic DNA of the plant cell using techniques such as electroporation and microinjection of plant cell protoplasts, or the DNA constructs can be introduced directly to plant tissue using ballistic methods, such as DNA particle bombardment. Alternatively, the DNA constructs may be combined with suitable T-DNA flanking regions and introduced into a conventional *Agrobacterium tumefaciens* host vector. The virulence functions of the *Agrobacterium tumefaciens* host will direct the insertion of the construct and adjacent marker into the plant cell DNA when the cell is infected by the bacteria (McCormac et al., *Mol. Biotechnol.* 8:199 (1997); Hamilton, *Gene* 200:107 (1997)); Salomon et al. *EMBO J.* 3:141 (1984); Herrera-Estrella et al. *EMBO J.* 2:987 (1983).

Microinjection techniques are known in the art and well described in the scientific and patent literature. The introduction of DNA constructs using polyethylene glycol precipitation is described in Paszkowski et al. *EMBO J.* 3:2717 (1984). Electroporation techniques are described in Fromm et al. *Proc. Natl Acad. Sci. USA* 82:5824 (1985). Ballistic transformation techniques are described in Klein et al. *Nature* 327:773 (1987). *Agrobacterium tumefaciens*-mediated transformation techniques, including disarming and use of binary or co-integrate vectors, are well described in the scientific literature. See, for example Hamilton, *CM, Gene* 200:107 (1997); Müller et al. *Mol. Gen. Genet.* 207:171 (1987); Komari et al. *Plant J.* 10:165 (1996); Venkateswarlu et al. *Biotechnology* 9:1103 (1991) and Gleave, *AP., Plant Mol. Biol.* 20:1203 (1992); Graves and Goldman, *Plant Mol. Biol.* 7:34 (1986) and Gould et al., *Plant Physiology* 95:426 (1991).

Transformed plant cells which are derived by any of the above transformation techniques can be cultured to regenerate a whole plant that possesses the transformed genotype and thus the desired phenotype such as seedlessness. Such regeneration techniques rely on manipulation of certain phytohormones in a tissue culture growth medium, typically relying on a biocide and/or herbicide marker which has been introduced together with the desired nucleotide sequences. Plant regeneration from cultured protoplasts is described in Evans et al., *Protoplasts Isolation and Culture* in "Handbook of Plant Cell Culture," pp. 124-176, MacMillan Publishing Company, New York, 1983; and Binding, *Regeneration of Plants, Plant Protoplasts*, pp. 21-73,

CRC Press, Boca Raton, 1988. Regeneration can also be obtained from plant callus, explants, organs, or parts thereof. Such regeneration techniques are described generally in Klee et al. *Ann. Rev. of Plant Phys.* 38:467 (1987). Regeneration of monocots (rice) is described by Hosoyama et al. (*Biosci. Biotechnol. Biochem.* 58:1500 (1994)) and by Ghosh et al. (*J. Biotechnol.* 32:1 (1994)). The nucleic acids of the invention can be used to confer desired traits on essentially any plant.

Thus, the invention has use over a broad range of plants, including species from the genera *Anacardium*, *Arachis*, *Asparagus*, *Atropa*, *Avena*, *Brassica*, *Citrus*, *Citrullus*, *Capsicum*, *Carthamus*, *Cocos*, *Coffea*, *Cucumis*, *Cucurbita*, *Daucus*, *Elaeis*, *Fragaria*, *Glycine*, *Gossypium*, *Helianthus*, *Heterocallis*, *Hordeum*, *Hyoscyamus*, *Lactuca*, *Linum*, *Lolium*, *Lupinus*, *Lycopersicon*, *Malus*, *Manihot*, *Majorana*, *Medicago*, *Nicotiana*, *Olea*, *Oryza*, *Panicum*, *Pennisetum*, *Persea*, *Phaseolus*, *Pistachia*, *Pisum*, *Pyrus*, *Prunus*, *Raphanus*, *Ricinus*, *Secale*, *Senecio*, *Sinapis*, *Solanum*, *Sorghum*, *Theobromus*, *Trigonella*, *Triticum*, *Vicia*, *Vitis*, *Vigna*, and, *Zea*.

One of skill will recognize that after the expression cassette is stably incorporated in transgenic plants and confirmed to be operable, it can be introduced into other plants by sexual crossing. Any of a number of standard breeding techniques can be used, depending upon the species to be crossed.

The particular sequences of SDFs identified are provided in the attached TABLE 1.

One of ordinary skill in the art, having this data, can obtain cloned DNA fragments, synthetic DNA fragments or polypeptides constituting desired sequences by recombinant methodology known in the art or described herein.

EXAMPLES

The invention is illustrated by way of the following examples. The invention is not limited by these examples as the scope of the invention is defined solely by the claims following.

EXAMPLE 1: cDNA PREPARATION

A number of the nucleotide sequences disclosed in TABLE 1 herein as representative of the SDFs of the invention can be obtained by sequencing genomic DNA (gDNA) and/or cDNA from corn plants grown from HYBRID SEED # 35A19, purchased from Pioneer Hi-Bred International, Inc., Supply Management, P.O. Box 256, Johnston, Iowa 50131-0256.

A number of the nucleotide sequences disclosed in TABLE 1 herein as representative of the SDFs of the invention can also be obtained by sequencing genomic DNA from *Arabidopsis thaliana*, Wassilewskija ecotype or by sequencing cDNA obtained from mRNA from such plants as described below. This is a true breeding strain. Seeds of the plant are
5 available from the Arabidopsis Biological Resource Center at the Ohio State University, under the accession number CS2360. Seeds of this plant were deposited under the terms and conditions of the Budapest Treaty at the American Type Culture Collection, Manassas, VA on August 31, 1999, and were assigned ATCC No. PTA-595.

Other methods for cloning full-length cDNA are described, for example, by Seki et al., *Plant Journal* 15:707-720 (1998) "High-efficiency cloning of Arabidopsis full-length cDNA by biotinylated Cap trapper"; Maruyama et al., *Gene* 138:171 (1994) "Oligo-capping a
10 simple method to replace the cap structure of eukaryotic mRNAs with oligoribonucleotides"; and WO 96/34981.

Tissues were, or each organ was, individually pulverized and frozen in liquid
15 nitrogen. Next, the samples were homogenized in the presence of detergents and then centrifuged. The debris and nuclei were removed from the sample and more detergents were added to the sample. The sample was centrifuged and the debris was removed. Then the sample was applied to a 2M sucrose cushion to isolate polysomes. The RNA was isolated by treatment with detergents and proteinase K followed by ethanol precipitation and
20 centrifugation. The polysomal RNA from the different tissues was pooled according to the following mass ratios: 15/15/1 for male inflorescences, female inflorescences and root, respectively. The pooled material was then used for cDNA synthesis by the methods described below.

Starting material for cDNA synthesis for the exemplary corn cDNA clones
25 with sequences presented in TABLE 1 was poly(A)-containing polysomal mRNAs from inflorescences and root tissues of corn plants grown from HYBRID SEED # 35A19. Male inflorescences and female (pre-and post-fertilization) inflorescences were isolated at various stages of development. Selection for poly(A) containing polysomal RNA was done using oligo d(T) cellulose columns, as described by Cox and Goldberg, "Plant Molecular Biology:
30 A Practical Approach", pp. 1-35, Shaw ed., c. 1988 by IRL, Oxford. The quality and the integrity of the polyA⁺ RNAs were evaluated.

Starting material for cDNA synthesis for the exemplary *Arabidopsis* cDNA clones with sequences presented in TABLE 1 was polysomal RNA isolated from the top-most inflorescence tissues of *Arabidopsis thaliana* Wassilewskija (Ws.) and from roots of *Arabidopsis thaliana* Landsberg erecta (L. er.), also obtained from the Arabidopsis

5 Biological Resource Center. Nine parts inflorescence to every part root was used, as measured by wet mass. Tissue was pulverized and exposed to liquid nitrogen. Next, the sample was homogenized in the presence of detergents and then centrifuged. The debris and nuclei were removed from the sample and more detergents were added to the sample. The sample was centrifuged and the debris was removed and the sample was applied to a 2M
10 sucrose cushion to isolate polysomal RNA. Cox et al., "Plant Molecular Biology: A Practical Approach", pp. 1-35, Shaw ed., c. 1988 by IRL, Oxford. The polysomal RNA was used for cDNA synthesis by the methods described below. Polysomal mRNA was then isolated as described above for corn cDNA. The quality of the RNA was assessed electrophoretically.

Following preparation of the mRNAs from various tissues as described above, selection
15 of mRNA with intact 5' ends and specific attachment of an oligonucleotide tag to the 5' end of such mRNA was performed using either a chemical or enzymatic approach. Both techniques take advantage of the presence of the "cap" structure, which characterizes the 5' end of most intact mRNAs and which comprises a guanosine generally methylated once, at the 7 position.

The chemical modification approach involves the optional elimination of the 2', 3'-cis
20 diol of the 3' terminal ribose, the oxidation of the 2', 3'-cis diol of the ribose linked to the cap of the 5' ends of the mRNAs into a dialdehyde, and the coupling of the such obtained dialdehyde to a derivatized oligonucleotide tag. Further detail regarding the chemical approaches for obtaining mRNAs having intact 5' ends are disclosed in International Application No. WO96/34981 published November 7, 1996.

25 The enzymatic approach for ligating the oligonucleotide tag to the intact 5' ends of mRNAs involves the removal of the phosphate groups present on the 5' ends of uncapped incomplete mRNAs, the subsequent decapping of mRNAs having intact 5' ends and the ligation of the phosphate present at the 5' end of the decapped mRNA to an oligonucleotide tag. Further detail regarding the enzymatic approaches for obtaining mRNAs having intact 5' ends are
30 disclosed in Dumas Milne Edwards J.B. (Doctoral Thesis of Paris VI University, Le clonage des ADNc complets: difficultés et perspectives nouvelles. Apports pour l'étude de la régulation de l'expression de la tryptophane hydroxylase de rat, 20 Dec. 1993), EP0 625572 and Kato et al., *Gene* 150:243-250 (1994).

In both the chemical and the enzymatic approach, the oligonucleotide tag has a restriction enzyme site (e.g. an EcoRI site) therein to facilitate later cloning procedures. Following attachment of the oligonucleotide tag to the mRNA, the integrity of the mRNA is examined by performing a Northern blot using a probe complementary to the oligonucleotide tag.

For the mRNAs joined to oligonucleotide tags using either the chemical or the enzymatic method, first strand cDNA synthesis is performed using an oligo-dT primer with reverse transcriptase. This oligo-dT primer can contain an internal tag of at least 4 nucleotides, which can be different from one mRNA preparation to another. Methylated dCTP is used for cDNA first strand synthesis to protect the internal EcoRI sites from digestion during subsequent steps. The first strand cDNA is precipitated using isopropanol after removal of RNA by alkaline hydrolysis to eliminate residual primers.

Second strand cDNA synthesis is conducted using a DNA polymerase, such as Klenow fragment and a primer corresponding to the 5' end of the ligated oligonucleotide. The primer is typically 20-25 bases in length. Methylated dCTP is used for second strand synthesis in order to protect internal EcoRI sites in the cDNA from digestion during the cloning process.

Following second strand synthesis, the full-length cDNAs are cloned into a phagemid vector, such as pBlueScriptTM (Stratagene). The ends of the full-length cDNAs are blunted with T4 DNA polymerase (Biolabs) and the cDNA is digested with EcoRI. Since methylated dCTP is used during cDNA synthesis, the EcoRI site present in the tag is the only hemi-methylated site; hence the only site susceptible to EcoRI digestion. In some instances, to facilitate subcloning, an Hind III adapter is added to the 3' end of full-length cDNAs.

The full-length cDNAs are then size fractionated using either exclusion chromatography (AcA, Biosepra) or electrophoretic separation which yields 3 to 6 different fractions. The full-length cDNAs are then directionally cloned either into pBlueScriptTM using either the EcoRI and SmaI restriction sites or, when the Hind III adapter is present in the full-length cDNAs, the EcoRI and Hind III restriction sites. The ligation mixture is transformed, preferably by electroporation, into bacteria, which are then propagated under appropriate antibiotic selection.

Clones containing the oligonucleotide tag attached to full-length cDNAs are selected as follows.

The plasmid cDNA libraries made as described above are purified (e.g. by a column available from Qiagen). A positive selection of the tagged clones is performed as follows. Briefly, in this selection procedure, the plasmid DNA is converted to single stranded DNA using

phage F1 gene II endonuclease in combination with an exonuclease (Chang et al., *Gene* 127:95 (1993)) such as exonuclease III or T7 gene 6 exonuclease. The resulting single stranded DNA is then purified using paramagnetic beads as described by Fry et al., *Biotechniques* 13: 124 (1992). Here the single stranded DNA is hybridized with a biotinylated oligonucleotide having a sequence corresponding to the 3' end of the oligonucleotide tag. Preferably, the primer has a length of 20-25 bases. Clones including a sequence complementary to the biotinylated oligonucleotide are selected by incubation with streptavidin coated magnetic beads followed by magnetic capture. After capture of the positive clones, the plasmid DNA is released from the magnetic beads and converted into double stranded DNA using a DNA polymerase such as ThermoSequenase™ (obtained from Amersham Pharmacia Biotech). Alternatively, protocols such as the Gene Trapper™ kit (Gibco BRL) can be used. The double stranded DNA is then transformed, preferably by electroporation, into bacteria. The percentage of positive clones having the 5' tag oligonucleotide is typically estimated to be between 90 and 98% from dot blot analysis.

Following transformation, the libraries are ordered in microtiter plates and sequenced. The *Arabidopsis* library was deposited at the American Type Culture Collection on January 7, 2000 as "*E-coli* liba 010600" under the accession number **PTA-1161**.

EXAMPLE 2: SOUTHERN HYBRIDIZATIONS

The SDFs of the invention can be used in Southern hybridizations as described above. The following describes extraction of DNA from nuclei of plant cells, digestion of the nuclear DNA and separation by length, transfer of the separated fragments to membranes, preparation of probes for hybridization, hybridization and detection of the hybridized probe.

The procedures described herein can be used to isolate related polynucleotides or for diagnostic purposes. Moderate stringency hybridization conditions, as defined above, are described in the present example. These conditions result in detection of hybridization between sequences having at least 70% sequence identity. As described above, the hybridization and wash conditions can be changed to reflect the desired percentatge of sequence identity between probe and target sequences that can be detected.

In the following procedure, a probe for hybridization is produced from two PCR reactions using two primers from genomic sequence of *Arabidopsis thaliana*. As described above, the particular template for generating the probe can be any desired template.

The first PCR product is assessed to validate the size of the primer to assure it is of the expected size. Then the product of the first PCR is used as a template, with the same pair

of primers used in the first PCR, in a second PCR that produces a labeled product used as the probe.

Fragments detected by hybridization, or other bands of interest, can be isolated from gels used to separate genomic DNA fragments by known methods for further purification and/or characterization.

Buffers for nuclear DNA extraction

1. 10X HB

	1000 ml	
40 mM spermidine	10.2 g	Spermine (Sigma S-2876) and spermidine (Sigma S-2501)
10 mM spermine	3.5 g	Stabilize chromatin and the nuclear membrane
0.1 M EDTA (disodium)	37.2 g	EDTA inhibits nuclease
0.1 M Tris	12.1 g	Buffer
0.8 M KCl	59.6 g	Adjusts ionic strength for stability of nuclei

Adjust pH to 9.5 with 10 N NaOH. It appears that there is a nuclease present in leaves. Use of pH 9.5 appears to inactivate this nuclease.

2. 2 M sucrose (684 g per 1000 ml)

Heat about half the final volume of water to about 50°C. Add the sucrose slowly then bring the mixture to close to final volume; stir constantly until it has dissolved. Bring the solution to volume.

3. Sarkosyl solution (lyses nuclear membranes)

	865	
N-lauroyl sarcosine (Sarkosyl)		20.0 g
0.1 M Tris		12.1 g
0.04 M EDTA (Disodium)	14.9 g	

Adjust the pH to 9.5 after all the components are dissolved and bring up to the proper volume.

4. 20% Triton X-100
80 ml Triton X-100
320 ml 1xHB (w/o β -ME and PMSF)
Prepare in advance; Triton takes some time to dissolve

10 A. Procedure

1. Prepare 1X "H" buffer (keep ice-cold during use)

	<u>1000 ml</u>	
10X HB	100 ml	
2 M sucrose	250 ml a non-ionic osmoticum	
15 Water	634 ml	

Added just before use:

100 mM PMSF*	10 ml a protease inhibitor; protects nuclear membrane proteins
β -mercaptoethanol	1 ml inactivates nuclease by reducing disulfide bonds

*100 mM PMSF

(phenyl methyl sulfonyl fluoride, Sigma P-7626)

(add 0.0875 g to 5 ml 100% ethanol)

2. Homogenize the tissue in a blender (use 300-400 ml of 1xHB per blender). Be sure that you use 5-10 ml of HB buffer per gram of tissue. Blenders generate heat so be

sure to keep the homogenate cold. It is necessary to put the blenders in ice periodically.

3. Add the 20% Triton X-100 (25 ml per liter of homogenate) and gently stir on ice for 20 min. This lyses plastid, but not nuclear, membranes.

- 5 4. Filter the tissue suspension through several nylon filters into an ice-cold beaker. The first filtration is through a 250-micron membrane; the second is through an 85-micron membrane; the third is through a 50-micron membrane; and the fourth is through a 20-micron membrane. Use a large funnel to hold the filters. Filtration can be sped up by gently squeezing the liquid through the filters.

- 10 5. Centrifuge the filtrate at 1200 x g for 20 min. at 4°C to pellet the nuclei.

6. Discard the dark green supernatant. The pellet will have several layers to it. One is starch; it is white and gritty. The nuclei are gray and soft. In the early steps, there may be a dark green and somewhat viscous layer of chloroplasts.

15 Wash the pellets in about 25 ml cold H buffer (with Triton X-100) and resuspend by swirling gently and pipetting. After the pellets are resuspended.

Pellet the nuclei again at 1200 - 1300 x g. Discard the supernatant.

20 Repeat the wash 3-4 times until the supernatant has changed from a dark green to a pale green. This usually happens after 3 or 4 resuspensions. At this point, the pellet is typically grayish white and very slippery. The Triton X-100 in these repeated steps helps to destroy the chloroplasts and mitochondria that contaminate the prep.

Resuspend the nuclei for a final time in a total of 15 ml of H buffer and transfer the suspension to a sterile 125 ml Erlenmeyer flask.

7. Add 15 ml, dropwise, cold 2% Sarkosyl, 0.1 M Tris, 0.04 M EDTA solution (pH 9.5) while swirling gently. This lyses the nuclei. The solution will become very viscous.

8. Add 30 grams of CsCl and gently swirl at room temperature until the CsCl is in solution. The mixture will be gray, white and viscous.

9. Centrifuge the solution at 11,400 x g at 4°C for at least 30 min. The longer this spin is, the firmer the protein pellicle.

5

10. The result is typically a clear green supernatant over a white pellet, and (perhaps) under a protein pellicle. Carefully remove the solution under the protein pellicle and above the pellet. Determine the density of the solution by weighing 1 ml of solution and add CsCl if necessary to bring to 1.57 g/ml. The solution contains dissolved solids (sucrose etc) and the refractive index alone will not be an accurate guide to CsCl concentration.

10

11. Add 20 µl of 10 mg/ml EtBr per ml of solution.

12. Centrifuge at 184,000 x g for 16 to 20 hours in a fixed-angle rotor.

13. Remove the dark red supernatant that is at the top of the tube with a plastic transfer pipette and discard. Carefully remove the DNA band with another transfer pipette. The DNA band is usually visible in room light; otherwise, use a long wave UV light to locate the band.

15

14. Extract the ethidium bromide with isopropanol saturated with water and salt. Once the solution is clear, extract at least two more times to ensure that all of the EtBr is gone. Be very gentle, as it is very easy to shear the DNA at this step. This extraction may take a while because the DNA solution tends to be very viscous. If the solution is too viscous, dilute it with TE.

20

15. Dialyze the DNA for at least two days against several changes (at least three times) of TE (10 mM Tris, 1mM EDTA, pH 8) to remove the cesium chloride.

16. Remove the dialyzed DNA from the tubing. If the dialyzed DNA solution contains a lot of debris, centrifuge the DNA solution at least at 2500 x g for 10 min. and carefully transfer the clear supernatant to a new tube. Read the A260 concentration of the DNA.

- 5 17. Assess the quality of the DNA by agarose gel electrophoresis (1% agarose gel) of the DNA. Load 50 ng and 100 ng (based on the OD reading) and compare it with known and good quality DNA. Undigested lambda DNA and a lambda-HindIII-digested DNA are good molecular weight makers.

Protocol for Digestion of Genomic DNA

Protocol:

- 10 1. The relative amounts of DNA for different crop plants that provide approximately a balanced number of genome equivalent is given in Table 3. Note that due to the size of the wheat genome, wheat DNA will be underrepresented. Lambda DNA provides a useful control for complete digestion.
- 15 2. Precipitate the DNA by adding 3 volumes of 100% ethanol. Incubate at -20°C for at least two hours. Yeast DNA can be purchased and made up at the necessary concentration, therefore no precipitation is necessary for yeast DNA.
- 20 3. Centrifuge the solution at 11,400 x g for 20 min. Decant the ethanol carefully (be careful not to disturb the pellet). Be sure that the residual ethanol is completely removed either by vacuum desiccation or by carefully wiping the sides of the tubes with a clean tissue.
4. Resuspend the pellet in an appropriate volume of water. Be sure the pellet is fully resuspended before proceeding to the next step. This may take about 30 min.
- 25 5. Add the appropriate volume of 10X reaction buffer provided by the manufacturer of the restriction enzyme to the resuspended DNA followed by the appropriate volume of enzymes. Be sure to mix it properly by slowly swirling the tubes.

6. Set-up the lambda digestion-control for each DNA that you are digesting.
7. Incubate both the experimental and lambda digests overnight at 37°C. Spin down condensation in a microfuge before proceeding.
8. After digestion, add 2 µl of loading dye (typically 0.25% bromophenol blue, 0.25% xylene cyanol in 15% Ficoll or 30% glycerol) to the lambda-control digests and load in 1% TPE-agarose gel (TPE is 90 mM Tris-phosphate, 2 mM EDTA, pH 8). If the lambda DNA in the lambda control digests are completely digested, proceed with the precipitation of the genomic DNA in the digests.
9. Precipitate the digested DNA by adding 3 volumes of 100% ethanol and incubating in -20°C for at least 2 hours (preferably overnight).

EXCEPTION: *Arabidopsis* and yeast DNA are digested in an appropriate volume; they don't have to be precipitated.

10. Resuspend the DNA in an appropriate volume of TE (e.g., 22 µl x 50 blots = 1100 µl) and an appropriate volume of 10X loading dye (e.g., 2.4 µl x 50 blots = 120 µl). Be careful in pipetting the loading dye - it is viscous. Be sure you are pipetting the correct volume.

Table 3

Some guide points in digesting genomic DNA.

Species	Genome Size	Size Relative to Arabidopsis	Genome Equivalent to 2 µg Arabidopsis DNA	Amount of DNA per blot
Arabidopsis	120 Mb	1X	1X	2 µg
Brassica	1,100 Mb	9.2X	0.54X	10 µg
Corn	2,800 Mb	23.3X	0.43X	20 µg

870

Cotton	2,300 Mb	19.2X	0.52X	20 µg
Oat	11,300 Mb	94X	0.11X	20 µg
Rice	400 Mb	3.3X	0.75X	5 µg
Soybean	1,100 Mb	9.2X	0.54X	10 µg
Sugarbeet	758 Mb	6.3X	0.8X	10 µg
Sweetclover	1,100 Mb	9.2X	0.54X	10 µg
Wheat	16,000 Mb	133X	0.08X	20 µg
Yeast	15 Mb	0.12X	1X	0.25 µg

Protocol for Southern Blot Analysis

The digested DNA samples are electrophoresed in 1% agarose gels in 1x TPE buffer. Low voltage; overnight separations are preferred. The gels are stained with EtBr and photographed.

1. For blotting the gels, first incubate the gel in 0.25 N HCl (with gentle shaking) for about 15 min.
2. Then briefly rinse with water. The DNA is denatured by 2 incubations. Incubate (with shaking) in 0.5 M NaOH in 1.5 M NaCl for 15 min.
3. The gel is then briefly rinsed in water and neutralized by incubating twice (with shaking) in 1.5 M Tris pH 7.5 in 1.5 M NaCl for 15 min.
4. A nylon membrane is prepared by soaking it in water for at least 5 min, then in 6X SSC for at least 15 min. before use. (20x SSC is 175.3 g NaCl, 88.2 g sodium citrate per liter, adjusted to pH 7.0.)
5. The nylon membrane is placed on top of the gel and all bubbles in between are removed. The DNA is blotted from the gel to the membrane using an absorbent medium, such as paper toweling and 6x SCC buffer. After the transfer, the membrane may be lightly brushed with a gloved hand to remove any agarose sticking to the surface.

6. The DNA is then fixed to the membrane by UV crosslinking and baking at 80°C. The membrane is stored at 4°C until use.

B. Protocol for PCR Amplification of Genomic Fragments in Arabidopsis

Amplification procedures:

- 5 1. Mix the following in a 0.20 ml PCR tube or 96-well PCR plate:

Volume	Stock	Final Amount or Conc.
0.5 µl	~ 10 ng/µl genomic DNA ¹	5 ng
2.5 µl	10X PCR buffer	20 mM Tris, 50 mM KCl
0.75 µl	50 mM MgCl ₂	1.5 mM
1 µl	10 pmol/µl Primer 1 (Forward)	10 pmol
1 µl	10 pmol/µl Primer 2 (Reverse)	10 pmol
0.5 µl	5 mM dNTPs	0.1 mM
0.1 µl	5 units/µl Platinum Taq™ (Life Technologies, Gaithersburg, MD) DNA Polymerase	1 units
(to 25 µl)	Water	

2. The template DNA is amplified using a Perkin Elmer 9700 PCR machine:

¹ Arabidopsis DNA is used in the present experiment, but the procedure is a general one.

- 1) 94°C for 10 min. followed by

2) 5 cycles:	3) 5 cycles:	4) 25 cycles:
94 °C - 30 sec	94 °C - 30 sec	94 °C - 30 sec
62 °C - 30 sec	58 °C - 30 sec	53 °C - 30 sec
72 °C - 3 min	72 °C - 3 min	72 °C - 3 min

- 5) 72°C for 7 min. Then the reactions are stopped by chilling to 4°C.

The procedure can be adapted to a multi-well format if necessary.

Quantification and Dilution of PCR Products:

- 5 1. The product of the PCR is analyzed by electrophoresis in a 1% agarose gel. A linearized plasmid DNA can be used as a quantification standard (usually at 50, 100, 200, and 400 ng). These will be used as references to approximate the amount of PCR products. HindIII-digested Lambda DNA is useful as a molecular weight marker. The gel can be run fairly quickly; e.g., at 100 volts. The standard gel is examined to determine that the size of the PCR products is consistent with the expected size and if there are significant extra bands or smeary products in the PCR reactions.
2. The amounts of PCR products can be estimated on the basis of the plasmid standard.
3. For the small number of reactions that produce extraneous bands, a small amount of DNA from bands with the correct size can be isolated by dipping a sterile 10-μl tip into the band while viewing through a UV Transilluminator. The small amount of agarose gel (with the DNA fragment) is used in the labeling reaction.

C. Protocol for PCR-DIG-Labeling of DNA

Solutions:

873

Reagents in PCR reactions (diluted PCR products, 10X PCR Buffer, 50 mM MgCl₂, 5 U/μl Platinum Taq Polymerase, and the primers)

10X dNTP + DIG-11-dUTP [1:5]: (2 mM dATP, 2 mM dCTP, 2 mM dGTP, 1.65 mM dTTP, 0.35 mM DIG-11-dUTP)

5 10X dNTP + DIG-11-dUTP [1:10]: (2 mM dATP, 2 mM dCTP, 2 mM dGTP, 1.81 mM dTTP, 0.19 mM DIG-11-dUTP)

10X dNTP + DIG-11-dUTP [1:15]: (2 mM dATP, 2 mM dCTP, 2 mM dGTP, 1.875 mM dTTP, 0.125 mM DIG-11-dUTP)

TE buffer (10 mM Tris, 1 mM EDTA, pH 8)

10 Maleate buffer: In 700 ml of deionized distilled water, dissolve 11.61 g maleic acid and 8.77 g NaCl. Add NaOH to adjust the pH to 7.5. Bring the volume to 1 L. Stir for 15 min. and sterilize.

15 10% blocking solution: In 80 ml deionized distilled water, dissolve 1.16g maleic acid. Next, add NaOH to adjust the pH to 7.5. Add 10 g of the blocking reagent powder (Boehringer Mannheim, Indianapolis, IN, Cat. no. 1096176). Heat to 60°C while stirring to dissolve the powder. Adjust the volume to 100 ml with water. Stir and sterilize.

1% blocking solution: Dilute the 10% stock to 1% using the maleate buffer.

20 Buffer 3 (100 mM Tris, 100 mM NaCl, 50 mM MgCl₂, pH9.5). Prepared from autoclaved solutions of 1M Tris pH 9.5, 5 M NaCl, and 1 M MgCl₂ in autoclaved distilled water.

Procedure:

1. PCR reactions are performed in 25 µl volumes containing:

PCR buffer	1X
MgCl ₂	1.5 mM
10X dNTP + DIG-11-dUTP	1X (please see the note below)
Platinum Taq™ Polymerase	1 unit
10 pg probe DNA	
10 pmol primer 1	

Note:**Use for:**

10X dNTP + DIG-11-dUTP (1:5)	< 1 kb
10X dNTP + DIG-11-dUTP (1:10)	1 kb to 1.8 kb
10X dNTP + DIG-11-dUTP (1:15)	> 1.8 kb

2. The PCR reaction uses the following amplification cycles:

- 1) 94°C for 10 min.

<u>2)</u> 5 cycles:	<u>3)</u> 5 cycles:	<u>4)</u> 25 cycles:
95°C - 30 sec 61°C - 1 min 73°C - 5 min	95°C - 30 sec 59°C - 1 min 75°C - 5 min	95°C - 30 sec 51°C - 1 min 73°C - 5 min

- 5) 72°C for 8 min. The reactions are terminated by chilling to 4°C (hold).

3. The products are analyzed by electrophoresis- in a 1% agarose gel, comparing to an aliquot of the unlabelled probe starting material.

4. The amount of DIG-labeled probe is determined as follows:

875

Make serial dilutions of the diluted control DNA in dilution buffer (TE: 10 mM Tris and 1 mM EDTA, pH 8) as shown in the following table:

DIG-labeled control DNA starting conc.	Stepwise Dilution	Final Conc. (Dilution Name)
5 ng/μl	1 μl in 49 μl TE	100 pg/μl (A)
100 pg/μl (A)	25 μl in 25 μl TE	50 pg/μl (B)
50 pg/μl (B)	25 μl in 25 μl TE	25 pg/μl (C)
25 pg/μl (C)	20 μl in 30 μl TE	10 pg/μl (D)

- a. Serial deletions of a DIG-labeled standard DNA ranging from 100 pg to 10 pg are spotted onto a positively charged nylon membrane, marking the membrane lightly with a pencil to identify each dilution.
- b. Serial dilutions (e.g., 1:50, 1:2500, 1:10,000) of the newly labeled DNA probe are spotted.
- c. The membrane is fixed by UV crosslinking.
- d. The membrane is wetted with a small amount of maleate buffer and then incubated in 1% blocking solution for 15 min at room temp.
- e. The labeled DNA is then detected using alkaline phosphatase conjugated anti-DIG antibody (Boehringer Mannheim, Indianapolis, IN, cat. no. 1093274) and an NBT substrate according to the manufacture's instruction.
- f. Spot intensities of the control and experimental dilutions are then compared to estimate the concentration of the PCR-DIG-labeled probe.

D. Prehybridization and Hybridization of Southern Blots**Solutions:**

100% Formamide purchased from Gibco

20X SSC (1X = 0.15 M NaCl, 0.015 M Na₃citrate)

per L: 175 g NaCl
87.5 g Na₃citrate·2H₂O

20% Sarkosyl (N-lauroyl-sarcosine)

20% SDS (sodium dodecyl sulphate)

10% Blocking Reagent: In 80 ml deionized distilled water, dissolve 1.16 g maleic acid. Next, add NaOH to adjust the pH to 7.5. Add 10 g of the blocking reagent powder. Heat to 60°C while stirring to dissolve the powder. Adjust the volume to 100 ml with water. Stir and sterilize.

Prehybridization Mix:

Final Concentration	Components	Volume (per 100 ml)	Stock
50%	Formamide	50 ml	100%
5X	SSC	25 ml	20X
0.1%	Sarkosyl	0.5 ml	20%
0.02%	SDS	0.1 ml	20%
2%	Blocking Reagent	20 ml	10%
	Water	4.4 ml	

General Procedures:

- Place the blot in a heat-sealable plastic bag and add an appropriate volume of prehybridization solution (30 ml/100cm²) at room temperature. Seal the bag with a heat sealer, avoiding bubbles as much as possible. Lay down the bags in a large plastic tray (one tray can accommodate at least 4–5 bags). Ensure that the bags are

lying flat in the tray so that the prehybridization solution is evenly distributed throughout the bag. Incubate the blot for at least 2 hours with gentle agitation using a waver shaker.

2. Denature DIG-labeled DNA probe by incubating for 10 min. at 98°C using the PCR machine and immediately cool it to 4°C.

3. Add probe to prehybridization solution (25 ng/ml; 30 ml = 750 ng total probe) and mix well but avoid foaming. Bubbles may lead to background.

4. Pour off the prehybridization solution from the hybridization bags and add new prehybridization and probe solution mixture to the bags containing the membrane.

5. Incubate with gentle agitation for at least 16 hours.

6. Proceed to medium stringency post-hybridization wash:

Three times for 20 min. each with gentle agitation using 1X SSC, 1% SDS at 60°C.

All wash solutions must be prewarmed to 60°C. Use about 100 ml of wash solution per membrane.

To avoid background keep the membranes fully submerged to avoid drying in spots; agitate sufficiently to avoid having membranes stick to one another.

7. After the wash, proceed to immunological detection and CSPD development.

E. Procedure for Immunological Detection with CSPD

Solutions:

Buffer 1: Maleic acid buffer (0.1 M maleic acid, 0.15 M NaCl; adjusted to pH 7.5 with NaOH)

Washing buffer: Maleic acid buffer with 0.3% (v/v) Tween 20.

Blocking stock solution 10% blocking reagent in buffer 1. Dissolve (10X concentration): blocking reagent powder (Boehringer Mannheim, Indianapolis, IN, cat. no. 1096176) by constantly stirring on a 65°C heating block or heat in a microwave, autoclave and store at 4°C.

Buffer 2

(1X blocking solution): Dilute the stock solution 1:10 in Buffer 1.

Detection buffer: 0.1 M Tris, 0.1 M NaCl, pH 9.5

Procedure:

1. After the post-hybridization wash the blots are briefly rinsed (1-5 min.) in the maleate washing buffer with gentle shaking.
2. Then the membranes are incubated for 30 min. in Buffer 2 with gentle shaking.
3. Anti-DIG-AP conjugate (Boehringer Mannheim, Indianapolis, IN, cat. no. 1093274) at 75 mU/ml (1:10,000) in Buffer 2 is used for detection. 75 ml of solution can be used for 3 blots.
4. The membrane is incubated for 30 min. in the antibody solution with gentle shaking.
5. The membrane are washed twice in washing buffer with gentle shaking. About 250 mls is used per wash for 3 blots.
6. The blots are equilibrated for 2-5 min in 60 ml detection buffer.
7. Dilute CSPD (1:200) in detection buffer. (This can be prepared ahead of time and stored in the dark at 4°C).

The following steps must be done individually. Bags (one for detection and one for exposure) are generally cut and ready before doing the following steps.

8. The blot is carefully removed from the detection buffer and excess liquid removed without drying the membrane. The blot is immediately placed in a bag and 1.5 ml of CSPD solution is added. The CSPD solution can be spread over the membrane. Bubbles present at the edge and on the surface of the blot are typically removed by gentle rubbing. The membrane is incubated for 5 min. in CSPD solution.
9. Excess liquid is removed and the membrane is blotted briefly (DNA side up) on Whatman 3MM paper. Do not let the membrane dry completely.
10. Seal the damp membrane in a hybridization bag and incubate for 10 min at 37°C to enhance the luminescent reaction.
11. Expose for 2 hours at room temperature to X-ray film. Multiple exposures can be taken. Luminescence continues for at least 24 hours and signal intensity increases during the first hours.

Example 3: Transformation of Carrot Cells

Transformation of plant cells can be accomplished by a number of methods, as described above. Similarly, a number of plant genera can be regenerated from tissue culture following transformation. Transformation and regeneration of carrot cells as described herein is illustrative.

Single cell suspension cultures of carrot (*Daucus carota*) cells are established from hypocotyls of cultivar Early Nantes in B₅ growth medium (O.L. Gamborg et al., *Plant Physiol.* 45:372 (1970)) plus 2,4-D and 15 mM CaCl₂ (B₅-44 medium) by methods known in the art. The suspension cultures are subcultured by adding 10 ml of the suspension culture to 40 ml of B₅-44 medium in 250 ml flasks every 7 days and are maintained in a shaker at 150 rpm at 27 °C in the dark.

The suspension culture cells are transformed with exogenous DNA as described by Z. Chen et al. *Plant Mol. Bio.* 36:163 (1998). Briefly, 4-days post-subculture cells are incubated with cell wall digestion solution containing 0.4 M sorbitol, 2% driselase, 5mM MES (2-[N-

Morpholino] ethanesulfonic acid) pH 5.0 for 5 hours. The digested cells are pelleted gently at 60 xg for 5 min. and washed twice in W5 solution containing 154 mM NaCl, 5 mM KCl, 125 mM CaCl₂ and 5mM glucose, pH 6.0. The protoplasts are suspended in MC solution containing 5 mM MES, 20 mM CaCl₂, 0.5 M mannitol, pH 5.7 and the protoplast density is
5 adjusted to about 4×10^6 protoplasts per ml.

15-60 µg of plasmid DNA is mixed with 0.9 ml of protoplasts. The resulting suspension is mixed with 40% polyethylene glycol (MW 8000, PEG 8000), by gentle inversion a few times at room temperature for 5 to 25 min. Protoplast culture medium known in the art is added into the PEG-DNA-protoplast mixture. Protoplasts are incubated in the
10 culture medium for 24 hour to 5 days and cell extracts can be used for assay of transient expression of the introduced gene. Alternatively, transformed cells can be used to produce transgenic callus, which in turn can be used to produce transgenic plants, by methods known in the art. See, for example, Nomura and Komamine, *Plt. Phys.* 79:988-991 (1985),
Identification and Isolation of Single Cells that Produce Somatic Embryos in Carrot
15 *Suspension Cultures.*

An additional deposit, PTA-1411, of an *E. coli* Library, *E. coli*LibA021800, was made at the American Type Culture Collection in Manassas, Virginia, USA on February 22, 2000 to meet the requirements of Budapest Treaty for the international recognition of the deposit of microorganisms. This deposit was assigned ATCC accession no. PTA-1411.

20 The invention being thus described, it will be apparent to one of ordinary skill in the art that various modifications of the materials and methods for practicing the invention can be made. Such modifications are to be considered within the scope of the invention as defined by the following claims.

Each of the references from the patent and periodical literature cited herein is hereby
25 expressly incorporated in its entirety by such citation.